



Full wwPDB X-ray Structure Validation Report ⓘ

Sep 30, 2021 – 02:30 PM EDT

PDB ID : 3P3Q
Title : Crystal Structure of MmoQ Response regulator from *Methylococcus capsulatus* str. Bath at the resolution 2.4Å, Northeast Structural Genomics Consortium Target McR175M
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Deposited on : 2010-10-05
Resolution : 2.40 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.23.2
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)	:	2.23.2

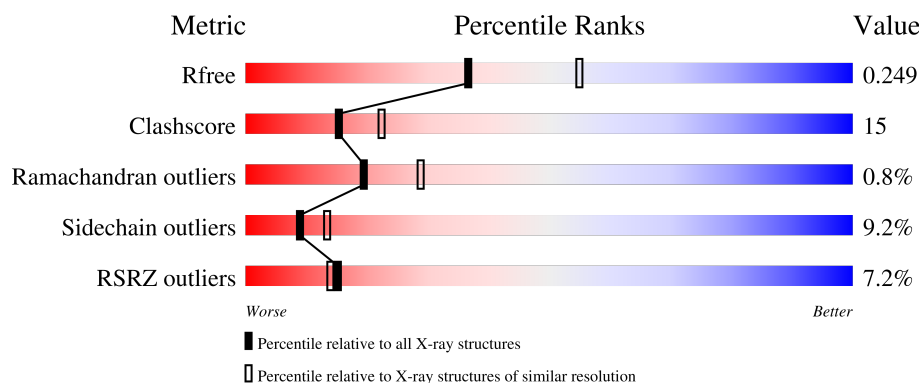
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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	3907 (2.40-2.40)
Clashscore	141614	4398 (2.40-2.40)
Ramachandran outliers	138981	4318 (2.40-2.40)
Sidechain outliers	138945	4319 (2.40-2.40)
RSRZ outliers	127900	3811 (2.40-2.40)

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	283	<div> <div>7%</div> <div>61%</div> <div>21%</div> <div>•</div> <div>15%</div> </div>
1	B	283	<div> <div>5%</div> <div>68%</div> <div>16%</div> <div>5%</div> <div>11%</div> </div>

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 3876 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 MmoQ.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	240	Total	C	N	O	S	Se	0	0	0
			1839	1154	331	348	4	2			
1	B	253	Total	C	N	O	S	Se	0	0	0
			1937	1210	352	369	4	2			

There are 26 discrepancies between the modelled and reference sequences:

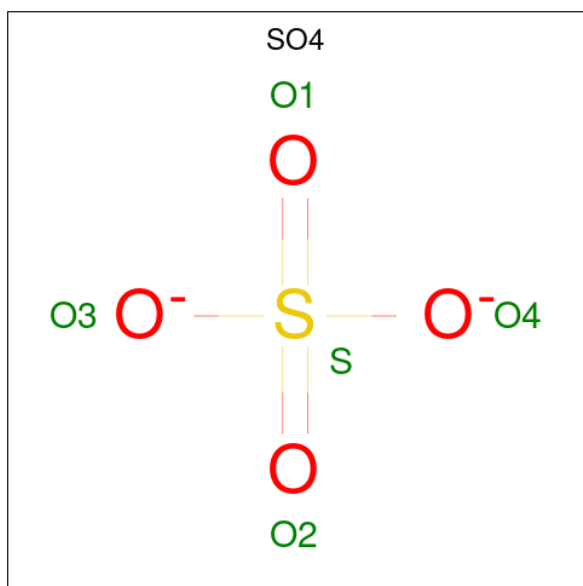
Chain	Residue	Modelled	Actual	Comment	Reference
A	28	MSE	-	expression tag	UNP Q7WZ31
A	49	SER	ARG	engineered mutation	UNP Q7WZ31
A	242	THR	ALA	engineered mutation	UNP Q7WZ31
A	293	ARG	TRP	engineered mutation	UNP Q7WZ31
A	300	GLY	PRO	engineered mutation	UNP Q7WZ31
A	303	LEU	-	expression tag	UNP Q7WZ31
A	304	GLU	-	expression tag	UNP Q7WZ31
A	305	HIS	-	expression tag	UNP Q7WZ31
A	306	HIS	-	expression tag	UNP Q7WZ31
A	307	HIS	-	expression tag	UNP Q7WZ31
A	308	HIS	-	expression tag	UNP Q7WZ31
A	309	HIS	-	expression tag	UNP Q7WZ31
A	310	HIS	-	expression tag	UNP Q7WZ31
B	28	MSE	-	expression tag	UNP Q7WZ31
B	49	SER	ARG	engineered mutation	UNP Q7WZ31
B	242	THR	ALA	engineered mutation	UNP Q7WZ31
B	293	ARG	TRP	engineered mutation	UNP Q7WZ31
B	300	GLY	PRO	engineered mutation	UNP Q7WZ31
B	303	LEU	-	expression tag	UNP Q7WZ31
B	304	GLU	-	expression tag	UNP Q7WZ31
B	305	HIS	-	expression tag	UNP Q7WZ31
B	306	HIS	-	expression tag	UNP Q7WZ31
B	307	HIS	-	expression tag	UNP Q7WZ31
B	308	HIS	-	expression tag	UNP Q7WZ31
B	309	HIS	-	expression tag	UNP Q7WZ31

