



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 10:30 AM GMT

PDB ID : 3M8N
Title : Crystal structure of a possible glutathione S-transferase from *Rhodospseudomonas palustris*
Authors : Damodharan, L.; Burley, S.K.; Swaminathan, S.; New York SGX Research Center for Structural Genomics (NYSGXRC)
Deposited on : 2010-03-18
Resolution : 2.04 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
<http://wwpdb.org/validation/2016/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 : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

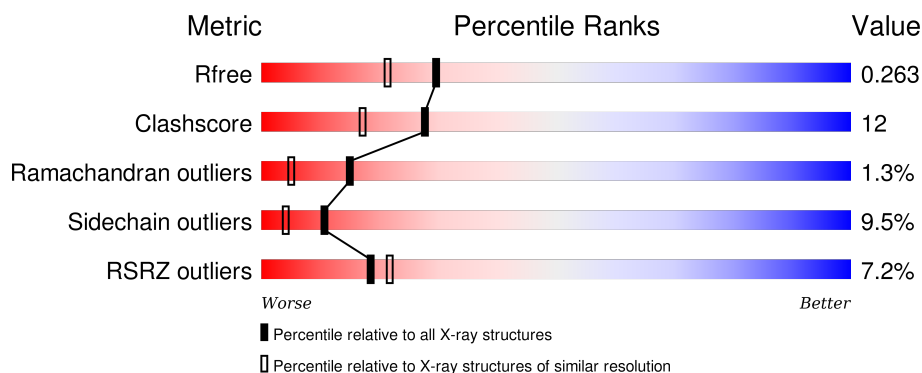
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.04 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}	91344	1192 (2.04-2.04)
Clashscore	102246	1269 (2.04-2.04)
Ramachandran outliers	100387	1258 (2.04-2.04)
Sidechain outliers	100360	1258 (2.04-2.04)
RSRZ outliers	91569	1194 (2.04-2.04)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	225	<div> <div>2%</div> <div> <div></div> <div>67%</div> <div>20%</div> <div>•</div> <div>9%</div> </div> </div>
1	B	225	<div> <div>3%</div> <div> <div></div> <div>62%</div> <div>16%</div> <div>•</div> <div>19%</div> </div> </div>
1	C	225	<div> <div>15%</div> <div> <div></div> <div>61%</div> <div>17%</div> <div>7%</div> <div>14%</div> </div> </div>
1	D	225	<div> <div>5%</div> <div> <div></div> <div>73%</div> <div>21%</div> <div>• •</div> </div> </div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 6636 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 Possible glutathione S-transferase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	204	Total	C	N	O	S	Se	0	0	0
			1629	1046	275	301	2	5			
1	B	183	Total	C	N	O	S	Se	0	0	0
			1459	935	245	273	1	5			
1	C	193	Total	C	N	O	S	Se	0	0	0
			1525	983	257	278	2	5			
1	D	222	Total	C	N	O	S	Se	0	0	0
			1769	1132	305	325	2	5			

There are 40 discrepancies between the modelled and reference sequences:

