wwPDB X-ray Structure Validation Summary Report (i)

Jun 12, 2024 – 09:01 PM EDT

PDB ID	:	3WSH
Title	:	EDTA-treated, oxidized HcgD from Methanocaldococcus jannaschii
Authors	:	Fujishiro, T.; Ermler, U.; Shima, S.
Deposited on	:	2014-03-13
Resolution	:	2.80 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 (i) 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 (i)) were used in the production of this report:

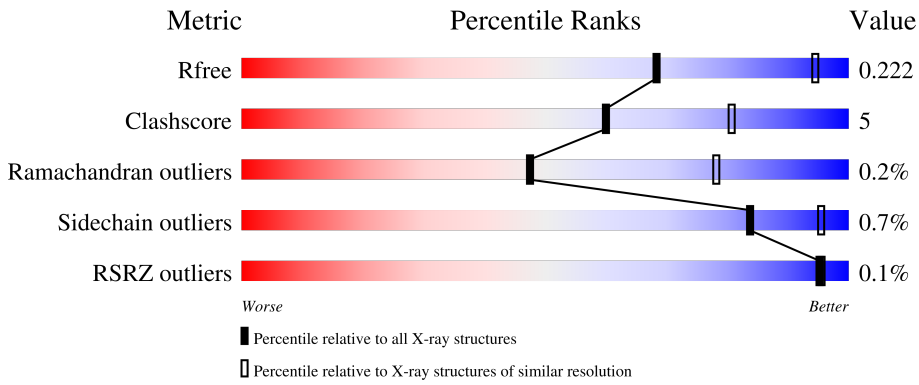
MolProbity	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.20.1
EDS	:	2.36.2
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

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 2.80 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	3140 (2.80-2.80)
Clashscore	141614	3569 (2.80-2.80)
Ramachandran outliers	138981	3498 (2.80-2.80)
Sidechain outliers	138945	3500 (2.80-2.80)
RSRZ outliers	127900	3078 (2.80-2.80)

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	252	84% 12% •
1	B	252	89% 7% •
1	C	252	88% 9% •
1	D	252	87% 10% •
1	E	252	86% 10% •

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Mol	Chain	Length	Quality of chain
1	F	252	83% 12%
1	G	252	81% 15%
1	H	252	87% 10%
1	I	252	89% 8%
1	J	252	87% 10%
1	K	252	87% 9%
1	L	252	% 77% 18%

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 23433 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 Putative GTP cyclohydrolase 1 type 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	244	1933	1255	307	368	3	0	0	0
1	B	244	1933	1255	307	368	3	0	0	0
1	C	244	1933	1255	307	368	3	0	0	0
1	D	244	1933	1255	307	368	3	0	0	0
1	E	244	1933	1255	307	368	3	0	0	0
1	F	244	1933	1255	307	368	3	0	0	0
1	G	244	1933	1255	307	368	3	0	0	0
1	H	244	1933	1255	307	368	3	0	0	0
1	I	244	1933	1255	307	368	3	0	0	0
1	J	244	1933	1255	307	368	3	0	0	0
1	K	244	1933	1255	307	368	3	0	0	0
1	L	244	1933	1255	307	368	3	0	0	0

- Molecule 2 is FE (III) ION (three-letter code: FE) (formula: Fe).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Fe		
2	A	1	1	1	0	0
2	B	1	1	1	0	0

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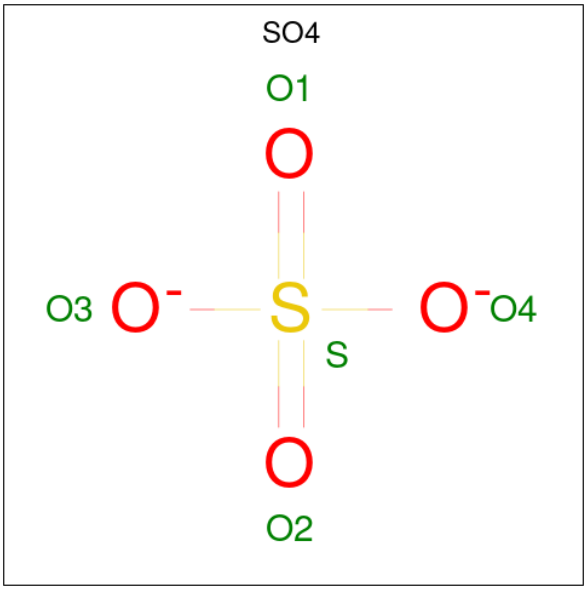
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	Fe			
2	C	1	1	1		0	0
2	D	1	1	1		0	0
2	E	1	1	1		0	0
2	F	1	1	1		0	0
2	G	1	1	1		0	0
2	H	1	1	1		0	0
2	I	1	1	1		0	0
2	J	1	1	1		0	0
2	K	1	1	1		0	0
2	L	1	1	1		0	0