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Chain	Residue	Modelled	Actual	Comment	Reference
B	310	HIS	-	expression tag	UNP Q7WZ31

- 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	B	1	Total	O	S	0	0
			5	4	1		

- Molecule 3 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Na	0	0
			1	1		

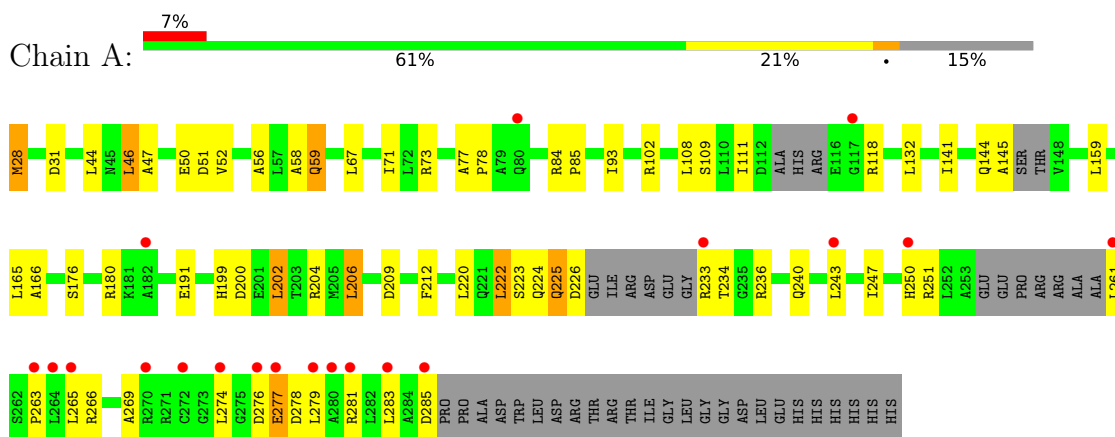
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	34	Total	O	0	0
			34	34		
4	B	50	Total	O	0	0
			50	50		