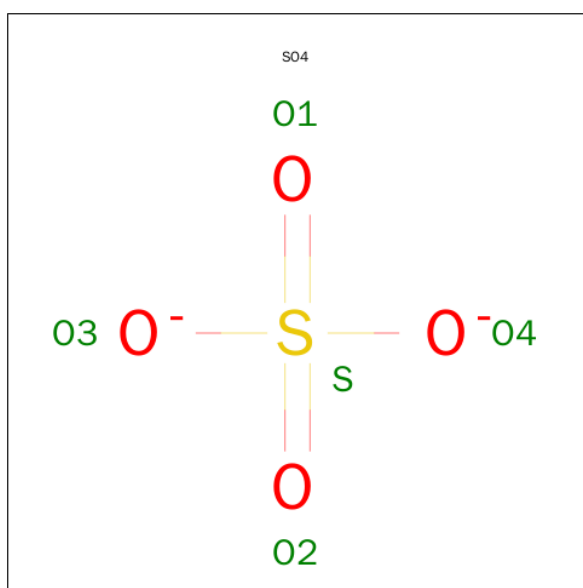
Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	MSE	-	expression tag	UNP Q6N1S2
A	0	SER	-	expression tag	UNP Q6N1S2
A	1	LEU	-	expression tag	UNP Q6N1S2
A	217	GLY	-	expression tag	UNP Q6N1S2
A	218	HIS	-	expression tag	UNP Q6N1S2
A	219	HIS	-	expression tag	UNP Q6N1S2
A	220	HIS	-	expression tag	UNP Q6N1S2
A	221	HIS	-	expression tag	UNP Q6N1S2
A	222	HIS	-	expression tag	UNP Q6N1S2
A	223	HIS	-	expression tag	UNP Q6N1S2
B	-1	MSE	-	expression tag	UNP Q6N1S2
B	0	SER	-	expression tag	UNP Q6N1S2
B	1	LEU	-	expression tag	UNP Q6N1S2
B	217	GLY	-	expression tag	UNP Q6N1S2
B	218	HIS	-	expression tag	UNP Q6N1S2
B	219	HIS	-	expression tag	UNP Q6N1S2
B	220	HIS	-	expression tag	UNP Q6N1S2
B	221	HIS	-	expression tag	UNP Q6N1S2
B	222	HIS	-	expression tag	UNP Q6N1S2
B	223	HIS	-	expression tag	UNP Q6N1S2
C	-1	MSE	-	expression tag	UNP Q6N1S2

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Chain	Residue	Modelled	Actual	Comment	Reference
C	0	SER	-	expression tag	UNP Q6N1S2
C	1	LEU	-	expression tag	UNP Q6N1S2
C	217	GLY	-	expression tag	UNP Q6N1S2
C	218	HIS	-	expression tag	UNP Q6N1S2
C	219	HIS	-	expression tag	UNP Q6N1S2
C	220	HIS	-	expression tag	UNP Q6N1S2
C	221	HIS	-	expression tag	UNP Q6N1S2
C	222	HIS	-	expression tag	UNP Q6N1S2
C	223	HIS	-	expression tag	UNP Q6N1S2
D	-1	MSE	-	expression tag	UNP Q6N1S2
D	0	SER	-	expression tag	UNP Q6N1S2
D	1	LEU	-	expression tag	UNP Q6N1S2
D	217	GLY	-	expression tag	UNP Q6N1S2
D	218	HIS	-	expression tag	UNP Q6N1S2
D	219	HIS	-	expression tag	UNP Q6N1S2
D	220	HIS	-	expression tag	UNP Q6N1S2
D	221	HIS	-	expression tag	UNP Q6N1S2
D	222	HIS	-	expression tag	UNP Q6N1S2
D	223	HIS	-	expression tag	UNP Q6N1S2

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



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

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

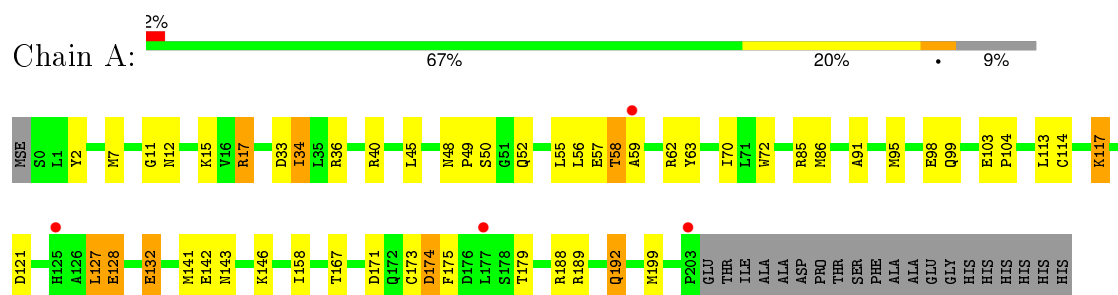
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	69	Total	O	0	0
			69	69		
3	B	73	Total	O	0	0
			73	73		
3	C	35	Total	O	0	0
			35	35		
3	D	62	Total	O	0	0
			62	62		

