



wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 4, 2026 – 11:13 PM EDT

PDB ID : 2FTK / pdb_00002ftk
Title : beryllofluoride Spo0F complex with Spo0B
Authors : Varughese, K.I.
Deposited on : 2006-01-24
Resolution : 3.05 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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

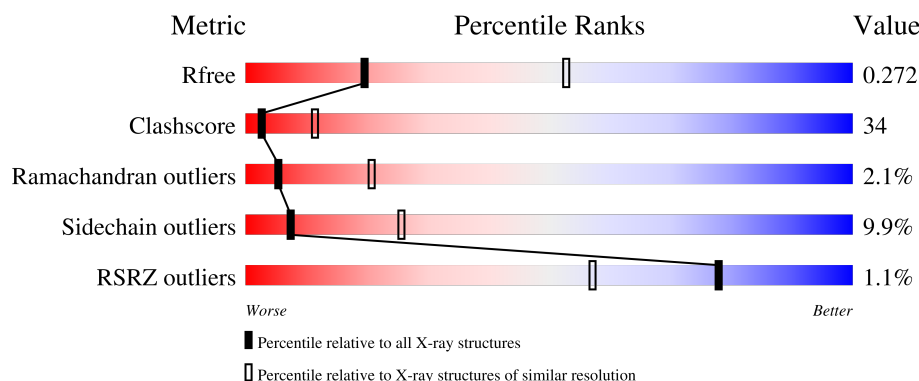
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.05 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	2469 (3.10-3.02)
Clashscore	190562	2569 (3.10-3.02)
Ramachandran outliers	187476	2424 (3.10-3.02)
Sidechain outliers	187428	2423 (3.10-3.02)
RSRZ outliers	180081	2469 (3.10-3.02)

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 $\leq 5\%$. 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	192	2% 47% 42% 5% 6%
1	B	192	45% 44% 6% 5%
1	C	192	38% 46% 9% 6%
1	D	192	2% 46% 42% 7% 5%
2	E	124	52% 38% 6% •

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Mol	Chain	Length	Quality of chain
2	F	124	2% 48% 42% 6%
2	G	124	3% 18% 60% 17%
2	H	124	2% 51% 38% 7%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 9834 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 Sporulation initiation phosphotransferase B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	181	Total	C	N	O	S	0	0	0
			1497	955	251	284	7			
1	B	182	Total	C	N	O	S	6	0	0
			1505	959	253	286	7			
1	C	181	Total	C	N	O	S	0	0	0
			1497	955	251	284	7			
1	D	182	Total	C	N	O	S	6	0	0
			1505	959	253	286	7			

- Molecule 2 is a protein called Sporulation initiation phosphotransferase F.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	E	119	Total	C	N	O	S	0	0	0
			950	609	156	180	5			
2	F	119	Total	C	N	O	S	0	0	0
			950	609	156	180	5			
2	G	119	Total	C	N	O	S	0	0	0
			950	609	156	180	5			
2	H	119	Total	C	N	O	S	0	1	0
			960	615	159	181	5			

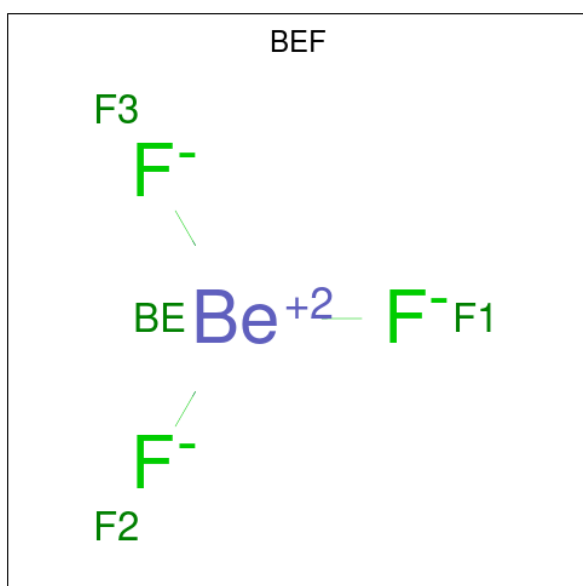
There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	1213	SER	TYR	engineered mutation	UNP P06628
F	1013	SER	TYR	engineered mutation	UNP P06628
G	1613	SER	TYR	engineered mutation	UNP P06628
H	1413	SER	TYR	engineered mutation	UNP P06628

