



Full wwPDB X-ray Structure Validation Report ⓘ

Jun 16, 2024 – 03:38 AM EDT

PDB ID : 2GFQ
Title : Structure of Protein of Unknown Function PH0006 from *Pyrococcus horikoshii*
Authors : Cuff, M.E.; Skarina, T.; Gorodichtchenskaia, E.; Edwards, A.; Savchenko, A.;
Joachimciak, A.; Midwest Center for Structural Genomics (MCSG)
Deposited on : 2006-03-22
Resolution : 1.75 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	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.20.1
EDS	:	2.37.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.37.1

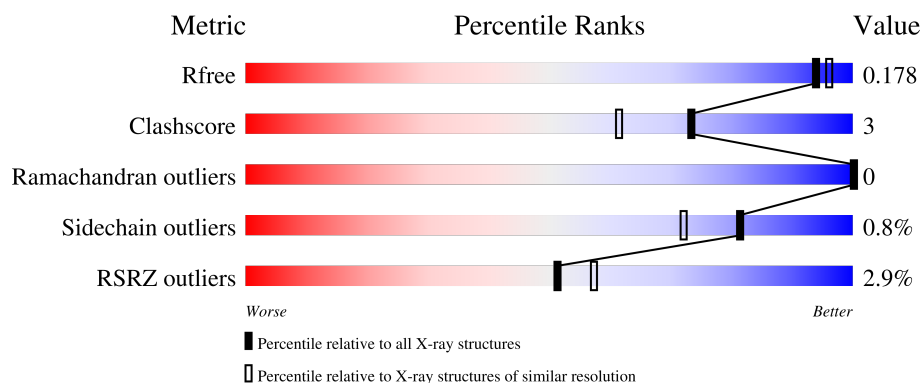
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.75 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}	130704	2340 (1.76-1.76)
Clashscore	141614	2466 (1.76-1.76)
Ramachandran outliers	138981	2437 (1.76-1.76)
Sidechain outliers	138945	2437 (1.76-1.76)
RSRZ outliers	127900	2298 (1.76-1.76)

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	298	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 0%, red 1%, orange 1%, orange 90%, yellow 90%, yellow 96%, green 96%, green 100%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> % 90% 6% . </div> </div>
1	B	298	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 0%, red 3%, orange 3%, orange 88%, yellow 88%, yellow 94%, green 94%, green 100%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> 3% 88% 6% 6% </div> </div>
1	C	298	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 0%, red 4%, orange 4%, orange 88%, yellow 88%, yellow 93%, green 93%, green 100%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> 4% 88% 5% 7% </div> </div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 7927 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 UPF0204 protein PH0006.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	288	Total	C	N	O	S	Se	0	4	0
			2326	1484	394	438	1	9			
1	B	280	Total	C	N	O	S	Se	0	2	0
			2244	1438	374	422	1	9			
1	C	278	Total	C	N	O	S	Se	0	3	0
			2233	1428	373	422	1	9			

There are 102 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-21	MET	-	CLONING ARTIFACT	UNP O57774
A	-20	GLY	-	CLONING ARTIFACT	UNP O57774
A	-19	SER	-	CLONING ARTIFACT	UNP O57774
A	-18	SER	-	CLONING ARTIFACT	UNP O57774
A	-17	HIS	-	EXPRESSION TAG	UNP O57774
A	-16	HIS	-	EXPRESSION TAG	UNP O57774
A	-15	HIS	-	EXPRESSION TAG	UNP O57774
A	-14	HIS	-	EXPRESSION TAG	UNP O57774
A	-13	HIS	-	EXPRESSION TAG	UNP O57774
A	-12	HIS	-	EXPRESSION TAG	UNP O57774
A	-11	SER	-	CLONING ARTIFACT	UNP O57774
A	-10	SER	-	CLONING ARTIFACT	UNP O57774
A	-9	GLY	-	CLONING ARTIFACT	UNP O57774
A	-8	ARG	-	CLONING ARTIFACT	UNP O57774
A	-7	GLU	-	CLONING ARTIFACT	UNP O57774
A	-6	ASN	-	CLONING ARTIFACT	UNP O57774
A	-5	LEU	-	CLONING ARTIFACT	UNP O57774
A	-4	TYR	-	CLONING ARTIFACT	UNP O57774
A	-3	PHE	-	CLONING ARTIFACT	UNP O57774
A	-2	GLN	-	CLONING ARTIFACT	UNP O57774
A	-1	GLY	-	CLONING ARTIFACT	UNP O57774
A	0	HIS	-	CLONING ARTIFACT	UNP O57774
A	1	MSE	MET	MODIFIED RESIDUE	UNP O57774

