Full wwPDB X-ray Structure Validation Report ⓘ

Aug 5, 2026 – 09:00 AM EDT

PDB ID	:	1ULI / pdb_00001uli
Title	:	Biphenyl dioxygenase (BphA1A2) derived from Rhodococcus sp. strain RHA1
Authors	:	Furusawa, Y.; Nagarajan, V.; Masai, E.; Tanokura, M.; Fukuda, M.; Senda, T.
Deposited on	:	2003-09-12
Resolution	:	2.20 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references ⓘ) were used in the production of this report:

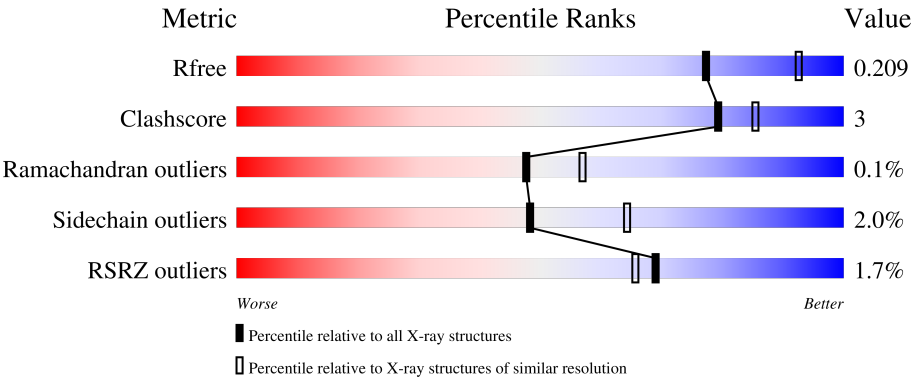
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.015 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.50

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



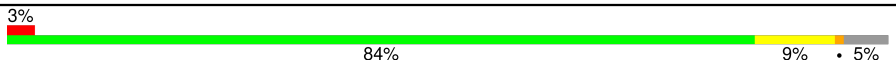
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	6164 (2.20-2.20)
Clashscore	190562	6851 (2.20-2.20)
Ramachandran outliers	187476	6768 (2.20-2.20)
Sidechain outliers	187428	6769 (2.20-2.20)
RSRZ outliers	180081	6166 (2.20-2.20)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	460	87% • 8%
1	C	460	86% 5% • 8%
1	E	460	87% • 8%
2	B	187	83% 10% • 5%
2	D	187	3% 84% 10% • 5%

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Mol	Chain	Length	Quality of chain
2	F	187	

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 15345 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called biphenyl dioxygenase large subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	424	Total	C	N	O	S	0	0	0
			3370	2124	584	641	21			
1	C	425	Total	C	N	O	S	0	0	0
			3375	2127	585	642	21			
1	E	425	Total	C	N	O	S	0	0	0
			3377	2129	585	642	21			

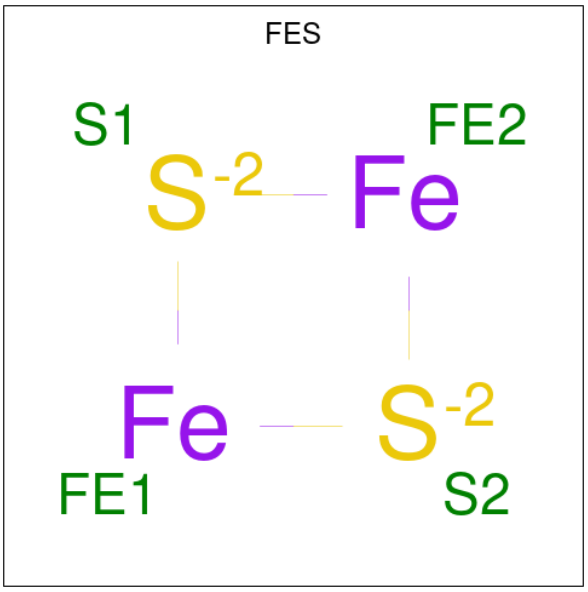
- Molecule 2 is a protein called biphenyl dioxygenase small subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	177	Total	C	N	O	S	0	0	0
			1484	939	267	273	5			
2	D	178	Total	C	N	O	S	0	0	0
			1489	942	268	274	5			
2	F	177	Total	C	N	O	S	0	0	0
			1484	939	267	273	5			