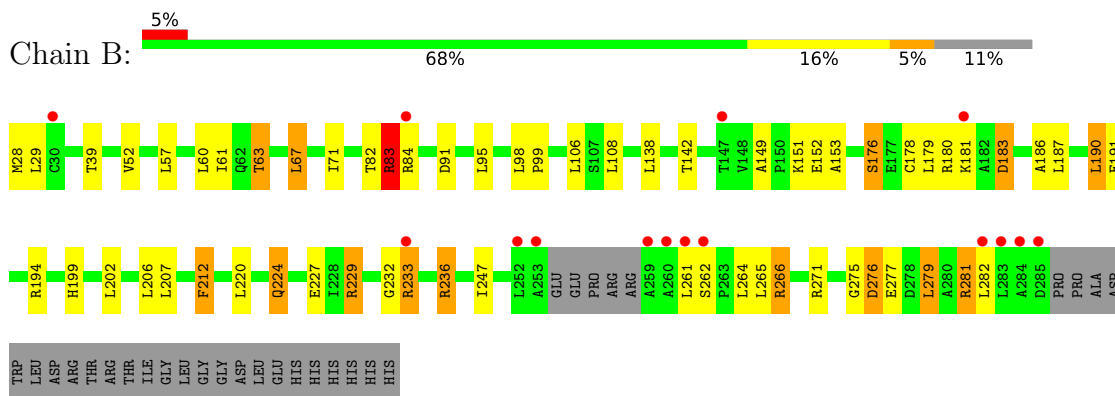
3 Residue-property plots [i](#)

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: MmoQ



• Molecule 1: MmoQ



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	44.23Å 76.16Å 160.28Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	38.25 – 2.40 40.07 – 2.40	Depositor EDS
% Data completeness (in resolution range)	98.6 (38.25-2.40) 98.6 (40.07-2.40)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.21 (at 2.39Å)	Xtriage
Refinement program	PHENIX 1.6.4 _486	Depositor
R, R_{free}	0.194 , 0.255 0.190 , 0.249	Depositor DCC
R_{free} test set	1110 reflections (5.12%)	wwPDB-VP
Wilson B-factor (Å ²)	34.9	Xtriage
Anisotropy	0.558	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 60.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	3876	wwPDB-VP
Average B, all atoms (Å ²)	47.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.44% 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: NA, 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	0.38	0/1862	0.55	0/2523
1	B	0.40	0/1964	0.55	0/2665
All	All	0.39	0/3826	0.55	0/5188

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	1839	0	1848	55	0
1	B	1937	0	1941	59	0
2	A	10	0	0	0	0
2	B	5	0	0	0	0
3	A	1	0	0	0	0
4	A	34	0	0	0	0
4	B	50	0	0	1	0
All	All	3876	0	3789	113	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 15.