- Molecule 3 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	E	1	Total 1	Mg 1	0	0
3	F	1	Total 1	Mg 1	0	0
3	G	1	Total 1	Mg 1	0	0
3	H	1	Total 1	Mg 1	0	0

- Molecule 4 is BERYLLIUM TRIFLUORIDE ION (CCD ID: BEF) (formula: BeF₃).

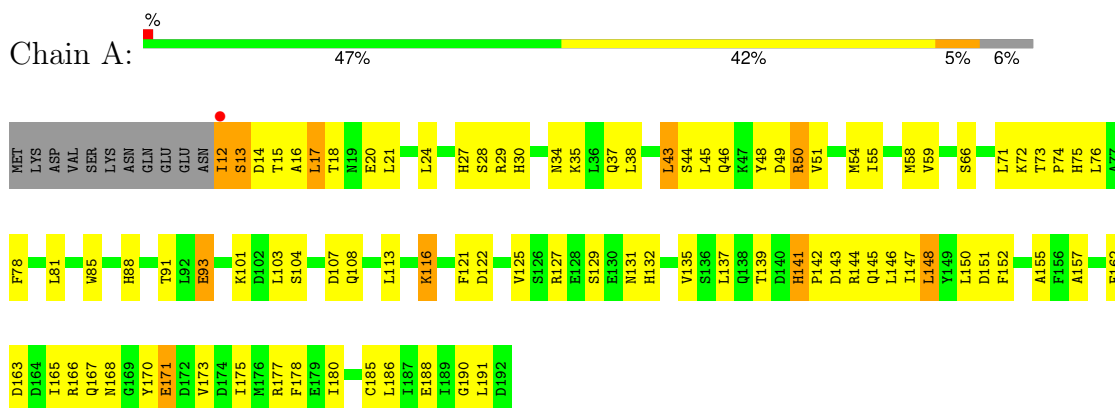


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	E	1	Total 4	Be 1	F 3	0	0
4	F	1	Total 4	Be 1	F 3	0	0
4	G	1	Total 4	Be 1	F 3	0	0
4	H	1	Total 4	Be 1	F 3	0	0

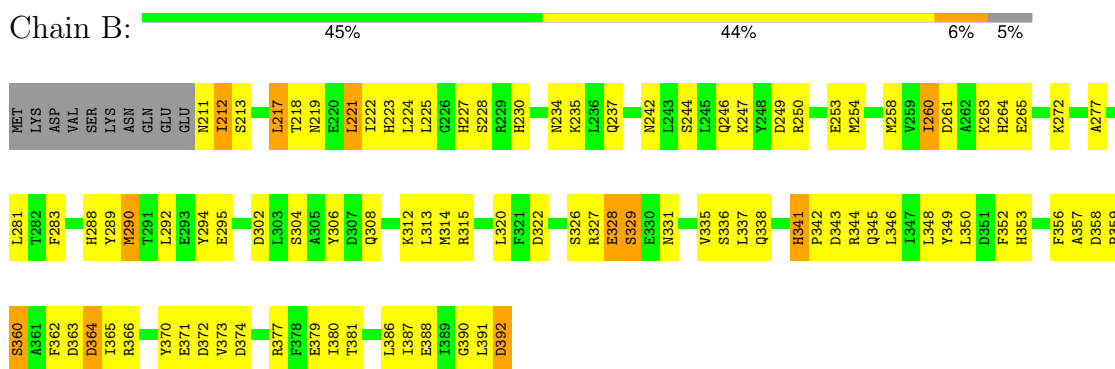
3 Residue-property plots [i](#)

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.