- Molecule 3 is FE (II) ION (CCD ID: FE2) (formula: Fe).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Fe	0	0
			1	1		
3	B	1	Total	Fe	0	0
			1	1		
3	C	1	Total	Fe	0	0
			1	1		
3	E	1	Total	Fe	0	0
			1	1		

- Molecule 4 is FE2/S2 (INORGANIC) CLUSTER (CCD ID: FES) (formula: Fe_2S_2).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total Fe S 4 2 2	0	0
4	C	1	Total Fe S 4 2 2	0	0
4	E	1	Total Fe S 4 2 2	0	0

- Molecule 5 is water.

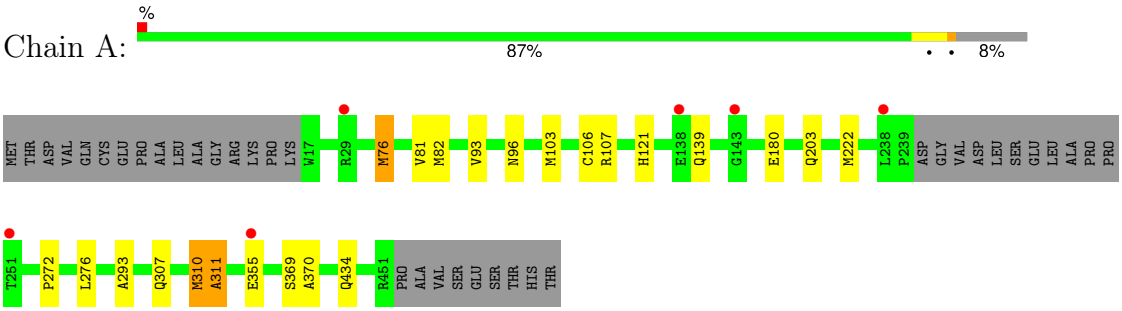
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	170	Total O 170 170	0	0
5	B	84	Total O 84 84	0	0
5	C	155	Total O 155 155	0	0
5	D	89	Total O 89 89	0	0
5	E	171	Total O 171 171	0	0
5	F	81	Total O 81 81	0	0

3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density (RSRZ > 2). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

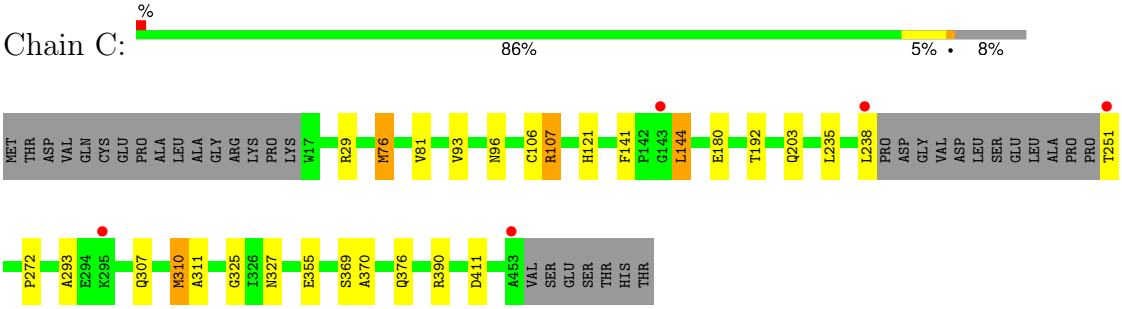
• Molecule 1: biphenyl dioxygenase large subunit

Chain A:



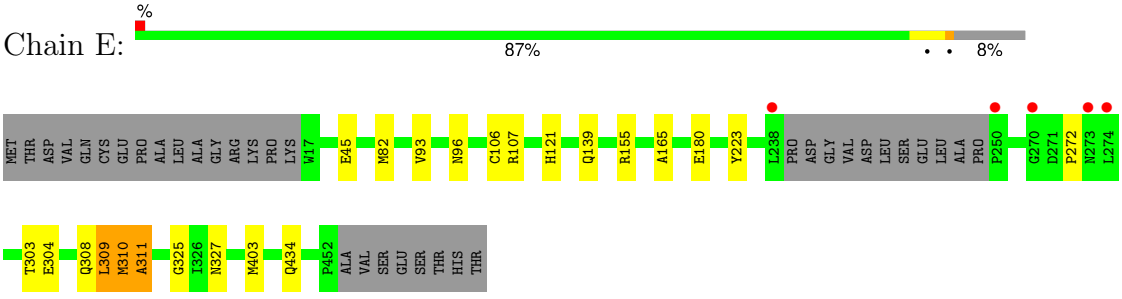
• Molecule 1: biphenyl dioxygenase large subunit