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Chain	Residue	Modelled	Actual	Comment	Reference
A	5	MSE	MET	MODIFIED RESIDUE	UNP O57774
A	14	MSE	MET	MODIFIED RESIDUE	UNP O57774
A	17	MSE	MET	MODIFIED RESIDUE	UNP O57774
A	34	GLU	ASP	SEE REMARK 999	UNP O57774
A	53	MSE	MET	MODIFIED RESIDUE	UNP O57774
A	101	MSE	MET	MODIFIED RESIDUE	UNP O57774
A	117	MSE	MET	MODIFIED RESIDUE	UNP O57774
A	124	MSE	MET	MODIFIED RESIDUE	UNP O57774
A	231	MSE	MET	MODIFIED RESIDUE	UNP O57774
A	275	GLY	-	CLONING ARTIFACT	UNP O57774
A	276	SER	-	CLONING ARTIFACT	UNP O57774
B	-21	MET	-	CLONING ARTIFACT	UNP O57774
B	-20	GLY	-	CLONING ARTIFACT	UNP O57774
B	-19	SER	-	CLONING ARTIFACT	UNP O57774
B	-18	SER	-	CLONING ARTIFACT	UNP O57774
B	-17	HIS	-	EXPRESSION TAG	UNP O57774
B	-16	HIS	-	EXPRESSION TAG	UNP O57774
B	-15	HIS	-	EXPRESSION TAG	UNP O57774
B	-14	HIS	-	EXPRESSION TAG	UNP O57774
B	-13	HIS	-	EXPRESSION TAG	UNP O57774
B	-12	HIS	-	EXPRESSION TAG	UNP O57774
B	-11	SER	-	CLONING ARTIFACT	UNP O57774
B	-10	SER	-	CLONING ARTIFACT	UNP O57774
B	-9	GLY	-	CLONING ARTIFACT	UNP O57774
B	-8	ARG	-	CLONING ARTIFACT	UNP O57774
B	-7	GLU	-	CLONING ARTIFACT	UNP O57774
B	-6	ASN	-	CLONING ARTIFACT	UNP O57774
B	-5	LEU	-	CLONING ARTIFACT	UNP O57774
B	-4	TYR	-	CLONING ARTIFACT	UNP O57774
B	-3	PHE	-	CLONING ARTIFACT	UNP O57774
B	-2	GLN	-	CLONING ARTIFACT	UNP O57774
B	-1	GLY	-	CLONING ARTIFACT	UNP O57774
B	0	HIS	-	CLONING ARTIFACT	UNP O57774
B	1	MSE	MET	MODIFIED RESIDUE	UNP O57774
B	5	MSE	MET	MODIFIED RESIDUE	UNP O57774
B	14	MSE	MET	MODIFIED RESIDUE	UNP O57774
B	17	MSE	MET	MODIFIED RESIDUE	UNP O57774
B	34	GLU	ASP	SEE REMARK 999	UNP O57774
B	53	MSE	MET	MODIFIED RESIDUE	UNP O57774
B	101	MSE	MET	MODIFIED RESIDUE	UNP O57774
B	117	MSE	MET	MODIFIED RESIDUE	UNP O57774
B	124	MSE	MET	MODIFIED RESIDUE	UNP O57774