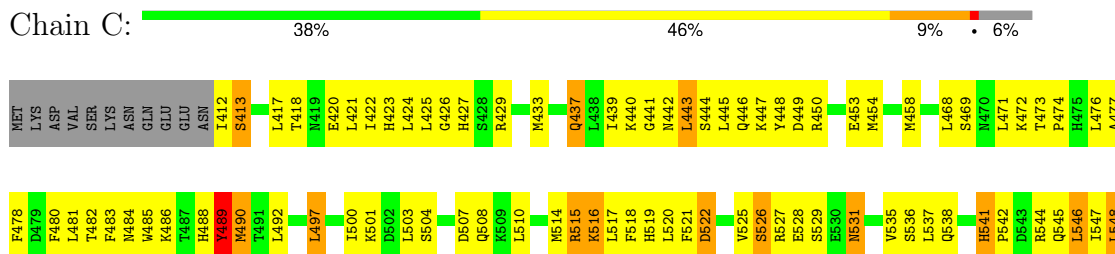
• Molecule 1: Sporulation initiation phosphotransferase B



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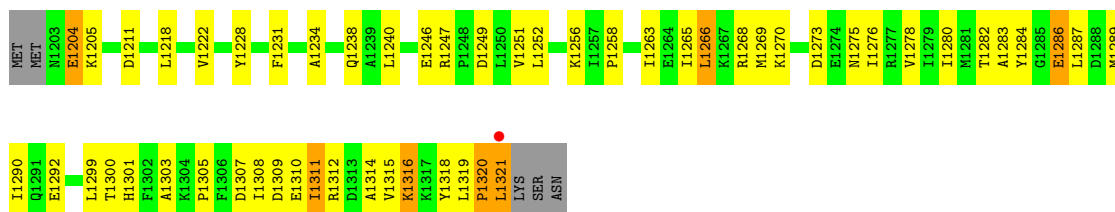




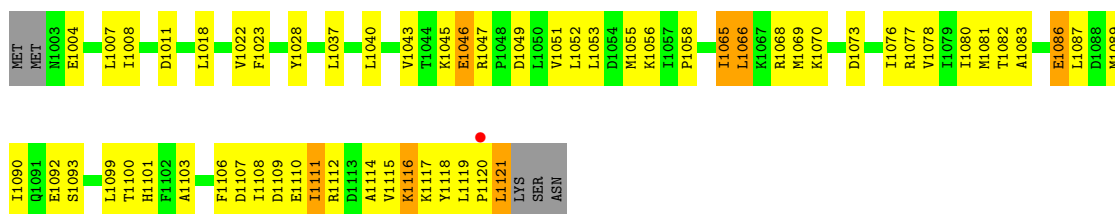
• Molecule 1: Sporulation initiation phosphotransferase B



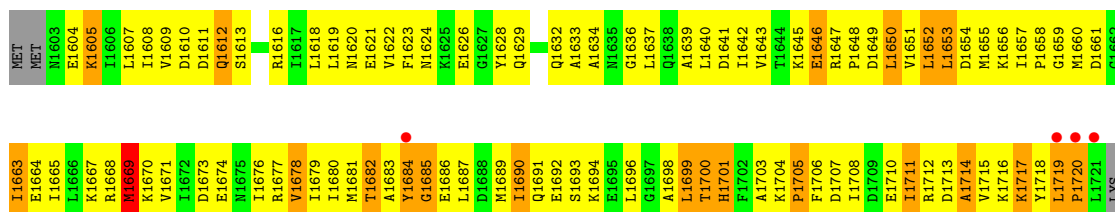
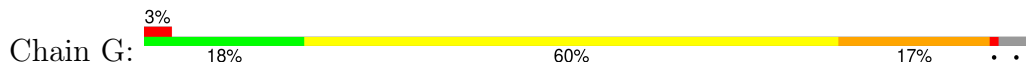
• Molecule 2: Sporulation initiation phosphotransferase F