Chain C:



• Molecule 1: biphenyl dioxygenase large subunit

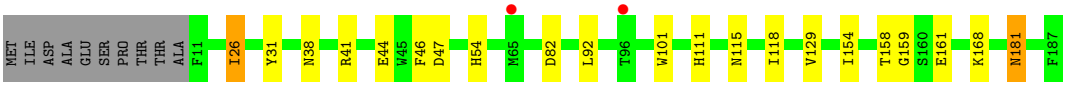
Chain E:



• Molecule 2: biphenyl dioxygenase small subunit

Chain B:

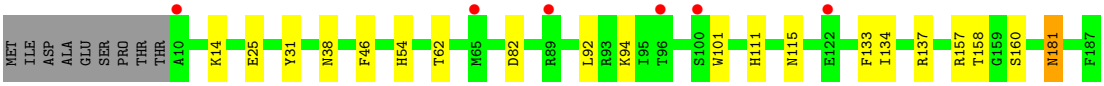




• Molecule 2: biphenyl dioxygenase small subunit

Chain D:

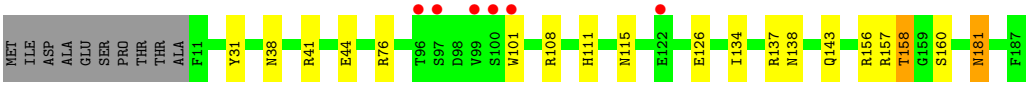




• Molecule 2: biphenyl dioxygenase small subunit

Chain F:





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α, β, γ	137.74Å 137.74Å 237.74Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	38.07 – 2.20 38.07 – 2.20	Depositor EDS
% Data completeness (in resolution range)	98.8 (38.07-2.20) 98.8 (38.07-2.20)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	0.07	Depositor
$< I/\sigma(I) >$ [1]	3.21 (at 1.89Å)	Xtriage
Refinement program	REFMAC 5.1.24	Depositor
R, R_{free}	0.167 , 0.201 0.179 , 0.209	Depositor DCC
R_{free} test set	7700 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å^2)	16.1	Xtriage
Anisotropy	0.013	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.36 , 34.3	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	15345	wwPDB-VP
Average B, all atoms (Å^2)	17.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.19% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: FE2, FES

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$\|Z\|$ >5	RMSZ	#$\|Z\|$ >5
1	A	0.67	2/3462 (0.1%)	0.83	0/4699
1	C	0.70	1/3467 (0.0%)	0.83	0/4706
1	E	0.63	0/3470	0.81	0/4710
2	B	0.66	0/1519	0.80	0/2047
2	D	0.69	0/1524	0.81	0/2054
2	F	0.71	0/1519	0.84	0/2047
All	All	0.67	3/14961 (0.0%)	0.82	0/20263

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
2	D	0	1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	76	MET	SD-CE	-16.00	1.39	1.79
1	A	76	MET	SD-CE	-14.02	1.44	1.79
1	A	222	MET	SD-CE	-5.81	1.65	1.79

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	D	133	PHE	Peptide

5.2 Too-close contacts (i)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3370	0	3172	17	0
1	C	3375	0	3177	16	0
1	E	3377	0	3180	13	0
2	B	1484	0	1441	15	0
2	D	1489	0	1446	15	0
2	F	1484	0	1441	13	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	E	1	0	0	0	0
4	A	4	0	0	1	0
4	C	4	0	0	1	0
4	E	4	0	0	1	0
5	A	170	0	0	2	0
5	B	84	0	0	0	0
5	C	155	0	0	1	0
5	D	89	0	0	0	0
5	E	171	0	0	1	0
5	F	81	0	0	1	0
All	All	15345	0	13857	77	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 3.

