



Full wwPDB X-ray Structure Validation Report ⓘ

Sep 5, 2023 – 03:01 PM EDT

PDB ID : 4DLL
Title : Crystal structure of a 2-hydroxy-3-oxopropionate reductase from *Polaromonas* sp. JS666
Authors : Agarwal, R.; Chamala, S.; Evans, B.; Foti, R.; Gizzi, A.; Hillerich, B.; Kar, A.; Lafleur, J.; Seidel, R.; Villigas, G.; Zencheck, W.; Almo, S.C.; Swaminathan, S.; New York Structural Genomics Research Consortium (NYSGRG)
Deposited on : 2012-02-06
Resolution : 2.11 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 : 1.8.5 (274361), CSD as541be (2020)
Xtrriage (Phenix) : 1.13
EDS : 2.35
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) : 2.35

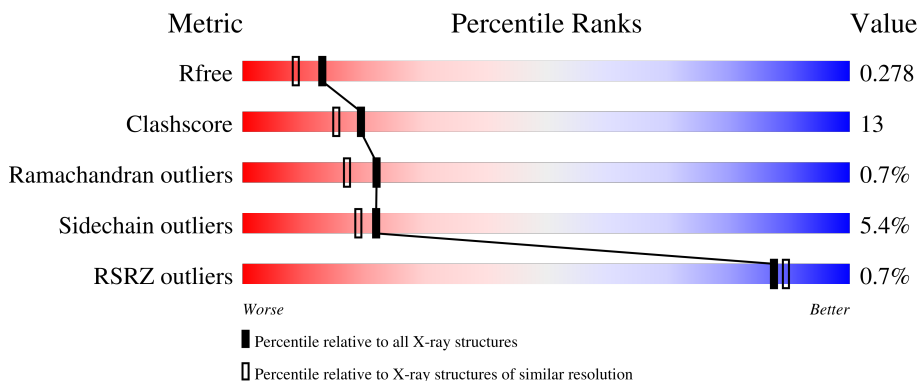
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.11 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	6241 (2.14-2.10)
Clashscore	141614	6778 (2.14-2.10)
Ramachandran outliers	138981	6705 (2.14-2.10)
Sidechain outliers	138945	6706 (2.14-2.10)
RSRZ outliers	127900	6112 (2.14-2.10)

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	320	 69% 18% 10%
1	B	320	 66% 20% 11%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	SO4	A	401	-	-	X	-

2 Entry composition i

There are 3 unique types of molecules in this entry. The entry contains 4240 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 2-hydroxy-3-oxopropionate reductase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	S	Se			
1	A	288	2081	1311	374	385	1	10	0	0	0
1	B	285	2034	1275	363	385	1	10	0	0	0

There are 44 discrepancies between the modelled and reference sequences:

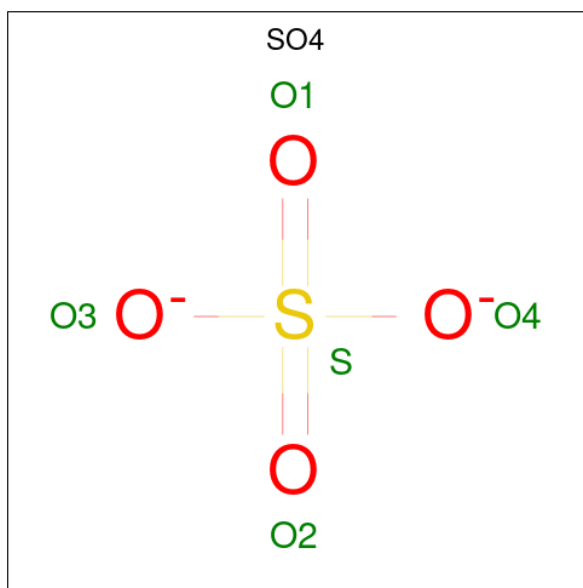
Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MSE	-	expression tag	UNP Q12CU4
A	2	HIS	-	expression tag	UNP Q12CU4
A	3	HIS	-	expression tag	UNP Q12CU4
A	4	HIS	-	expression tag	UNP Q12CU4
A	5	HIS	-	expression tag	UNP Q12CU4
A	6	HIS	-	expression tag	UNP Q12CU4
A	7	HIS	-	expression tag	UNP Q12CU4
A	8	SER	-	expression tag	UNP Q12CU4
A	9	SER	-	expression tag	UNP Q12CU4
A	10	GLY	-	expression tag	UNP Q12CU4
A	11	VAL	-	expression tag	UNP Q12CU4
A	12	ASP	-	expression tag	UNP Q12CU4
A	13	LEU	-	expression tag	UNP Q12CU4
A	14	GLY	-	expression tag	UNP Q12CU4
A	15	THR	-	expression tag	UNP Q12CU4
A	16	GLU	-	expression tag	UNP Q12CU4
A	17	ASN	-	expression tag	UNP Q12CU4
A	18	LEU	-	expression tag	UNP Q12CU4
A	19	TYR	-	expression tag	UNP Q12CU4
A	20	PHE	-	expression tag	UNP Q12CU4
A	21	GLN	-	expression tag	UNP Q12CU4
A	22	SER	-	expression tag	UNP Q12CU4
B	1	MSE	-	expression tag	UNP Q12CU4
B	2	HIS	-	expression tag	UNP Q12CU4
B	3	HIS	-	expression tag	UNP Q12CU4