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	O	S		
3	A	1	5	4	1	0	0

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	O	S		
3	B	1	5	4	1	0	0
3	C	1	5	4	1	0	0
3	D	1	5	4	1	0	0
3	E	1	5	4	1	0	0
3	F	1	5	4	1	0	0
3	G	1	5	4	1	0	0
3	H	1	5	4	1	0	0
3	I	1	5	4	1	0	0
3	J	1	5	4	1	0	0
3	K	1	5	4	1	0	0
3	L	1	5	4	1	0	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
4	A	30	30	30	0	0
4	B	25	25	25	0	0
4	C	5	5	5	0	0
4	D	9	9	9	0	0
4	E	13	13	13	0	0
4	F	7	7	7	0	0
4	G	3	3	3	0	0
4	H	18	18	18	0	0

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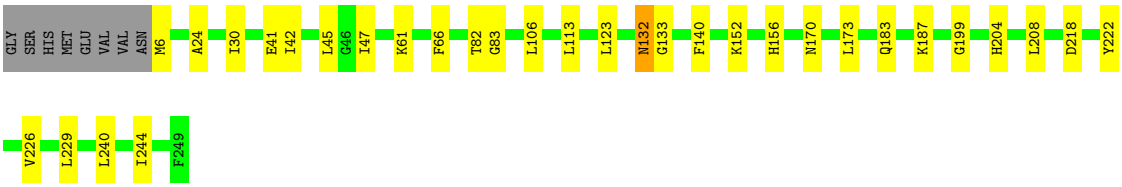
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
4	I	20	20	20	0	0
			Total	O		
4	J	21	21	21	0	0
			Total	O		
4	K	10	10	10	0	0
			Total	O		
4	L	4	4	4	0	0

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.

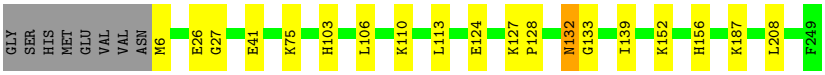
• Molecule 1: Putative GTP cyclohydrolase 1 type 2

Chain A:



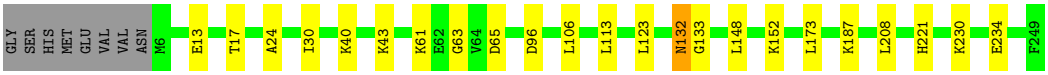
• Molecule 1: Putative GTP cyclohydrolase 1 type 2

Chain B:



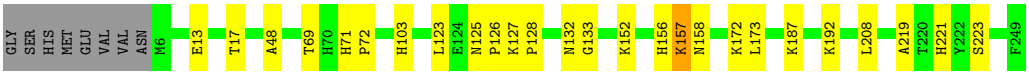
• Molecule 1: Putative GTP cyclohydrolase 1 type 2

Chain C:



• Molecule 1: Putative GTP cyclohydrolase 1 type 2

Chain D:

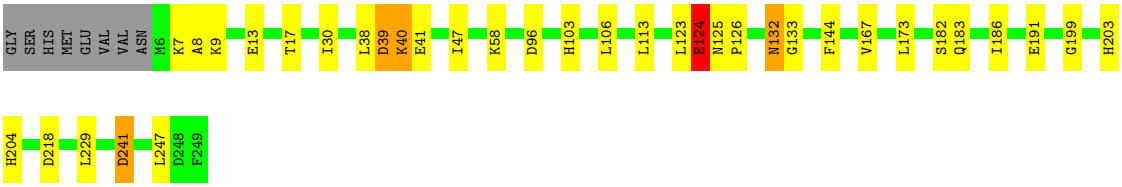


• Molecule 1: Putative GTP cyclohydrolase 1 type 2

Chain E:

• Molecule 1: Putative GTP cyclohydrolase 1 type 2

Chain F:

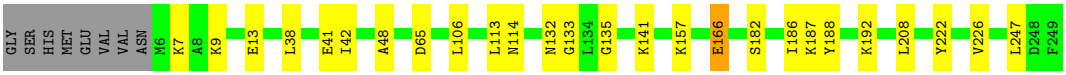


• Molecule 1: Putative GTP cyclohydrolase 1 type 2

Chain G:

• Molecule 1: Putative GTP cyclohydrolase 1 type 2

Chain H:

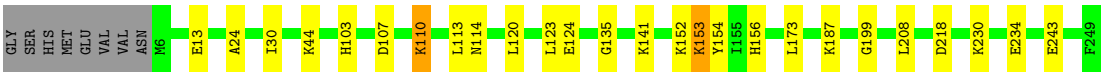


• Molecule 1: Putative GTP cyclohydrolase 1 type 2

Chain I:

• Molecule 1: Putative GTP cyclohydrolase 1 type 2

Chain J:



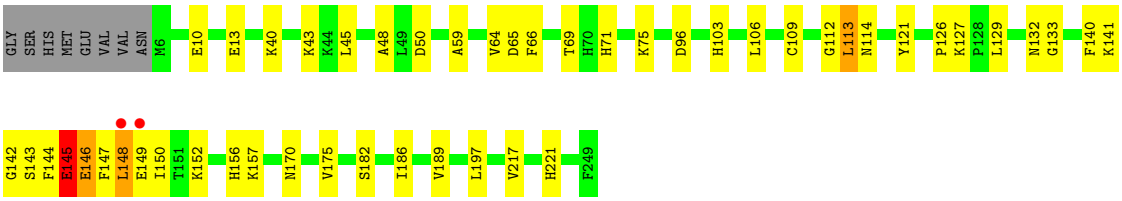
• Molecule 1: Putative GTP cyclohydrolase 1 type 2

Chain K:

• Molecule 1: Putative GTP cyclohydrolase 1 type 2

Chain L:

%
77%
18%


GLY
SER
HIS
MET
GLU
VAL
VAL
ASN
M6
E10
E13
K40
K43
K44
L45
A48
L49
D50
A59
V64
D65
F66
T69
H70
H71
K75
D96
H103
L106
C109
G112
L113
N114
Y121
P126
K127
P128
L129
N132
G133
F140
K141

G142
S143
F144
E145
E146
F147
L148
E149
I150
T151
K152
H156
K157
N170
V175
S182
I186
V189
L197
V217
H221
F249

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 63	Depositor
Cell constants a, b, c, α, β, γ	157.37Å 157.37Å 258.15Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	44.20 – 2.80 44.20 – 2.80	Depositor EDS
% Data completeness (in resolution range)	98.9 (44.20-2.80) 98.9 (44.20-2.80)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	4.03 (at 2.81Å)	Xtriage
Refinement program	PHENIX 1.8.4_1496	Depositor
R, R_{free}	0.176 , 0.218 0.180 , 0.222	Depositor DCC
R_{free} test set	4390 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å^2)	45.9	Xtriage
Anisotropy	0.061	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.31 , 13.9	EDS
L-test for twinning[2]	$< \|L\| > = 0.47$, $< L^2 > = 0.30$	Xtriage
Estimated twinning fraction	0.135 for h,-h-k,-l	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	23433	wwPDB-VP
Average B, all atoms (Å^2)	50.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 9.60% 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 (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: FE, SO4

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	0.32	0/1968	0.52	0/2651
1	B	0.31	0/1968	0.53	0/2651
1	C	0.31	0/1968	0.56	0/2651
1	D	0.33	0/1968	0.52	0/2651
1	E	0.31	0/1968	0.52	0/2651
1	F	0.33	0/1968	0.59	1/2651 (0.0%)
1	G	0.36	0/1968	0.63	1/2651 (0.0%)
1	H	0.32	0/1968	0.55	0/2651
1	I	0.33	0/1968	0.53	0/2651
1	J	0.31	0/1968	0.51	0/2651
1	K	0.31	0/1968	0.54	0/2651
1	L	0.41	1/1968 (0.1%)	0.61	1/2651 (0.0%)
All	All	0.33	1/23616 (0.0%)	0.55	3/31812 (0.0%)

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	A	0	1
1	B	0	1
1	C	0	1
1	E	0	1
1	F	0	2
1	G	0	1
All	All	0	7

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	L	145	GLU	CG-CD	5.41	1.60	1.51

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	G	65	ASP	CB-CG-OD2	-6.28	112.65	118.30
1	F	241	ASP	CB-CG-OD1	6.08	123.77	118.30
1	L	148	LEU	CB-CG-CD1	-5.24	102.09	111.00

There are no chirality outliers.