All (77) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:76:MET:HE3	1:A:81:VAL:HG11	1.45	0.98
1:C:76:MET:HE3	1:C:81:VAL:HG11	1.53	0.89
1:A:96:ASN:HD21	1:A:106:CYS:H	1.32	0.76
1:C:96:ASN:HD21	1:C:106:CYS:H	1.36	0.74
2:F:158:THR:HG22	2:F:160:SER:H	1.55	0.71
1:E:96:ASN:HD21	1:E:106:CYS:H	1.39	0.70
2:B:38:ASN:HD21	2:B:111:HIS:H	1.42	0.66
2:D:38:ASN:HD21	2:D:111:HIS:H	1.43	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:38:ASN:HD21	2:F:111:HIS:H	1.42	0.65
1:A:203:GLN:HE22	1:A:369:SER:HB2	1.63	0.62
2:F:181:ASN:H	2:F:181:ASN:HD22	1.49	0.61
1:A:434:GLN:NE2	5:A:670:HOH:O	2.34	0.61
1:E:310:MET:O	1:E:311:ALA:O	2.19	0.59
1:E:303:THR:HG22	1:E:308:GLN:HE21	1.68	0.59
2:D:115:ASN:HA	2:F:31:TYR:CD1	2.37	0.59
1:C:272:PRO:HA	1:C:310:MET:HG2	1.85	0.58
2:B:181:ASN:H	2:B:181:ASN:HD22	1.50	0.58
2:D:181:ASN:HD22	2:D:181:ASN:H	1.51	0.58
1:C:203:GLN:HE22	1:C:369:SER:HB2	1.69	0.57
2:D:25:GLU:OE2	2:D:157:ARG:NH1	2.37	0.56
2:B:26:ILE:HG12	2:B:118:ILE:HD11	1.87	0.56
2:B:115:ASN:HA	2:D:31:TYR:CD1	2.41	0.56
2:B:31:TYR:CD1	2:F:115:ASN:HA	2.43	0.53
2:B:31:TYR:CG	2:F:115:ASN:HA	2.44	0.53
2:B:46:PHE:CD1	2:B:92:LEU:HD13	2.43	0.53
2:B:101:TRP:O	1:E:107:ARG:NH2	2.41	0.53
1:C:76:MET:CE	1:C:93:VAL:HG11	2.38	0.53
2:D:14:LYS:HE2	5:F:223:HOH:O	2.08	0.53
2:B:41:ARG:HD2	2:B:44:GLU:OE1	2.10	0.51
1:E:223:TYR:CD1	1:E:403:MET:HE1	2.45	0.51
2:B:54:HIS:NE2	2:B:82:ASP:OD2	2.41	0.51
1:A:76:MET:HE2	1:A:93:VAL:HG11	1.92	0.51
1:C:76:MET:HE2	1:C:93:VAL:HG11	1.94	0.50
2:D:115:ASN:HA	2:F:31:TYR:CG	2.46	0.50
1:A:107:ARG:NH2	2:D:101:TRP:O	2.44	0.49
1:A:272:PRO:HA	1:A:310:MET:HG3	1.93	0.49
1:A:103:MET:HE3	1:A:107:ARG:HD2	1.94	0.49
1:C:141:PHE:HB3	1:C:144:LEU:HB2	1.95	0.49
1:A:76:MET:CE	1:A:93:VAL:HG11	2.43	0.48
1:C:203:GLN:HE22	1:C:370:ALA:H	1.62	0.48
2:F:41:ARG:HD2	2:F:44:GLU:OE1	2.14	0.48
2:D:62:THR:OG1	2:F:108:ARG:NH2	2.42	0.47
1:A:293:ALA:HB1	1:A:307:GLN:HG2	1.97	0.47
5:A:683:HOH:O	1:E:45:GLU:HG3	2.14	0.47
2:B:158:THR:HG22	2:B:159:GLY:N	2.29	0.47
2:B:26:ILE:HD11	2:B:129:VAL:HG11	1.97	0.47
1:C:310:MET:O	1:C:311:ALA:HB3	2.15	0.47
1:A:310:MET:O	1:A:311:ALA:HB3	2.15	0.46
1:C:376:GLN:OE1	2:D:94:LYS:HE3	2.14	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:46:PHE:CD1	2:D:92:LEU:HD13	2.51	0.46
1:E:325:GLY:H	1:E:327:ASN:ND2	2.13	0.46
1:A:203:GLN:NE2	1:A:370:ALA:H	2.14	0.45
2:B:115:ASN:HA	2:D:31:TYR:CG	2.50	0.45
1:E:121:HIS:HB2	4:E:500:FES:S1	2.56	0.45
1:A:203:GLN:HE22	1:A:370:ALA:H	1.63	0.45
1:C:121:HIS:HB2	4:C:500:FES:S1	2.56	0.45
1:E:434:GLN:NE2	5:E:728:HOH:O	2.49	0.45
2:D:134:ILE:HD13	2:F:134:ILE:HD13	1.99	0.44
1:E:82:MET:O	1:E:93:VAL:HA	2.17	0.44
1:A:121:HIS:HB2	4:A:500:FES:S1	2.58	0.44
1:A:203:GLN:NE2	1:A:369:SER:HB2	2.30	0.44
2:B:26:ILE:HG12	2:B:118:ILE:CD1	2.48	0.44
2:F:126:GLU:OE1	2:F:156:ARG:HD3	2.18	0.44
1:C:203:GLN:NE2	1:C:370:ALA:H	2.16	0.44
1:C:293:ALA:HB1	1:C:307:GLN:HG2	2.00	0.43
1:A:82:MET:O	1:A:93:VAL:HA	2.19	0.43
2:D:54:HIS:NE2	2:D:82:ASP:OD2	2.35	0.42
1:A:203:GLN:HE22	1:A:369:SER:CB	2.31	0.42
2:D:158:THR:HG23	2:D:160:SER:H	1.84	0.42
2:B:154:ILE:HD12	2:B:168:LYS:HD3	2.01	0.42
2:F:138:ASN:HA	2:F:143:GLN:O	2.19	0.42
1:E:272:PRO:HA	1:E:310:MET:CG	2.50	0.41
1:C:355:GLU:HG3	5:C:733:HOH:O	2.21	0.41
1:C:107:ARG:NH2	2:F:101:TRP:O	2.53	0.41
1:E:304:GLU:O	1:E:309:LEU:HD13	2.20	0.41
1:E:155:ARG:O	1:E:165:ALA:HA	2.21	0.40
1:C:325:GLY:H	1:C:327:ASN:ND2	2.19	0.40