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Chain	Residue	Modelled	Actual	Comment	Reference
B	4	HIS	-	expression tag	UNP Q12CU4
B	5	HIS	-	expression tag	UNP Q12CU4
B	6	HIS	-	expression tag	UNP Q12CU4
B	7	HIS	-	expression tag	UNP Q12CU4
B	8	SER	-	expression tag	UNP Q12CU4
B	9	SER	-	expression tag	UNP Q12CU4
B	10	GLY	-	expression tag	UNP Q12CU4
B	11	VAL	-	expression tag	UNP Q12CU4
B	12	ASP	-	expression tag	UNP Q12CU4
B	13	LEU	-	expression tag	UNP Q12CU4
B	14	GLY	-	expression tag	UNP Q12CU4
B	15	THR	-	expression tag	UNP Q12CU4
B	16	GLU	-	expression tag	UNP Q12CU4
B	17	ASN	-	expression tag	UNP Q12CU4
B	18	LEU	-	expression tag	UNP Q12CU4
B	19	TYR	-	expression tag	UNP Q12CU4
B	20	PHE	-	expression tag	UNP Q12CU4
B	21	GLN	-	expression tag	UNP Q12CU4
B	22	SER	-	expression tag	UNP Q12CU4

- 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	B	1	Total	O	S	0	0
			5	4	1		

- Molecule 3 is water.

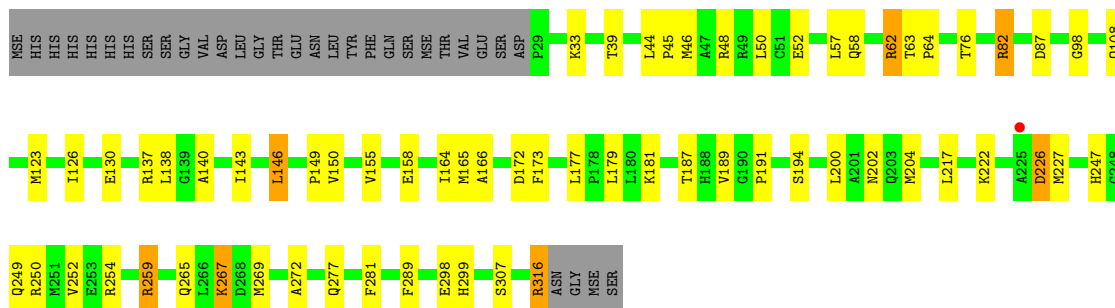
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	59	Total 59	O 59	0	0
3	B	56	Total 56	O 56	0	0

3 Residue-property plots

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.

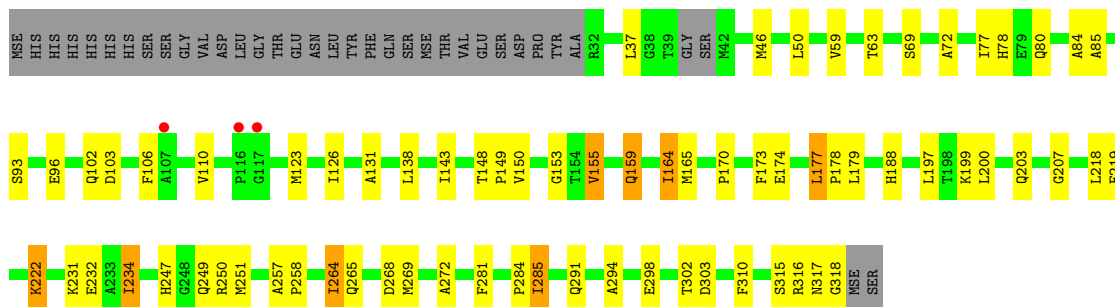
- Molecule 1: 2-hydroxy-3-oxopropionate reductase