All (113) 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:206:LEU:HD13	1:B:28:MSE:HE2	1.41	1.01
1:A:276:ASP:HB3	1:A:277:GLU:HA	1.51	0.93
1:B:82:THR:HG21	1:B:95:LEU:HD21	1.55	0.87
1:A:251:ARG:HH22	1:A:285:ASP:HA	1.45	0.80
1:B:29:LEU:HD22	1:B:29:LEU:H	1.46	0.80
1:A:46:LEU:HD22	1:A:52:VAL:HG23	1.62	0.79
1:A:204:ARG:NH1	1:A:224:GLN:HE22	1.82	0.77
1:B:276:ASP:CB	1:B:277:GLU:HA	2.17	0.74
1:B:233:ARG:N	1:B:233:ARG:HE	1.86	0.73
1:A:67:LEU:O	1:A:71:ILE:HG12	1.90	0.72
1:A:233:ARG:HG3	1:A:234:THR:H	1.54	0.71
1:B:67:LEU:O	1:B:71:ILE:HG12	1.92	0.69
1:A:204:ARG:HH11	1:A:224:GLN:HE22	1.41	0.68
1:A:111:ILE:HD12	1:A:111:ILE:H	1.58	0.68
1:B:233:ARG:HE	1:B:233:ARG:H	1.43	0.67
1:A:220:LEU:O	1:A:224:GLN:HG3	1.95	0.66
1:A:56:ALA:O	1:A:59:GLN:HG3	1.95	0.65
1:B:82:THR:CG2	1:B:95:LEU:HD21	2.27	0.65
1:B:276:ASP:OD2	1:B:277:GLU:HA	1.97	0.65
1:B:178:CYS:SG	1:B:194:ARG:HG3	2.37	0.65
1:B:262:SER:HB3	1:B:265:LEU:HD13	1.79	0.64
1:B:191:GLU:OE2	1:B:199:HIS:HD2	1.80	0.64
1:A:47:ALA:O	1:A:102:ARG:HD2	1.98	0.64
1:B:60:LEU:O	1:B:63:THR:HB	1.97	0.64
1:A:118:ARG:HG3	1:A:118:ARG:HH11	1.64	0.63
1:A:269:ALA:CB	1:A:279:LEU:HD12	2.29	0.63
1:A:111:ILE:HD12	1:A:111:ILE:N	2.15	0.62
1:B:233:ARG:H	1:B:233:ARG:NE	1.97	0.61
1:B:233:ARG:N	1:B:233:ARG:NE	2.49	0.60
1:B:232:GLY:O	1:B:236:ARG:HG2	2.02	0.59
1:B:276:ASP:HB3	1:B:277:GLU:HA	1.84	0.59
1:A:233:ARG:N	1:A:236:ARG:HD3	2.17	0.59
1:A:276:ASP:CB	1:A:277:GLU:HA	2.19	0.59
1:A:269:ALA:HB2	1:A:279:LEU:HD12	1.84	0.58
1:B:29:LEU:H	1:B:29:LEU:CD2	2.15	0.58
1:B:261:LEU:HB2	1:B:266:ARG:HH21	1.69	0.58
1:A:144:GLN:O	1:A:145:ALA:HB2	2.04	0.57
1:B:183:ASP:HA	1:B:187:LEU:HB2	1.87	0.57
1:B:39:THR:OG1	1:B:63:THR:HG22	2.04	0.57
1:A:250:HIS:CE1	1:A:265:LEU:HD22	2.40	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:28:MSE:HB3	1:A:31:ASP:OD2	2.05	0.56
1:A:200:ASP:HB3	1:A:224:GLN:NE2	2.21	0.55
1:A:261:LEU:HB2	1:A:266:ARG:HH21	1.72	0.54
1:B:233:ARG:H	1:B:233:ARG:CD	2.20	0.54
1:A:191:GLU:OE2	1:A:199:HIS:HD2	1.91	0.53
1:B:181:LYS:HB3	1:B:190:LEU:HD21	1.91	0.53
1:A:278:ASP:HA	1:A:281:ARG:HD2	1.91	0.53
1:A:176:SER:O	1:A:180:ARG:HG3	2.09	0.52
1:A:111:ILE:H	1:A:111:ILE:CD1	2.22	0.52
1:B:261:LEU:O	1:B:261:LEU:HG	2.10	0.52
1:A:118:ARG:HG3	1:A:118:ARG:NH1	2.23	0.52
1:B:261:LEU:H	1:B:261:LEU:HD23	1.74	0.51
1:B:82:THR:HG21	1:B:95:LEU:HD11	1.93	0.51
1:B:138:LEU:HD23	1:B:153:ALA:O	2.11	0.51
1:B:191:GLU:OE2	1:B:199:HIS:CD2	2.64	0.51
1:B:176:SER:O	1:B:180:ARG:HG3	2.11	0.50