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Chain	Residue	Modelled	Actual	Comment	Reference
B	231	MSE	MET	MODIFIED RESIDUE	UNP O57774
B	275	GLY	-	CLONING ARTIFACT	UNP O57774
B	276	SER	-	CLONING ARTIFACT	UNP O57774
C	-21	MET	-	CLONING ARTIFACT	UNP O57774
C	-20	GLY	-	CLONING ARTIFACT	UNP O57774
C	-19	SER	-	CLONING ARTIFACT	UNP O57774
C	-18	SER	-	CLONING ARTIFACT	UNP O57774
C	-17	HIS	-	EXPRESSION TAG	UNP O57774
C	-16	HIS	-	EXPRESSION TAG	UNP O57774
C	-15	HIS	-	EXPRESSION TAG	UNP O57774
C	-14	HIS	-	EXPRESSION TAG	UNP O57774
C	-13	HIS	-	EXPRESSION TAG	UNP O57774
C	-12	HIS	-	EXPRESSION TAG	UNP O57774
C	-11	SER	-	CLONING ARTIFACT	UNP O57774
C	-10	SER	-	CLONING ARTIFACT	UNP O57774
C	-9	GLY	-	CLONING ARTIFACT	UNP O57774
C	-8	ARG	-	CLONING ARTIFACT	UNP O57774
C	-7	GLU	-	CLONING ARTIFACT	UNP O57774
C	-6	ASN	-	CLONING ARTIFACT	UNP O57774
C	-5	LEU	-	CLONING ARTIFACT	UNP O57774
C	-4	TYR	-	CLONING ARTIFACT	UNP O57774
C	-3	PHE	-	CLONING ARTIFACT	UNP O57774
C	-2	GLN	-	CLONING ARTIFACT	UNP O57774
C	-1	GLY	-	CLONING ARTIFACT	UNP O57774
C	0	HIS	-	CLONING ARTIFACT	UNP O57774
C	1	MSE	MET	MODIFIED RESIDUE	UNP O57774
C	5	MSE	MET	MODIFIED RESIDUE	UNP O57774
C	14	MSE	MET	MODIFIED RESIDUE	UNP O57774
C	17	MSE	MET	MODIFIED RESIDUE	UNP O57774
C	34	GLU	ASP	SEE REMARK 999	UNP O57774
C	53	MSE	MET	MODIFIED RESIDUE	UNP O57774
C	101	MSE	MET	MODIFIED RESIDUE	UNP O57774
C	117	MSE	MET	MODIFIED RESIDUE	UNP O57774
C	124	MSE	MET	MODIFIED RESIDUE	UNP O57774
C	231	MSE	MET	MODIFIED RESIDUE	UNP O57774
C	275	GLY	-	CLONING ARTIFACT	UNP O57774
C	276	SER	-	CLONING ARTIFACT	UNP O57774

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	C	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

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

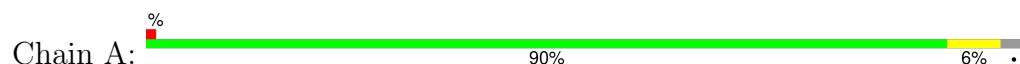
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	422	Total	O	0	0
			422	422		
4	B	353	Total	O	0	0
			353	353		
4	C	261	Total	O	0	0
			261	261		

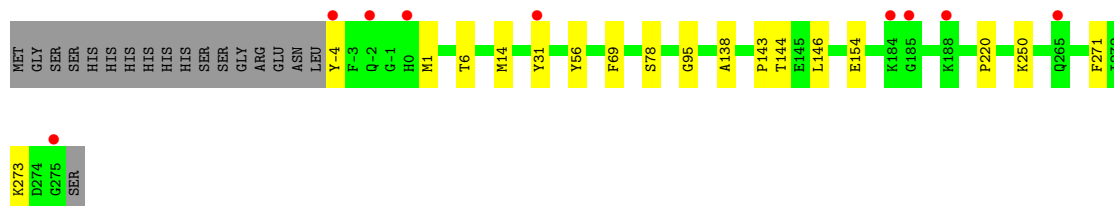
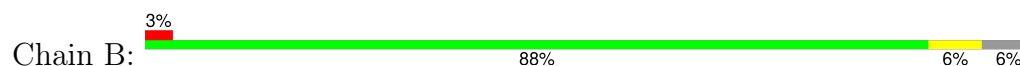
3 Residue-property plots [i](#)

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.