Chain A: 



- Molecule 1: 2-hydroxy-3-oxopropionate reductase

Chain B: 



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	39.87Å 47.01Å 77.50Å 92.14° 95.30° 101.19°	Depositor
Resolution (Å)	38.52 – 2.11 38.52 – 2.11	Depositor EDS
% Data completeness (in resolution range)	93.8 (38.52-2.11) 93.8 (38.52-2.11)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.86 (at 2.12Å)	Xtrriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.218 , 0.278 0.220 , 0.278	Depositor DCC
R_{free} test set	1484 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	37.4	Xtrriage
Anisotropy	0.134	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 41.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	4240	wwPDB-VP
Average B, all atoms (Å ²)	40.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.84% 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

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	0.94	0/2103	0.91	2/2830 (0.1%)
1	B	0.85	1/2054 (0.0%)	0.90	2/2770 (0.1%)
All	All	0.89	1/4157 (0.0%)	0.90	4/5600 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	222	LYS	CE-NZ	-5.07	1.36	1.49

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	250	ARG	NE-CZ-NH1	5.81	123.20	120.30
1	A	146	LEU	CB-CG-CD1	-5.61	101.45	111.00
1	A	146	LEU	CB-CG-CD2	-5.60	101.47	111.00
1	B	250	ARG	NE-CZ-NH2	-5.23	117.69	120.30

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	2081	0	2079	61	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	2034	0	1999	54	0
2	A	5	0	0	2	0
2	B	5	0	0	1	0
3	A	59	0	0	2	0
3	B	56	0	0	3	0
All	All	4240	0	4078	105	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 13.