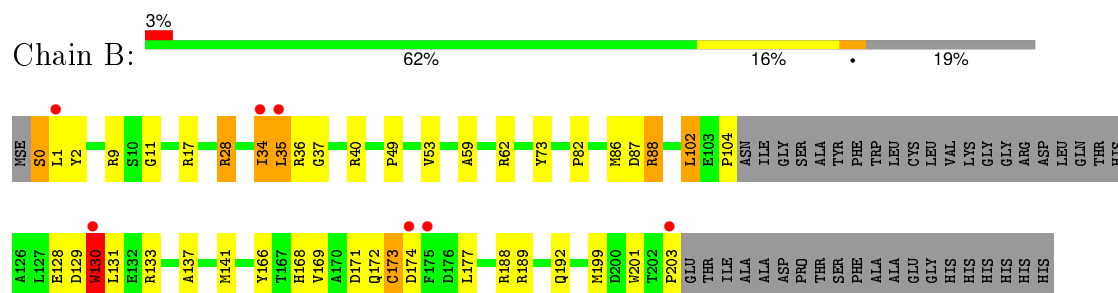
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

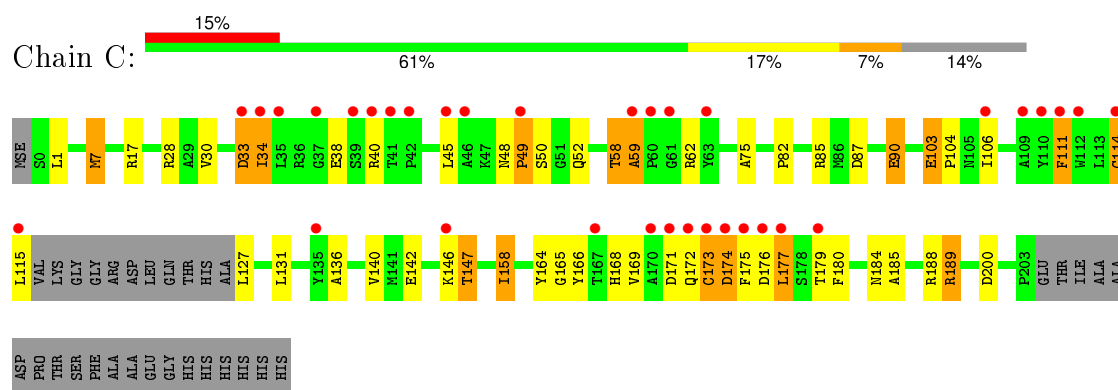
- Molecule 1: Possible glutathione S-transferase



- Molecule 1: Possible glutathione S-transferase

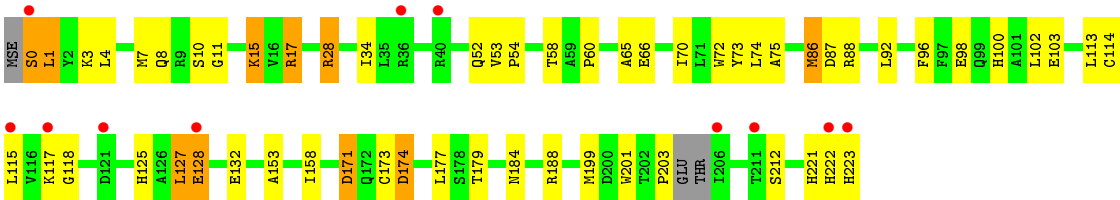


- Molecule 1: Possible glutathione S-transferase



- Molecule 1: Possible glutathione S-transferase





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	56.97Å 105.09Å 152.13Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	45.67 – 2.04 45.67 – 2.04	Depositor EDS
% Data completeness (in resolution range)	91.3 (45.67-2.04) 91.3 (45.67-2.04)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.73 (at 2.05Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.199 , 0.259 0.205 , 0.263	Depositor DCC
R_{free} test set	1718 reflections (3.30%)	DCC
Wilson B-factor (Å ²)	35.5	Xtriage
Anisotropy	0.112	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 54.3	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 53728 reflections	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	6636	wwPDB-VP
Average B, all atoms (Å ²)	38.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.95% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: 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	1.07	0/1668	1.00	5/2266 (0.2%)
1	B	1.14	1/1492 (0.1%)	1.07	4/2026 (0.2%)
1	C	0.95	1/1561 (0.1%)	0.93	1/2122 (0.0%)
1	D	1.01	0/1815	0.98	4/2466 (0.2%)
All	All	1.04	2/6536 (0.0%)	0.99	14/8880 (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	B	0	1
1	D	0	1
All	All	0	2