• Molecule 2: Sporulation initiation phosphotransferase F



• Molecule 2: Sporulation initiation phosphotransferase F



SER

ASN

● Molecule 2: Sporulation initiation phosphotransferase F



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	73.47Å 118.33Å 168.24Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.86 – 3.05 19.86 – 3.05	Depositor EDS
% Data completeness (in resolution range)	98.6 (19.86-3.05) 98.2 (19.86-3.05)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.21 (at 3.04Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.232 , 0.282 0.220 , 0.272	Depositor DCC
R_{free} test set	1404 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	74.1	Xtriage
Anisotropy	0.113	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 42.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	9834	wwPDB-VP
Average B, all atoms (Å ²)	67.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.48% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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	0.66	0/1530	0.94	3/2064 (0.1%)
1	B	0.66	0/1538	0.97	4/2075 (0.2%)
1	C	0.55	0/1530	0.95	6/2064 (0.3%)
1	D	0.54	0/1538	0.90	1/2075 (0.0%)
2	E	0.47	0/961	0.91	2/1293 (0.2%)
2	F	0.60	0/961	1.00	3/1293 (0.2%)
2	G	0.41	0/961	1.03	6/1293 (0.5%)
2	H	0.44	0/972	0.89	1/1308 (0.1%)
All	All	0.56	0/9991	0.95	26/13465 (0.2%)

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
1	C	0	1

There are no bond length outliers.

The worst 5 of 26 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	1086	GLU	N-CA-C	-8.20	100.60	110.44
2	G	1719	LEU	CA-C-N	7.40	129.09	119.84
2	G	1719	LEU	C-N-CA	7.40	129.09	119.84
1	B	341	HIS	CA-C-N	6.84	126.44	119.19
1	B	341	HIS	C-N-CA	6.84	126.44	119.19

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	489	TYR	Sidechain

5.2 Too-close contacts ⓘ

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	1497	0	1457	91	0
1	B	1505	0	1463	87	0
1	C	1497	0	1457	141	0
1	D	1505	0	1463	103	0
2	E	950	0	987	45	0
2	F	950	0	987	48	0
2	G	950	0	987	136	0
2	H	960	0	993	55	0
3	E	1	0	0	0	0
3	F	1	0	0	0	0
3	G	1	0	0	0	0
3	H	1	0	0	0	0
4	E	4	0	0	1	0
4	F	4	0	0	1	0
4	G	4	0	0	0	0
4	H	4	0	0	1	0
All	All	9834	0	9794	660	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 34.

The worst 5 of 660 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)
2:G:1687:LEU:HA	2:G:1690:ILE:HD13	1.26	1.10
2:E:1251:VAL:HG11	2:E:1269:MET:HE1	1.41	1.02
1:C:565:ILE:HD12	1:C:565:ILE:H	1.25	1.01
2:G:1620:ASN:ND2	2:G:1632:GLN:HE21	1.60	0.98
1:B:381:THR:HG23	1:C:581:THR:HG23	1.48	0.94

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	179/192 (93%)	165 (92%)	12 (7%)	2 (1%)	11	34
1	B	180/192 (94%)	166 (92%)	13 (7%)	1 (1%)	21	48
1	C	179/192 (93%)	165 (92%)	12 (7%)	2 (1%)	11	34
1	D	180/192 (94%)	168 (93%)	11 (6%)	1 (1%)	21	48
2	E	117/124 (94%)	101 (86%)	15 (13%)	1 (1%)	14	39
2	F	117/124 (94%)	100 (86%)	14 (12%)	3 (3%)	4	17
2	G	117/124 (94%)	84 (72%)	21 (18%)	12 (10%)	0	2
2	H	118/124 (95%)	101 (86%)	14 (12%)	3 (2%)	4	17
All	All	1187/1264 (94%)	1050 (88%)	112 (9%)	25 (2%)	5	21