5 of 7 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	132	ASN	Peptide
1	B	132	ASN	Peptide
1	C	132	ASN	Peptide
1	E	132	ASN	Peptide
1	F	124	GLU	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	1933	0	1978	19	0
1	B	1933	0	1978	12	0
1	C	1933	0	1978	13	0
1	D	1933	0	1978	18	0
1	E	1933	0	1978	15	0
1	F	1933	0	1978	28	0
1	G	1933	0	1978	31	0
1	H	1933	0	1978	17	0
1	I	1933	0	1978	10	0
1	J	1933	0	1978	14	0
1	K	1933	0	1978	14	0
1	L	1933	0	1978	30	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	D	1	0	0	0	0
2	E	1	0	0	0	0
2	F	1	0	0	0	0
2	G	1	0	0	0	0
2	H	1	0	0	0	0
2	I	1	0	0	0	0
2	J	1	0	0	0	0
2	K	1	0	0	0	0
2	L	1	0	0	0	0
3	A	5	0	0	0	0
3	B	5	0	0	1	0
3	C	5	0	0	0	0
3	D	5	0	0	1	0
3	E	5	0	0	0	0
3	F	5	0	0	1	0
3	G	5	0	0	1	0
3	H	5	0	0	0	0
3	I	5	0	0	0	0
3	J	5	0	0	1	0
3	K	5	0	0	1	0
3	L	5	0	0	1	0
4	A	30	0	0	0	0
4	B	25	0	0	0	0
4	C	5	0	0	0	0
4	D	9	0	0	0	0
4	E	13	0	0	0	0
4	F	7	0	0	0	0
4	G	3	0	0	0	0
4	H	18	0	0	1	0
4	I	20	0	0	0	0
4	J	21	0	0	0	0
4	K	10	0	0	0	0
4	L	4	0	0	0	0
All	All	23433	0	23736	216	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 5.

The worst 5 of 216 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:L:147:PHE:HE2	1:L:217:VAL:HG21	1.28	0.97
1:F:124:GLU:HG3	1:F:125:ASN:H	1.30	0.95
1:G:110:LYS:H	1:G:110:LYS:HD3	1.33	0.90
1:G:44:LYS:N	1:G:65:ASP:OD2	2.08	0.86
1:E:28:ASP:OD1	1:E:75:LYS:NZ	2.11	0.84

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	242/252 (96%)	232 (96%)	10 (4%)	0	100	100
1	B	242/252 (96%)	232 (96%)	10 (4%)	0	100	100
1	C	242/252 (96%)	231 (96%)	11 (4%)	0	100	100
1	D	242/252 (96%)	232 (96%)	10 (4%)	0	100	100
1	E	242/252 (96%)	233 (96%)	9 (4%)	0	100	100
1	F	242/252 (96%)	233 (96%)	9 (4%)	0	100	100
1	G	242/252 (96%)	230 (95%)	8 (3%)	4 (2%)	9	29
1	H	242/252 (96%)	232 (96%)	10 (4%)	0	100	100
1	I	242/252 (96%)	232 (96%)	10 (4%)	0	100	100
1	J	242/252 (96%)	233 (96%)	9 (4%)	0	100	100
1	K	242/252 (96%)	232 (96%)	10 (4%)	0	100	100
1	L	242/252 (96%)	228 (94%)	11 (4%)	3 (1%)	13	39
All	All	2904/3024 (96%)	2780 (96%)	117 (4%)	7 (0%)	47	78

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	G	111	ASN

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Mol	Chain	Res	Type
1	L	109	CYS
1	L	113	LEU
1	L	145	GLU
1	G	110	LYS

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	215/222 (97%)	215 (100%)	0	100	100
1	B	215/222 (97%)	214 (100%)	1 (0%)	88	96
1	C	215/222 (97%)	215 (100%)	0	100	100
1	D	215/222 (97%)	214 (100%)	1 (0%)	88	96
1	E	215/222 (97%)	215 (100%)	0	100	100
1	F	215/222 (97%)	211 (98%)	4 (2%)	57	85
1	G	215/222 (97%)	214 (100%)	1 (0%)	88	96
1	H	215/222 (97%)	214 (100%)	1 (0%)	88	96
1	I	215/222 (97%)	214 (100%)	1 (0%)	88	96
1	J	215/222 (97%)	212 (99%)	3 (1%)	67	90
1	K	215/222 (97%)	213 (99%)	2 (1%)	78	94
1	L	215/222 (97%)	212 (99%)	3 (1%)	67	90
All	All	2580/2664 (97%)	2563 (99%)	17 (1%)	84	95

5 of 17 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	L	143	SER
1	L	146	GLU
1	H	166	GLU
1	I	241	ASP
1	J	13	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	183	GLN
1	E	183	GLN
1	E	239	ASN
1	F	183	GLN
1	I	183	GLN