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	130	TRP	CB-CG	5.71	1.60	1.50
1	C	90	GLU	CG-CD	5.71	1.60	1.51

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	17	ARG	NE-CZ-NH2	-12.72	113.94	120.30
1	A	17	ARG	NE-CZ-NH1	9.00	124.80	120.30
1	B	189	ARG	NE-CZ-NH2	-9.00	115.80	120.30
1	D	17	ARG	NE-CZ-NH2	-7.85	116.37	120.30
1	B	88	ARG	NE-CZ-NH1	-7.57	116.51	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	17	ARG	NE-CZ-NH2	-7.25	116.67	120.30
1	B	87	ASP	CB-CG-OD1	6.41	124.06	118.30
1	A	189	ARG	NE-CZ-NH1	6.08	123.34	120.30
1	D	17	ARG	NE-CZ-NH1	5.66	123.13	120.30
1	A	17	ARG	CD-NE-CZ	5.51	131.31	123.60
1	D	1	LEU	CB-CA-C	5.29	120.25	110.20
1	D	88	ARG	NE-CZ-NH2	-5.24	117.68	120.30
1	A	98	GLU	OE1-CD-OE2	-5.08	117.20	123.30
1	B	189	ARG	CG-CD-NE	-5.05	101.19	111.80

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	0	SER	Peptide
1	D	0	SER	Peptide

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	1629	0	1582	36	0
1	B	1459	0	1409	37	0
1	C	1525	0	1470	46	0
1	D	1769	0	1695	39	0
2	B	10	0	0	0	0
2	D	5	0	0	0	0
3	A	69	0	0	3	0
3	B	73	0	0	4	0
3	C	35	0	0	0	0
3	D	62	0	0	8	0
All	All	6636	0	6156	148	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 12.