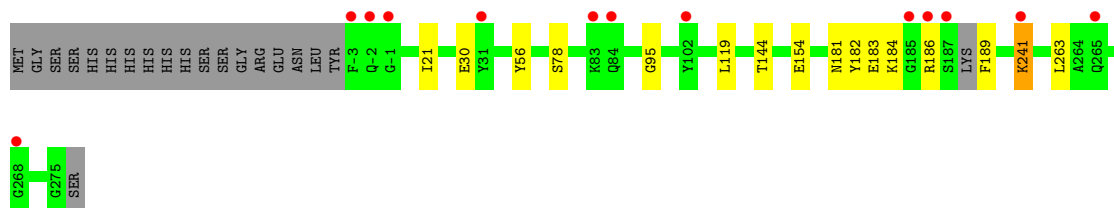
- Molecule 1: UPF0204 protein PH0006



- Molecule 1: UPF0204 protein PH0006



- Molecule 1: UPF0204 protein PH0006



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	65.02Å 67.03Å 111.57Å 90.00° 90.09° 90.00°	Depositor
Resolution (Å)	35.80 – 1.75 35.82 – 1.75	Depositor EDS
% Data completeness (in resolution range)	94.3 (35.80-1.75) 94.3 (35.82-1.75)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	0.05	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.33 (at 1.75Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.150 , 0.179 0.149 , 0.178	Depositor DCC
R_{free} test set	4552 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	19.2	Xtriage
Anisotropy	0.671	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 63.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.013 for -k,-h,-l 0.016 for k,h,-l 0.027 for h,-k,-l	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	7927	wwPDB-VP
Average B, all atoms (Å ²)	18.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.27% 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: SO4, 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	0.67	0/2368	0.68	0/3174
1	B	0.63	0/2285	0.65	0/3064
1	C	0.58	0/2271	0.63	0/3043
All	All	0.63	0/6924	0.65	0/9281

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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	2326	0	2298	21	0
1	B	2244	0	2222	12	0
1	C	2233	0	2210	12	0
2	A	30	0	0	0	0
2	B	35	0	0	0	0
2	C	20	0	0	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
4	A	422	0	0	5	1

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	B	353	0	0	3	1
4	C	261	0	0	4	0
All	All	7927	0	6730	45	1