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 24 ligands modelled in this entry, 12 are monoatomic - leaving 12 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	$\#\|Z\| > 2$
3	SO4	C	302	2	4,4,4	0.84	0	6,6,6	0.52	0
3	SO4	J	302	2	4,4,4	0.79	0	6,6,6	0.58	0
3	SO4	L	302	2	4,4,4	0.82	0	6,6,6	0.57	0
3	SO4	A	302	2	4,4,4	0.79	0	6,6,6	0.52	0
3	SO4	K	302	2	4,4,4	0.75	0	6,6,6	0.60	0
3	SO4	H	302	2	4,4,4	0.82	0	6,6,6	0.53	0
3	SO4	E	302	2	4,4,4	0.79	0	6,6,6	0.59	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
3	SO4	G	302	2	4,4,4	0.77	0	6,6,6	0.69	0
3	SO4	F	302	2	4,4,4	0.80	0	6,6,6	0.53	0
3	SO4	B	302	2	4,4,4	0.82	0	6,6,6	0.56	0
3	SO4	D	302	2	4,4,4	0.78	0	6,6,6	0.67	0
3	SO4	I	302	2	4,4,4	0.79	0	6,6,6	0.64	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.

7 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	J	302	SO4	1	0
3	L	302	SO4	1	0
3	K	302	SO4	1	0
3	G	302	SO4	1	0
3	F	302	SO4	1	0
3	B	302	SO4	1	0
3	D	302	SO4	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 (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	244/252 (96%)	-0.50	0	100	100	18, 34, 55, 68	0
1	B	244/252 (96%)	-0.49	0	100	100	20, 36, 59, 77	0
1	C	244/252 (96%)	-0.39	0	100	100	37, 50, 70, 85	0
1	D	244/252 (96%)	-0.41	0	100	100	27, 43, 66, 86	0
1	E	244/252 (96%)	-0.54	0	100	100	19, 37, 64, 78	0
1	F	244/252 (96%)	-0.32	0	100	100	39, 59, 82, 99	0
1	G	244/252 (96%)	-0.11	0	100	100	35, 69, 97, 109	0
1	H	244/252 (96%)	-0.48	0	100	100	26, 42, 69, 91	0
1	I	244/252 (96%)	-0.47	0	100	100	23, 40, 66, 79	0
1	J	244/252 (96%)	-0.50	0	100	100	21, 41, 68, 83	0
1	K	244/252 (96%)	-0.36	0	100	100	29, 49, 79, 90	0
1	L	244/252 (96%)	-0.12	2 (0%)	86	81	39, 72, 105, 117	0
All	All	2928/3024 (96%)	-0.39	2 (0%)	95	95	18, 47, 84, 117	0

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	L	149	GLU	2.9
1	L	148	LEU	2.6

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(Å^2)	Q<0.9
3	SO4	I	302	5/5	0.90	0.16	106,107,110,113	0
3	SO4	F	302	5/5	0.91	0.15	119,121,123,125	0
3	SO4	K	302	5/5	0.91	0.19	106,108,109,110	0
3	SO4	L	302	5/5	0.91	0.15	120,121,122,123	0
3	SO4	E	302	5/5	0.92	0.14	83,84,84,87	0
3	SO4	B	302	5/5	0.93	0.20	87,89,89,92	0
3	SO4	G	302	5/5	0.93	0.21	99,101,102,105	0
3	SO4	H	302	5/5	0.93	0.22	101,101,103,106	0
3	SO4	C	302	5/5	0.94	0.11	86,87,89,93	0
3	SO4	J	302	5/5	0.94	0.21	101,104,106,107	0
3	SO4	A	302	5/5	0.96	0.25	91,92,96,98	0
3	SO4	D	302	5/5	0.96	0.12	90,90,91,91	0
2	FE	L	301	1/1	0.97	0.09	34,34,34,34	1
2	FE	F	301	1/1	0.98	0.11	35,35,35,35	1
2	FE	G	301	1/1	0.98	0.08	31,31,31,31	1
2	FE	D	301	1/1	0.98	0.09	24,24,24,24	1
2	FE	I	301	1/1	0.99	0.11	26,26,26,26	1
2	FE	J	301	1/1	0.99	0.10	13,13,13,13	1
2	FE	K	301	1/1	0.99	0.10	28,28,28,28	1
2	FE	A	301	1/1	0.99	0.10	19,19,19,19	1
2	FE	E	301	1/1	0.99	0.11	28,28,28,28	1
2	FE	B	301	1/1	0.99	0.12	11,11,11,11	1
2	FE	C	301	1/1	0.99	0.09	37,37,37,37	1
2	FE	H	301	1/1	0.99	0.12	23,23,23,23	1

6.5 Other polymers (i)

There are no such residues in this entry.