All (148) 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:B:102:LEU:O	1:B:130:TRP:HZ3	1.35	1.08
1:D:28:ARG:HH11	1:D:28:ARG:HG3	1.21	1.02
1:A:58:THR:HG21	1:B:86:MSE:SE	2.10	1.02
1:D:28:ARG:CG	1:D:28:ARG:HH11	1.78	0.95
1:B:102:LEU:O	1:B:130:TRP:CZ3	2.24	0.91
1:B:28:ARG:HH11	1:B:28:ARG:HG2	1.37	0.90
1:B:59:ALA:HB3	1:B:62:ARG:HB3	1.62	0.81
1:B:36:ARG:HG2	1:B:37:GLY:H	1.46	0.81
1:D:28:ARG:NH1	1:D:28:ARG:HG3	1.92	0.81
1:A:57:GLU:HG2	1:A:63:TYR:CE1	2.16	0.80
1:D:34:ILE:HD11	1:D:53:VAL:HG22	1.65	0.78
1:A:58:THR:HG22	1:A:59:ALA:N	1.96	0.78
1:D:113:LEU:HD11	1:D:127:LEU:HD21	1.69	0.75
1:B:36:ARG:HG2	1:B:37:GLY:N	2.03	0.74
1:A:188:ARG:O	1:A:192:GLN:HG2	1.87	0.73
1:B:129:ASP:O	1:B:133:ARG:HB2	1.89	0.72
1:B:36:ARG:CG	1:B:37:GLY:H	2.05	0.70
1:C:127:LEU:O	1:C:131:LEU:HD12	1.91	0.69
1:C:172:GLN:C	1:C:174:ASP:H	1.95	0.69
1:A:173:CYS:O	1:A:174:ASP:HB2	1.91	0.69
1:D:28:ARG:CG	1:D:28:ARG:NH1	2.48	0.69
1:A:57:GLU:CG	1:A:63:TYR:CE1	2.78	0.67
1:C:7:MSE:CG	1:C:34:ILE:HD13	2.26	0.66
1:D:113:LEU:HD21	1:D:127:LEU:HD11	1.78	0.65
1:D:171:ASP:HB2	3:D:276:HOH:O	1.96	0.64
1:D:128:GLU:O	1:D:132:GLU:HG3	1.97	0.64
1:C:111:PHE:C	1:C:111:PHE:HD1	2.03	0.62
1:C:7:MSE:HB2	1:C:34:ILE:HD13	1.83	0.61
1:C:28:ARG:NH1	1:C:30:VAL:HG22	2.15	0.61
1:C:111:PHE:C	1:C:111:PHE:CD1	2.73	0.61
1:A:12:ASN:HA	1:A:15:LYS:HD3	1.83	0.60
3:A:256:HOH:O	1:D:60:PRO:HD3	2.02	0.59
1:A:128:GLU:O	1:A:132:GLU:HB3	2.02	0.59
1:A:11:GLY:HA2	1:A:199:MSE:CE	2.33	0.59
1:D:173:CYS:O	1:D:174:ASP:HB2	2.02	0.58
1:C:185:ALA:C	1:C:189:ARG:HH21	2.06	0.58
1:A:117:LYS:HZ2	1:C:147:THR:HG22	1.67	0.58
1:C:166:TYR:O	1:C:169:VAL:HG22	2.03	0.58
1:A:113:LEU:HD21	1:A:127:LEU:HD11	1.87	0.57
1:A:117:LYS:NZ	1:C:147:THR:HG22	2.20	0.57
1:C:114:CYS:O	1:C:115:LEU:HG	2.05	0.57
1:D:201:TRP:CH2	1:D:203:PRO:HA	2.40	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:58:THR:CG2	1:A:59:ALA:H	2.19	0.56
1:D:34:ILE:HD11	1:D:53:VAL:CG2	2.36	0.55
1:A:95:MSE:SE	1:A:158:ILE:HD12	2.57	0.55
1:C:172:GLN:O	1:C:174:ASP:N	2.38	0.55
1:C:7:MSE:CB	1:C:34:ILE:HD13	2.37	0.54
1:C:33:ASP:HB2	1:C:38:GLU:OE1	2.09	0.53
1:B:34:ILE:C	1:B:36:ARG:H	2.11	0.53
1:B:173:CYS:O	1:B:173:CYS:SG	2.67	0.53
1:C:172:GLN:OE1	1:C:172:GLN:N	2.42	0.53
1:B:34:ILE:HD11	1:B:53:VAL:HG12	1.90	0.53
1:D:127:LEU:O	1:D:128:GLU:C	2.48	0.52
1:B:36:ARG:CG	1:B:37:GLY:N	2.69	0.52
1:A:40:ARG:NH1	3:A:252:HOH:O	2.43	0.52
1:D:8:GLN:O	1:D:17:ARG:NH2	2.42	0.52
1:A:58:THR:HG23	3:A:283:HOH:O	2.09	0.52
1:A:91:ALA:O	1:A:95:MSE:HG3	2.10	0.51
1:B:28:ARG:NH1	1:B:28:ARG:HG2	2.16	0.51
1:C:172:GLN:C	1:C:174:ASP:N	2.63	0.51
1:C:28:ARG:HH12	1:C:30:VAL:HG22	1.75	0.51
1:C:111:PHE:HD1	1:C:111:PHE:O	1.94	0.51
1:B:82:PRO:O	1:B:88:ARG:HD2	2.11	0.51
1:B:166:TYR:O	1:B:169:VAL:HG22	2.11	0.51
1:B:133:ARG:HB3	3:B:286:HOH:O	2.10	0.51
1:D:15:LYS:NZ	1:D:98:GLU:OE2	2.42	0.51
1:D:11:GLY:HA2	1:D:199:MSE:CE	2.41	0.50
1:C:90:GLU:HG3	3:D:235:HOH:O	2.12	0.50
1:C:85:ARG:NH1	1:D:73:TYR:O	2.45	0.50
1:D:52:GLN:HB2	3:D:262:HOH:O	2.10	0.50
1:C:34:ILE:HD12	1:C:34:ILE:N	2.25	0.50
1:B:192:GLN:NE2	3:B:266:HOH:O	2.45	0.49
1:A:171:ASP:HA	1:A:175:PHE:O	2.11	0.49
1:A:103:GLU:HB3	1:A:104:PRO:HD3	1.94	0.49
1:C:7:MSE:HG3	1:C:34:ILE:HD13	1.93	0.49