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 (45) 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:253[B]:ARG:HH11	1:A:253[B]:ARG:HG3	1.15	1.07
1:A:64[A]:GLU:HG3	4:A:2434:HOH:O	1.77	0.84
1:A:253[B]:ARG:HG3	1:A:253[B]:ARG:NH1	1.93	0.83
1:A:253[B]:ARG:HH11	1:A:253[B]:ARG:CG	1.95	0.79
1:B:14:MSE:HE2	1:B:14:MSE:HA	1.77	0.66
1:A:64[A]:GLU:CG	4:A:2434:HOH:O	2.41	0.65
1:B:250:LYS:HE3	4:B:2348:HOH:O	2.02	0.59
1:A:61:ARG:HH21	1:A:61:ARG:CG	2.16	0.58
1:A:253[B]:ARG:NH1	1:A:253[B]:ARG:CG	2.59	0.57
1:C:181:ASN:HA	1:C:184:LYS:HE3	1.88	0.56
1:B:6:THR:HB	1:B:14:MSE:CE	2.39	0.52
1:A:19:LYS:HE3	1:A:165:ASP:OD1	2.10	0.51
1:B:138:ALA:HB1	1:B:220:PRO:HD3	1.92	0.51
1:C:189:PHE:N	4:C:2271:HOH:O	2.43	0.51
1:B:143:PRO:HG2	1:B:146:LEU:HD11	1.93	0.50
1:A:61:ARG:CZ	4:A:2066:HOH:O	2.59	0.50
1:B:271:PHE:HE2	1:B:273:LYS:HE2	1.76	0.50
1:C:119:LEU:CD1	1:C:182:TYR:HA	2.43	0.49
1:A:61:ARG:HH21	1:A:61:ARG:HG2	1.78	0.49
1:B:-4:TYR:N	4:B:2352:HOH:O	2.45	0.48
1:B:1:MSE:HB2	1:B:69:PHE:CE1	2.47	0.48
1:C:181:ASN:O	1:C:184:LYS:HG2	2.15	0.47
1:C:21:ILE:HG23	4:C:2079:HOH:O	2.14	0.47
1:A:61:ARG:CG	1:A:61:ARG:NH2	2.76	0.46
1:A:-8:ARG:HD2	4:A:2157:HOH:O	2.15	0.46
1:C:95:GLY:HA2	1:C:144:THR:HG22	1.97	0.46
1:C:183:GLU:HA	1:C:186:ARG:HH21	1.80	0.46
1:B:78:SER:O	1:B:154:GLU:HA	2.16	0.45
1:B:-4:TYR:CG	1:B:31:TYR:HE1	2.34	0.45
1:C:241:LYS:HG3	4:C:2135:HOH:O	2.16	0.45
1:B:78:SER:HB3	1:B:154:GLU:HG2	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:19:LYS:CE	1:A:165:ASP:OD1	2.66	0.44
1:C:119:LEU:HD12	1:C:182:TYR:HA	2.00	0.44
1:A:159:GLU:HA	1:A:162:TRP:CE3	2.53	0.43
1:A:5:MSE:HE3	1:A:59:LEU:HD21	2.00	0.43
1:A:253[A]:ARG:HD2	4:B:2087:HOH:O	2.19	0.43
1:C:30[B]:GLU:HG2	4:C:2087:HOH:O	2.19	0.42
1:C:182:TYR:O	1:C:186:ARG:HD2	2.19	0.42
1:A:78:SER:O	1:A:154:GLU:HA	2.19	0.42
1:A:95:GLY:HA2	1:A:144:THR:HG22	2.02	0.41
1:B:95:GLY:HA2	1:B:144:THR:HG22	2.02	0.41
1:A:19:LYS:HD3	1:A:19:LYS:HA	1.88	0.41
1:C:78:SER:O	1:C:154:GLU:HA	2.19	0.41
1:A:85:LYS:HE3	4:A:2372:HOH:O	2.20	0.41
1:A:249:TRP:CD2	1:A:273:LYS:HE3	2.56	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:2394:HOH:O	4:B:2318:HOH:O[1_545]	2.04	0.16

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	290/298 (97%)	287 (99%)	3 (1%)	0	100	100
1	B	280/298 (94%)	275 (98%)	5 (2%)	0	100	100
1	C	277/298 (93%)	276 (100%)	1 (0%)	0	100	100
All	All	847/894 (95%)	838 (99%)	9 (1%)	0	100	100

There are no Ramachandran outliers to report.

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	246/242 (102%)	244 (99%)	2 (1%)	81	72
1	B	237/242 (98%)	236 (100%)	1 (0%)	91	87
1	C	236/242 (98%)	233 (99%)	3 (1%)	69	54
All	All	719/726 (99%)	713 (99%)	6 (1%)	81	72

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	27	LYS
1	A	56	TYR
1	B	56	TYR
1	C	56	TYR
1	C	241	LYS
1	C	263	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	23	ASN
1	B	84	GLN
1	B	96	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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 20 ligands modelled in this entry, 3 are monoatomic - leaving 17 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	$\# Z > 2$
2	SO4	A	2004	-	4,4,4	0.23	0	6,6,6	0.20	0
2	SO4	B	2008	-	4,4,4	0.33	0	6,6,6	0.22	0
2	SO4	A	2005	-	4,4,4	0.29	0	6,6,6	0.29	0
2	SO4	C	2017	-	4,4,4	0.23	0	6,6,6	0.08	0
2	SO4	A	2010	-	4,4,4	0.30	0	6,6,6	0.24	0
2	SO4	C	2011	-	4,4,4	0.23	0	6,6,6	0.13	0
2	SO4	B	2007	-	4,4,4	0.25	0	6,6,6	0.06	0
2	SO4	C	2016	-	4,4,4	0.27	0	6,6,6	0.16	0
2	SO4	A	2003	-	4,4,4	0.33	0	6,6,6	0.41	0
2	SO4	A	2012	-	4,4,4	0.23	0	6,6,6	0.18	0
2	SO4	A	2006	-	4,4,4	0.26	0	6,6,6	0.42	0
2	SO4	B	2001	-	4,4,4	0.29	0	6,6,6	0.21	0
2	SO4	B	2002	-	4,4,4	0.26	0	6,6,6	0.17	0
2	SO4	B	2014	-	4,4,4	0.24	0	6,6,6	0.13	0
2	SO4	B	2013	-	4,4,4	0.28	0	6,6,6	0.12	0
2	SO4	B	2009	-	4,4,4	0.28	0	6,6,6	0.17	0
2	SO4	C	2015	-	4,4,4	0.23	0	6,6,6	0.26	0