1:A:145:ALA:HB3	1:A:240:GLN:HE22	1.77	0.50
1:B:29:LEU:HD22	1:B:29:LEU:N	2.23	0.49
1:A:58:ALA:HB2	1:A:93:ILE:HD12	1.93	0.49
1:B:261:LEU:H	1:B:261:LEU:CD2	2.26	0.49
1:A:247:ILE:HG23	1:A:283:LEU:HD23	1.95	0.49
1:A:56:ALA:O	1:A:59:GLN:CG	2.62	0.47
1:B:247:ILE:CD1	1:B:282:LEU:HD13	2.44	0.47
1:B:281:ARG:HG3	1:B:281:ARG:NH1	2.28	0.47
1:A:50:GLU:HA	1:A:50:GLU:OE1	2.14	0.47
1:B:98:LEU:N	1:B:99:PRO:CD	2.78	0.47
1:B:265:LEU:HB3	1:B:279:LEU:HD11	1.97	0.46
1:A:223:SER:C	1:A:225:GLN:H	2.18	0.46
1:B:52:VAL:CG1	1:B:57:LEU:HB2	2.46	0.46
1:A:56:ALA:HA	1:A:59:GLN:HG2	1.98	0.46
1:A:225:GLN:O	1:A:226:ASP:C	2.54	0.46
1:A:67:LEU:HD11	1:A:108:LEU:HD11	1.98	0.46
1:A:84:ARG:CG	1:A:85:PRO:HD2	2.45	0.46
1:B:281:ARG:HG3	1:B:281:ARG:HH11	1.81	0.45
1:A:77:ALA:HB3	1:A:78:PRO:HD3	1.98	0.45
1:A:279:LEU:HD23	1:A:279:LEU:O	2.17	0.45
1:B:227:GLU:HG3	1:B:229:ARG:HD3	1.99	0.45
1:A:269:ALA:O	1:A:274:LEU:HB2	2.17	0.45
1:B:261:LEU:HD23	1:B:261:LEU:N	2.31	0.45
1:A:202:LEU:HD22	1:A:206:LEU:HD22	1.99	0.45
1:B:61:ILE:C	1:B:63:THR:H	2.19	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:224:GLN:HE21	1:B:224:GLN:HB3	1.52	0.44
1:A:141:ILE:HD13	1:A:243:LEU:HD23	1.99	0.44
1:B:183:ASP:O	1:B:186:ALA:HB3	2.18	0.44
1:A:108:LEU:HD23	1:A:108:LEU:HA	1.83	0.44
1:B:98:LEU:HB3	1:B:99:PRO:HD3	2.00	0.44
1:B:149:ALA:HB3	1:B:152:GLU:HG3	1.98	0.44
1:B:179:LEU:HD23	1:B:179:LEU:HA	1.85	0.44
1:A:28:MSE:HE3	1:A:28:MSE:HB2	1.92	0.43
1:B:281:ARG:H	1:B:281:ARG:HG2	1.52	0.43
1:B:91:ASP:OD1	1:B:151:LYS:HE3	2.18	0.43
1:B:227:GLU:HG3	1:B:229:ARG:CD	2.49	0.43
1:B:95:LEU:HD23	1:B:95:LEU:O	2.19	0.43
1:A:77:ALA:N	1:A:78:PRO:CD	2.82	0.43
1:B:183:ASP:CA	1:B:187:LEU:HB2	2.49	0.43
1:B:276:ASP:CG	1:B:277:GLU:HA	2.39	0.42
1:B:82:THR:HG21	1:B:95:LEU:CD2	2.38	0.42
1:A:274:LEU:HD23	1:A:274:LEU:HA	1.78	0.42
1:A:276:ASP:HB3	1:A:277:GLU:CA	2.36	0.42
1:A:279:LEU:HD23	1:A:279:LEU:C	2.40	0.42
1:B:83:ARG:H	1:B:83:ARG:HG2	1.57	0.41
1:A:261:LEU:HB3	1:A:266:ARG:HE	1.86	0.41
1:B:264:LEU:C	1:B:264:LEU:HD23	2.40	0.41
1:B:39:THR:OG1	1:B:63:THR:CG2	2.67	0.41
1:B:271:ARG:HD3	4:B:333:HOH:O	2.19	0.41
1:A:144:GLN:O	1:A:145:ALA:CB	2.68	0.41
1:A:73:ARG:HD2	1:A:209:ASP:OD2	2.21	0.41
1:B:52:VAL:H	1:B:52:VAL:HG23	1.64	0.41
1:A:261:LEU:CB	1:A:266:ARG:HH21	2.34	0.41
1:A:166:ALA:HB3	1:A:202:LEU:HD13	2.04	0.40
1:A:222:LEU:HD22	1:A:234:THR:HG22	2.04	0.40
1:B:108:LEU:HA	1:B:108:LEU:HD12	1.91	0.40
1:B:207:LEU:O	1:B:212:PHE:HB2	2.22	0.40