1:B:129:ASP:HB2	1:D:222:HIS:CE1	2.48	0.49
1:C:142:GLU:O	1:C:146:LYS:HG3	2.12	0.49
1:A:55:LEU:HG	1:A:63:TYR:HB3	1.95	0.48
1:B:17:ARG:NH1	3:B:243:HOH:O	2.43	0.48
1:C:7:MSE:SE	1:C:34:ILE:HB	2.63	0.48
1:A:114:CYS:SG	1:A:173:CYS:HB3	2.53	0.48
1:D:75:ALA:HB2	1:D:158:ILE:HG21	1.96	0.48
1:B:34:ILE:HB	1:B:35:LEU:HD23	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:87:ASP:HB3	1:D:153:ALA:HB2	1.96	0.48
1:B:86:MSE:HE2	3:B:253:HOH:O	2.14	0.47
1:B:34:ILE:HD11	1:B:53:VAL:CG1	2.45	0.47
1:A:48:ASN:HA	1:A:49:PRO:HD3	1.81	0.47
1:A:50:SER:HB2	1:A:52:GLN:HG3	1.96	0.47
1:A:7:MSE:SE	1:A:34:ILE:HB	2.65	0.47
1:D:114:CYS:SG	1:D:173:CYS:HB3	2.54	0.47
1:A:7:MSE:O	1:A:17:ARG:NH2	2.48	0.46
1:D:7:MSE:SE	1:D:34:ILE:HG12	2.66	0.46
1:A:33:ASP:OD2	1:A:36:ARG:HD2	2.15	0.46
1:B:11:GLY:HA2	1:B:199:MSE:CE	2.45	0.46
1:D:70:ILE:O	1:D:74:LEU:HG	2.16	0.46
1:A:142:GLU:HG3	1:A:146:LYS:HE2	1.96	0.46
1:B:172:GLN:OE1	1:B:172:GLN:HA	2.16	0.46
1:C:7:MSE:HB2	1:C:34:ILE:CD1	2.45	0.45
1:B:11:GLY:HA2	1:B:199:MSE:HE1	1.97	0.45
1:A:57:GLU:HG2	1:A:63:TYR:CD1	2.50	0.45
1:C:48:ASN:HA	1:C:49:PRO:HD2	1.67	0.45
1:D:102:LEU:HD23	3:D:229:HOH:O	2.17	0.45
1:D:177:LEU:HD23	1:D:184:ASN:HD21	1.82	0.45
1:C:90:GLU:CG	3:D:235:HOH:O	2.64	0.45
1:A:85:ARG:NH2	1:B:73:TYR:O	2.47	0.45
1:A:34:ILE:HD13	1:A:34:ILE:N	2.31	0.45
1:C:158:ILE:HG13	1:C:158:ILE:H	1.54	0.45
1:C:136:ALA:O	1:C:140:VAL:HG23	2.18	0.44
1:C:103:GLU:N	1:C:104:PRO:CD	2.81	0.44
1:D:117:LYS:HD2	3:D:270:HOH:O	2.17	0.44
1:D:1:LEU:HD23	1:D:1:LEU:HA	1.85	0.44
1:D:212:SER:OG	1:D:221:HIS:HE1	2.00	0.44
1:D:96:PHE:O	1:D:100:HIS:CD2	2.70	0.44
1:C:82:PRO:HB2	1:C:87:ASP:HB3	2.00	0.44
1:C:40:ARG:HG2	1:C:45:LEU:HD21	2.00	0.43
1:C:75:ALA:CB	1:C:158:ILE:HG12	2.48	0.43
1:A:86:MSE:HE2	1:B:62:ARG:HG3	2.00	0.43
1:C:90:GLU:HB2	3:D:235:HOH:O	2.17	0.43
1:C:82:PRO:CB	1:C:87:ASP:HB3	2.49	0.43
1:D:4:LEU:HD11	1:D:54:PRO:HB2	2.00	0.43
1:A:62:ARG:NH1	1:B:86:MSE:HE3	2.33	0.43
1:B:201:TRP:CZ2	1:B:203:PRO:HA	2.54	0.43
1:C:177:LEU:HB3	1:C:184:ASN:HD21	1.83	0.42
1:D:113:LEU:HD12	1:D:173:CYS:O	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:65:ALA:O	1:D:66:GLU:HB2	2.19	0.42
1:C:82:PRO:HB2	1:C:87:ASP:CB	2.50	0.42
1:C:59:ALA:HB3	1:C:62:ARG:CB	2.50	0.42
1:C:48:ASN:OD1	1:C:52:GLN:HG3	2.19	0.42
1:B:133:ARG:HG3	1:D:221:HIS:CD2	2.55	0.42
1:B:137:ALA:O	1:B:141:MSE:HG3	2.20	0.41
1:C:106:ILE:O	1:C:106:ILE:HG22	2.20	0.41
1:A:45:LEU:HA	1:A:45:LEU:HD23	1.88	0.41
1:C:177:LEU:HD12	1:C:180:PHE:HB2	2.01	0.41
1:C:58:THR:HG23	1:D:86:MSE:SE	2.71	0.41
1:B:34:ILE:HG22	1:B:35:LEU:H	1.85	0.41
1:C:59:ALA:HB3	1:C:62:ARG:HB3	2.01	0.41
1:D:72:TRP:CZ3	1:D:92:LEU:HG	2.55	0.41
1:B:59:ALA:HB3	1:B:62:ARG:CB	2.42	0.41
1:B:34:ILE:C	1:B:36:ARG:N	2.74	0.41
1:C:34:ILE:CD1	1:C:34:ILE:N	2.83	0.41
1:B:168:HIS:O	1:B:171:ASP:HB3	2.21	0.41
1:A:141:MSE:HE1	1:A:167:THR:OG1	2.21	0.41
1:C:164:TYR:O	1:C:165:GLY:C	2.59	0.41
1:D:212:SER:OG	1:D:221:HIS:CE1	2.74	0.40
1:D:118:GLY:HA2	3:D:230:HOH:O	2.20	0.40
1:A:56:LEU:HD22	1:A:70:ILE:HG23	2.03	0.40
1:B:104:PRO:HA	1:B:130:TRP:CE3	2.56	0.40
1:A:72:TRP:HA	1:A:158:ILE:HD13	2.03	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	202/225 (90%)	196 (97%)	4 (2%)	2 (1%)	19 8