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.

No monomer is involved in short contacts.

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 [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	279/298 (93%)	-0.18	2 (0%) 87 92	9, 12, 20, 27	0
1	B	271/298 (90%)	-0.05	9 (3%) 46 53	9, 13, 22, 30	0
1	C	269/298 (90%)	0.11	13 (4%) 30 36	9, 16, 24, 37	0
All	All	819/894 (91%)	-0.04	24 (2%) 51 57	9, 14, 22, 37	0

All (24) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	185	GLY	5.7
1	C	-2	GLN	4.9
1	B	-4	TYR	4.8
1	C	83	LYS	4.5
1	C	84	GLN	4.2
1	B	184	LYS	3.8
1	C	268	GLY	3.8
1	C	186	ARG	3.4
1	A	-12	HIS	3.4
1	B	185	GLY	3.0
1	C	265	GLN	2.8
1	B	265	GLN	2.8
1	C	-1	GLY	2.7
1	B	188	LYS	2.6
1	B	31	TYR	2.5
1	B	-2	GLN	2.4
1	C	31	TYR	2.4
1	B	0	HIS	2.4
1	C	102	TYR	2.3
1	A	-8	ARG	2.3
1	C	241	LYS	2.3
1	C	187	SER	2.2
1	C	-3	PHE	2.1

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Mol	Chain	Res	Type	RSRZ
1	B	275	GLY	2.1

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 monosaccharides 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(\AA^2)	Q<0.9
2	SO4	C	2015	5/5	0.88	0.16	52,54,55,55	0
2	SO4	B	2002	5/5	0.92	0.14	59,60,60,60	0
2	SO4	A	2004	5/5	0.93	0.21	49,49,51,51	0
2	SO4	A	2010	5/5	0.93	0.17	49,50,52,52	0
2	SO4	B	2009	5/5	0.94	0.17	51,53,53,54	0
2	SO4	A	2012	5/5	0.95	0.18	59,60,60,60	0
2	SO4	B	2014	5/5	0.95	0.16	72,73,73,73	0
2	SO4	A	2006	5/5	0.95	0.17	44,45,46,46	0
2	SO4	C	2017	5/5	0.95	0.19	65,65,65,66	0
3	MG	A	2018	1/1	0.95	0.20	30,30,30,30	0
2	SO4	B	2001	5/5	0.96	0.18	39,39,39,42	0
2	SO4	C	2011	5/5	0.97	0.22	56,56,57,57	0
2	SO4	C	2016	5/5	0.97	0.23	48,49,50,50	0
3	MG	B	2020	1/1	0.97	0.32	40,40,40,40	0
3	MG	C	2019	1/1	0.97	0.11	32,32,32,32	0
2	SO4	B	2013	5/5	0.98	0.25	46,47,48,48	0
2	SO4	B	2008	5/5	0.98	0.18	36,37,38,40	0
2	SO4	B	2007	5/5	0.98	0.21	44,45,47,47	0
2	SO4	A	2005	5/5	0.99	0.12	31,32,33,34	0
2	SO4	A	2003	5/5	0.99	0.13	18,22,25,28	0

6.5 Other polymers [i](#)

There are no such residues in this entry.