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	420/460 (91%)	402 (96%)	17 (4%)	1 (0%)	43 51
1	C	421/460 (92%)	404 (96%)	17 (4%)	0	100 100
1	E	421/460 (92%)	405 (96%)	15 (4%)	1 (0%)	43 51
2	B	175/187 (94%)	170 (97%)	5 (3%)	0	100 100
2	D	176/187 (94%)	169 (96%)	7 (4%)	0	100 100
2	F	175/187 (94%)	169 (97%)	6 (3%)	0	100 100
All	All	1788/1941 (92%)	1719 (96%)	67 (4%)	2 (0%)	48 57

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	311	ALA
1	A	311	ALA

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	345/375 (92%)	340 (99%)	5 (1%)	59 75
1	C	345/375 (92%)	334 (97%)	11 (3%)	34 47
1	E	346/375 (92%)	342 (99%)	4 (1%)	63 78
2	B	159/167 (95%)	155 (98%)	4 (2%)	42 56
2	D	159/167 (95%)	157 (99%)	2 (1%)	61 76
2	F	159/167 (95%)	154 (97%)	5 (3%)	35 48
All	All	1513/1626 (93%)	1482 (98%)	31 (2%)	48 64

All (31) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	139	GLN
1	A	180	GLU
1	A	276	LEU

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Mol	Chain	Res	Type
1	A	310	MET
1	A	355	GLU
2	B	26	ILE
2	B	47	ASP
2	B	161	GLU
2	B	181	ASN
1	C	29	ARG
1	C	107	ARG
1	C	144	LEU
1	C	180	GLU
1	C	192	THR
1	C	235	LEU
1	C	238	LEU
1	C	251	THR
1	C	310	MET
1	C	390	ARG
1	C	411	ASP
2	D	137	ARG
2	D	181	ASN
1	E	139	GLN
1	E	180	GLU
1	E	309	LEU
1	E	310	MET
2	F	76	ARG
2	F	137	ARG
2	F	157	ARG
2	F	158	THR
2	F	181	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (35) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	96	ASN
1	A	139	GLN
1	A	203	GLN
1	A	217	GLN
1	A	308	GLN
1	A	362	GLN
1	A	381	ASN
1	A	392	HIS
1	A	407	GLN
1	A	434	GLN