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	179/225 (80%)	171 (96%)	7 (4%)	1 (1%)	30	18
1	C	189/225 (84%)	173 (92%)	10 (5%)	6 (3%)	5	0
1	D	218/225 (97%)	207 (95%)	10 (5%)	1 (0%)	34	22
All	All	788/900 (88%)	747 (95%)	31 (4%)	10 (1%)	15	5

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	49	PRO
1	C	173	CYS
1	C	175	PHE
1	B	2	TYR
1	A	58	THR
1	A	174	ASP
1	C	174	ASP
1	C	176	ASP
1	D	174	ASP
1	C	59	ALA

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	168/178 (94%)	157 (94%)	11 (6%)	21	11
1	B	150/178 (84%)	134 (89%)	16 (11%)	8	2
1	C	154/178 (86%)	135 (88%)	19 (12%)	6	1
1	D	181/178 (102%)	165 (91%)	16 (9%)	12	5
All	All	653/712 (92%)	591 (90%)	62 (10%)	11	4

All (62) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	TYR

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Mol	Chain	Res	Type
1	A	34	ILE
1	A	99	GLN
1	A	117	LYS
1	A	121	ASP
1	A	127	LEU
1	A	128	GLU
1	A	132	GLU
1	A	143	ASN
1	A	179	THR
1	A	192	GLN
1	B	0	SER
1	B	1	LEU
1	B	9	ARG
1	B	28	ARG
1	B	34	ILE
1	B	35	LEU
1	B	40	ARG
1	B	49	PRO
1	B	102	LEU
1	B	128	GLU
1	B	130	TRP
1	B	131	LEU
1	B	173	CYS
1	B	174	ASP
1	B	177	LEU
1	B	188	ARG
1	C	1	LEU
1	C	7	MSE
1	C	33	ASP
1	C	34	ILE
1	C	50	SER
1	C	58	THR
1	C	103	GLU
1	C	111	PHE
1	C	114	CYS
1	C	147	THR
1	C	158	ILE
1	C	168	HIS
1	C	171	ASP
1	C	173	CYS
1	C	177	LEU
1	C	179	THR