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	230/283 (81%)	220 (96%)	8 (4%)	2 (1%)	17	25
1	B	249/283 (88%)	239 (96%)	8 (3%)	2 (1%)	19	29
All	All	479/566 (85%)	459 (96%)	16 (3%)	4 (1%)	19	29

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	275	GLY
1	A	263	PRO
1	A	225	GLN
1	B	83	ARG

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	186/219 (85%)	172 (92%)	14 (8%)	13	21
1	B	195/219 (89%)	174 (89%)	21 (11%)	6	9
All	All	381/438 (87%)	346 (91%)	35 (9%)	9	13

All (35) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	28	MSE
1	A	44	LEU
1	A	46	LEU
1	A	51	ASP
1	A	59	GLN
1	A	109	SER
1	A	132	LEU
1	A	159	LEU

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Mol	Chain	Res	Type
1	A	165	LEU
1	A	202	LEU
1	A	206	LEU
1	A	212	PHE
1	A	222	LEU
1	A	277	GLU
1	B	63	THR
1	B	67	LEU
1	B	83	ARG
1	B	84	ARG
1	B	106	LEU
1	B	142	THR
1	B	176	SER
1	B	183	ASP
1	B	190	LEU
1	B	202	LEU
1	B	206	LEU
1	B	212	PHE
1	B	220	LEU
1	B	224	GLN
1	B	229	ARG
1	B	233	ARG
1	B	236	ARG
1	B	266	ARG
1	B	276	ASP
1	B	279	LEU
1	B	281	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	80	GLN
1	A	129	GLN
1	A	199	HIS
1	A	224	GLN
1	A	225	GLN
1	A	240	GLN
1	A	250	HIS
1	B	80	GLN
1	B	199	HIS
1	B	221	GLN
1	B	224	GLN

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Mol	Chain	Res	Type
1	B	250	HIS

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 4 ligands modelled in this entry, 1 is 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	$\# Z > 2$
2	SO4	A	1	-	4,4,4	0.14	0	6,6,6	0.08	0
2	SO4	B	2	-	4,4,4	0.12	0	6,6,6	0.12	0
2	SO4	A	3	3	4,4,4	0.15	0	6,6,6	0.08	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 ⓘ

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, 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	238/283 (84%)	0.08	20 (8%)	11 10	20, 46, 102, 128	0
1	B	251/283 (88%)	-0.06	15 (5%)	21 20	19, 34, 79, 108	1 (0%)
All	All	489/566 (86%)	0.01	35 (7%)	15 14	19, 39, 94, 128	1 (0%)

All (35) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	260	ALA	7.2
1	B	259	ALA	5.4
1	B	261	LEU	4.8
1	B	283	LEU	4.4
1	B	252	LEU	4.2
1	B	284	ALA	3.9
1	B	285	ASP	3.9
1	B	253	ALA	3.8
1	A	274	LEU	3.6
1	A	264	LEU	3.4
1	A	281	ARG	3.4
1	A	272	CYS	3.3
1	A	270	ARG	3.3
1	A	265	LEU	3.2
1	A	277	GLU	3.1
1	A	283	LEU	3.1
1	A	263	PRO	2.9
1	B	30	CYS	2.9
1	A	233	ARG	2.8
1	A	279	LEU	2.7
1	A	261	LEU	2.7
1	B	147	THR	2.7
1	B	262	SER	2.7
1	A	80	GLN	2.5

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Mol	Chain	Res	Type	RSRZ
1	B	84	ARG	2.4
1	B	282	LEU	2.4
1	A	182	ALA	2.4
1	A	280	ALA	2.4
1	A	243	LEU	2.4
1	A	117	GLY	2.4
1	B	181	LYS	2.4
1	A	250	HIS	2.3
1	A	285	ASP	2.2
1	B	233	ARG	2.2
1	A	276	ASP	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 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
2	SO4	A	3	5/5	0.72	0.21	123,124,125,126	0
2	SO4	B	2	5/5	0.88	0.20	114,121,121,124	0
3	NA	A	311	1/1	0.88	0.38	52,52,52,52	0
2	SO4	A	1	5/5	0.94	0.12	73,85,92,93	0

6.5 Other polymers [i](#)

There are no such residues in this entry.