5 of 25 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	E	1320	PRO
2	F	1120	PRO
2	G	1684	TYR
2	G	1700	THR
2	H	1520	PRO

5.3.2 Protein sidechains

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	166/177 (94%)	149 (90%)	17 (10%)	7	24

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	167/177 (94%)	152 (91%)	15 (9%)	9	29
1	C	166/177 (94%)	143 (86%)	23 (14%)	3	13
1	D	167/177 (94%)	147 (88%)	20 (12%)	5	17
2	E	105/110 (96%)	97 (92%)	8 (8%)	12	35
2	F	105/110 (96%)	98 (93%)	7 (7%)	15	39
2	G	105/110 (96%)	95 (90%)	10 (10%)	8	27
2	H	106/110 (96%)	98 (92%)	8 (8%)	12	36
All	All	1087/1148 (95%)	979 (90%)	108 (10%)	7	26

5 of 108 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	638	LEU
1	D	765	ILE
2	G	1711	ILE
1	D	656	GLU
1	D	709	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 56 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	531	ASN
2	H	1491	GLN
1	D	783	HIS
2	H	1475	ASN
2	G	1675	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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 8 ligands modelled in this entry, 4 are monoatomic - leaving 4 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	BEF	G	2005	2	0,3,3	-	-	-		
4	BEF	E	2002	2	0,3,3	-	-	-		
4	BEF	F	2003	2	0,3,3	-	-	-		
4	BEF	H	2004	2	0,3,3	-	-	-		

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	E	2002	BEF	1	0
4	F	2003	BEF	1	0
4	H	2004	BEF	1	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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, 95th 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	181/192 (94%)	-0.56	1 (0%) 85 69	28, 44, 74, 91	0
1	B	182/192 (94%)	-0.52	0 100 100	24, 46, 75, 96	3 (1%)
1	C	181/192 (94%)	-0.29	0 100 100	42, 71, 100, 115	0
1	D	182/192 (94%)	-0.26	4 (2%) 62 39	41, 63, 98, 114	3 (1%)
2	E	119/124 (95%)	-0.25	1 (0%) 82 63	56, 77, 96, 106	0
2	F	119/124 (95%)	-0.46	1 (0%) 82 63	36, 54, 77, 87	0
2	G	119/124 (95%)	0.07	4 (3%) 48 27	68, 90, 103, 104	0
2	H	119/124 (95%)	0.05	2 (1%) 69 46	34, 87, 112, 121	1 (0%)
All	All	1202/1264 (95%)	-0.30	13 (1%) 78 57	24, 64, 101, 121	7 (0%)

The worst 5 of 13 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	H	1501[A]	HIS	10.1
2	G	1721	LEU	3.1
2	G	1720	PRO	3.1
1	D	743	ASP	2.9
2	E	1321	LEU	2.4

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, 95th 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($\text{\AA}^2$)	Q<0.9
4	BEF	G	2005	4/4	0.45	0.18	86,86,87,87	4
4	BEF	H	2004	4/4	0.70	0.21	66,67,67,68	4
4	BEF	E	2002	4/4	0.92	0.10	60,61,61,62	4
4	BEF	F	2003	4/4	0.93	0.13	41,42,42,42	4
3	MG	H	2003	1/1	0.94	0.11	37,37,37,37	0
3	MG	F	2002	1/1	0.96	0.21	37,37,37,37	0
3	MG	E	2001	1/1	0.97	0.14	37,37,37,37	0
3	MG	G	2004	1/1	0.98	0.04	37,37,37,37	0

6.5 Other polymers [i](#)

There are no such residues in this entry.