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Mol	Chain	Res	Type
1	C	188	ARG
1	C	189	ARG
1	C	200	ASP
1	D	0	SER
1	D	3	LYS
1	D	10	SER
1	D	15	LYS
1	D	28	ARG
1	D	58	THR
1	D	86	MSE
1	D	103	GLU
1	D	115	LEU
1	D	125	HIS
1	D	127	LEU
1	D	128	GLU
1	D	171	ASP
1	D	179	THR
1	D	188	ARG
1	D	223	HIS

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

Mol	Chain	Res	Type
1	A	105	ASN
1	B	144	HIS
1	B	184	ASN
1	B	192	GLN
1	C	52	GLN
1	C	105	ASN
1	D	48	ASN
1	D	105	ASN
1	D	144	HIS
1	D	172	GLN
1	D	184	ASN
1	D	221	HIS

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 ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

3 ligands are modelled in this entry.

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	B	230	-	4,4,4	0.30	0	6,6,6	1.27	1 (16%)
2	SO4	B	232	-	4,4,4	0.14	0	6,6,6	0.33	0
2	SO4	D	231	-	4,4,4	0.21	0	6,6,6	0.96	0

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
2	SO4	B	230	-	-	0/0/0/0	0/0/0/0
2	SO4	B	232	-	-	0/0/0/0	0/0/0/0
2	SO4	D	231	-	-	0/0/0/0	0/0/0/0

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	230	SO4	O2-S-O1	2.38	117.05	109.50

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

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

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	199/225 (88%)	-0.05	4 (2%) 68 73	18, 31, 50, 55	0
1	B	178/225 (79%)	0.21	7 (3%) 43 48	18, 28, 59, 66	0
1	C	188/225 (83%)	0.82	34 (18%) 2 2	24, 46, 81, 88	0
1	D	217/225 (96%)	0.29	11 (5%) 32 36	23, 37, 59, 69	0
All	All	782/900 (86%)	0.31	56 (7%) 18 22	18, 35, 63, 88	0

All (56) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	35	LEU	6.1
1	C	40	ARG	5.3
1	C	114	CYS	5.1
1	D	206	ILE	4.6
1	C	110	TYR	4.6
1	C	33	ASP	4.1
1	B	35	LEU	4.0
1	D	0	SER	4.0
1	C	112	TRP	4.0
1	C	45	LEU	3.9
1	A	59	ALA	3.9
1	B	1	LEU	3.9
1	C	34	ILE	3.8
1	B	174	ASP	3.8
1	C	170	ALA	3.8
1	C	177	LEU	3.8
1	C	174	ASP	3.7
1	C	109	ALA	3.6
1	B	130	TRP	3.5
1	D	115	LEU	3.4
1	D	222	HIS	3.3

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Mol	Chain	Res	Type	RSRZ
1	C	41	THR	3.3
1	C	49	PRO	3.2
1	D	117	LYS	3.2
1	C	42	PRO	3.2
1	C	46	ALA	3.0
1	C	173	CYS	2.9
1	C	111	PHE	2.8
1	A	125	HIS	2.8
1	C	39	SER	2.8
1	D	121	ASP	2.8
1	D	211	THR	2.7
1	C	176	ASP	2.7
1	C	37	GLY	2.6
1	C	115	LEU	2.6
1	C	61	GLY	2.6
1	C	106	ILE	2.5
1	C	59	ALA	2.5
1	C	172	GLN	2.5
1	C	60	PRO	2.4
1	D	40	ARG	2.4
1	C	135	TYR	2.4
1	C	179	THR	2.4
1	A	203	PRO	2.3
1	B	203	PRO	2.3
1	C	171	ASP	2.3
1	D	128	GLU	2.3
1	C	63	TYR	2.3
1	C	167	THR	2.3
1	D	223	HIS	2.2
1	B	175	PHE	2.1
1	C	146	LYS	2.1
1	A	177	LEU	2.1
1	C	175	PHE	2.1
1	D	36	ARG	2.1
1	B	34	ILE	2.0

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

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

6.3 Carbohydrates [i](#)

There are no carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(\AA^2)	Q<0.9
2	SO4	B	232	5/5	0.96	0.12	-0.38	83,84,85,86	0
2	SO4	D	231	5/5	0.94	0.10	-	59,62,64,64	0
2	SO4	B	230	5/5	0.95	0.10	-	55,58,58,62	0

6.5 Other polymers [i](#)

There are no such residues in this entry.