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Mol	Chain	Res	Type
2	B	38	ASN
2	B	86	GLN
2	B	143	GLN
2	B	181	ASN
1	C	96	ASN
1	C	153	GLN
1	C	203	GLN
1	C	307	GLN
1	C	327	ASN
1	C	381	ASN
1	C	392	HIS
1	C	434	GLN
2	D	38	ASN
2	D	143	GLN
2	D	181	ASN
1	E	96	ASN
1	E	130	ASN
1	E	139	GLN
1	E	153	GLN
1	E	308	GLN
1	E	327	ASN
1	E	381	ASN
1	E	434	GLN
2	F	38	ASN
2	F	181	ASN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains (i)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

Of 7 ligands modelled in this entry, 4 are monoatomic - leaving 3 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
4	FES	A	500	1	0,4,4	-	-	-		
4	FES	C	500	1	0,4,4	-	-	-		
4	FES	E	500	1	0,4,4	-	-	-		

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	FES	A	500	1	-	-	0/1/1/1
4	FES	C	500	1	-	-	0/1/1/1
4	FES	E	500	1	-	-	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	500	FES	1	0
4	C	500	FES	1	0
4	E	500	FES	1	0

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95^{th} percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q< 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å^2)	Q<0.9
1	A	424/460 (92%)	-0.30	6 (1%)	73	71	8, 16, 30, 39	0
1	C	425/460 (92%)	-0.24	5 (1%)	76	74	7, 17, 32, 40	0
1	E	425/460 (92%)	-0.30	5 (1%)	76	74	8, 15, 29, 41	0
2	B	177/187 (94%)	-0.22	2 (1%)	78	76	8, 16, 31, 38	0
2	D	178/187 (95%)	-0.18	6 (3%)	48	45	8, 15, 31, 35	0
2	F	177/187 (94%)	-0.21	6 (3%)	48	45	8, 16, 29, 38	0
All	All	1806/1941 (93%)	-0.26	30 (1%)	69	66	7, 16, 30, 41	0

All (30) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	250	PRO	3.8
1	A	143	GLY	3.8
1	C	251	THR	3.1
1	C	238	LEU	2.7
2	F	97	SER	2.7
2	F	101	TRP	2.7
1	C	453	ALA	2.6
1	E	273	ASN	2.6
2	F	100	SER	2.6
1	E	274	LEU	2.6
2	D	65	MET	2.5
2	D	10	ALA	2.5
1	A	238	LEU	2.4
2	F	122	GLU	2.4
2	F	96	THR	2.4
1	A	138	GLU	2.3
2	B	65	MET	2.3
1	A	355	GLU	2.3
2	D	122	GLU	2.2

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Mol	Chain	Res	Type	RSRZ
2	F	99	VAL	2.2
1	C	143	GLY	2.2
2	D	100	SER	2.2
2	B	96	THR	2.2
1	A	251	THR	2.1
2	D	89	ARG	2.1
1	E	238	LEU	2.1
2	D	96	THR	2.1
1	E	270	GLY	2.1
1	A	29	ARG	2.1
1	C	295	LYS	2.0

6.2 Non-standard residues in protein, DNA, RNA chains (i)

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates (i)

There are no oligosaccharides in this entry.

6.4 Ligands (i)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	FE2	A	600	1/1	0.99	0.02	17,17,17,17	0
3	FE2	C	600	1/1	0.99	0.03	22,22,22,22	0
3	FE2	E	600	1/1	0.99	0.01	19,19,19,19	0
4	FES	A	500	4/4	0.99	0.04	14,16,19,20	0
4	FES	C	500	4/4	0.99	0.05	13,13,18,18	0
3	FE2	B	700	1/1	1.00	0.01	17,17,17,17	0
4	FES	E	500	4/4	1.00	0.03	10,11,14,15	0

6.5 Other polymers (i)

There are no such residues in this entry.