All (105) 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:207:GLY:HA3	1:B:269:MSE:HE1	1.25	1.13
1:A:204:MSE:HE2	1:A:272:ALA:HB1	1.25	1.10
1:A:62:ARG:HH11	1:A:62:ARG:HG3	1.02	1.10
1:A:222:LYS:HG3	1:B:281:PHE:HD1	1.33	0.91
1:A:204:MSE:HE2	1:A:272:ALA:CB	2.00	0.91
1:A:62:ARG:HG3	1:A:62:ARG:NH1	1.81	0.87
1:B:207:GLY:HA3	1:B:269:MSE:CE	2.04	0.86
1:A:217:LEU:HD13	1:A:227:MSE:HE3	1.60	0.83
1:A:222:LYS:HG3	1:B:281:PHE:CD1	2.13	0.83
1:A:166:ALA:O	1:A:189:VAL:HG22	1.80	0.81
1:A:62:ARG:HH11	1:A:62:ARG:CG	1.91	0.81
1:A:281:PHE:CD1	1:B:222:LYS:HG3	2.16	0.80
1:A:281:PHE:HD1	1:B:222:LYS:HG3	1.53	0.73
1:B:258:PRO:HG3	1:B:303:ASP:O	1.89	0.72
1:B:155:VAL:O	1:B:159:GLN:HG2	1.89	0.72
1:B:318:GLY:C	3:B:510:HOH:O	2.28	0.70
1:B:50:LEU:HD11	1:B:179:LEU:HD11	1.73	0.70
1:A:50:LEU:HD11	1:A:179:LEU:HD11	1.72	0.70
1:A:204:MSE:HE1	1:B:219:PHE:CE2	2.27	0.69
1:B:294:ALA:O	1:B:298:GLU:HG3	1.97	0.64
1:B:102:GLN:HG3	1:B:106:PHE:HD2	1.63	0.64
1:B:155:VAL:O	1:B:159:GLN:CG	2.47	0.63
1:B:265:GLN:HE21	1:B:269:MSE:HE2	1.64	0.63
1:A:298:GLU:CB	3:A:505:HOH:O	2.46	0.63
1:A:63:THR:HG22	2:A:401:SO4:O2	2.01	0.61
1:A:204:MSE:HE1	1:B:219:PHE:CZ	2.38	0.59
1:B:302:THR:HG22	3:B:538:HOH:O	2.01	0.58
1:A:227:MSE:HE2	1:A:252:VAL:HG22	1.84	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:218:LEU:O	1:B:222:LYS:HG2	2.05	0.57
1:A:50:LEU:HD11	1:A:179:LEU:CD1	2.35	0.57
1:A:177:LEU:HG	1:A:181:LYS:HE2	1.87	0.57
1:A:189:VAL:HG23	1:A:194:SER:HB3	1.87	0.57
1:A:146:LEU:HD12	1:A:146:LEU:N	2.21	0.56
1:A:58:GLN:OE1	1:A:76:THR:HB	2.06	0.56
1:B:265:GLN:HE21	1:B:269:MSE:CE	2.18	0.56
1:A:137:ARG:O	1:A:140:ALA:HB3	2.06	0.56
1:B:138:LEU:HB3	1:B:143:ILE:HB	1.88	0.55
1:B:46:MSE:HE1	1:B:123:MSE:SE	2.57	0.55
1:B:78:HIS:HB2	1:B:84:ALA:HB2	1.89	0.55
1:A:247:HIS:HB3	1:A:307:SER:HB3	1.87	0.55
1:B:85:ALA:CB	1:B:110:VAL:HG13	2.37	0.55
1:A:177:LEU:O	1:A:181:LYS:HG2	2.07	0.54
1:B:200:LEU:HD13	1:B:272:ALA:HA	1.89	0.54
1:B:247:HIS:O	1:B:251:MSE:HG3	2.08	0.54
1:A:45:PRO:HB3	1:A:158:GLU:HG2	1.90	0.53
1:B:291:GLN:HA	1:B:291:GLN:OE1	2.10	0.52
1:A:62:ARG:NH1	1:A:62:ARG:CG	2.58	0.52
1:B:203:GLN:HG3	1:B:268:ASP:OD2	2.10	0.52
1:B:123:MSE:HG2	1:B:148:THR:O	2.09	0.52
1:A:200:LEU:C	1:A:204:MSE:HE3	2.30	0.51
1:A:166:ALA:O	1:A:189:VAL:CG2	2.57	0.51
1:A:265:GLN:NE2	1:A:269:MSE:HE3	2.26	0.50
1:A:98:GLY:HA3	1:A:130:GLU:OE2	2.12	0.50
1:A:82:ARG:HG2	1:A:108:GLN:O	2.11	0.49
1:B:150:VAL:HG22	1:B:164:ILE:HD13	1.94	0.49
1:B:63:THR:HG23	2:B:401:SO4:O2	2.13	0.49
1:B:218:LEU:HD21	1:B:310:PHE:CZ	2.47	0.49
1:B:150:VAL:O	1:B:199:LYS:NZ	2.31	0.49
1:A:33:LYS:NZ	1:A:87:ASP:OD2	2.46	0.49
1:A:50:LEU:HD23	1:A:57:LEU:HD13	1.95	0.49
1:A:298:GLU:O	1:A:299:HIS:HB2	2.13	0.48
1:B:126:ILE:HD11	1:B:131:ALA:HB2	1.95	0.48
1:B:80:GLN:HG3	3:B:532:HOH:O	2.14	0.48
1:A:146:LEU:HD21	1:A:173:PHE:HA	1.95	0.48
1:B:231:LYS:NZ	1:B:249:GLN:HE21	2.11	0.48
1:B:69:SER:O	1:B:72:ALA:HB3	2.14	0.48
1:A:82:ARG:HG3	3:A:529:HOH:O	2.14	0.47
1:A:146:LEU:HD11	1:A:172:ASP:HB3	1.96	0.47
1:A:227:MSE:HE2	1:A:252:VAL:HA	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:265:GLN:HE21	1:A:269:MSE:HE3	1.80	0.47
1:B:59:VAL:HB	1:B:77:ILE:CD1	2.45	0.47
1:B:247:HIS:H	1:B:247:HIS:CD2	2.33	0.47
1:A:249:GLN:NE2	1:A:249:GLN:HA	2.30	0.46
1:A:63:THR:HA	1:A:64:PRO:HD3	1.81	0.46
1:A:204:MSE:CE	1:A:272:ALA:HB1	2.18	0.46
1:A:187:THR:HG23	1:B:232:GLU:OE2	2.16	0.46
1:A:289:PHE:CZ	1:B:285:ILE:HD12	2.49	0.46
1:A:150:VAL:HG12	1:A:164:ILE:HG12	1.97	0.46
1:A:316:ARG:NH2	1:B:284:PRO:HG3	2.32	0.45
1:A:39:THR:OG1	2:A:401:SO4:O2	2.33	0.45
1:A:149:PRO:O	1:A:165:MSE:HE3	2.17	0.44
1:A:149:PRO:HD2	1:A:165:MSE:O	2.18	0.44
1:B:265:GLN:HG3	1:B:269:MSE:HE2	1.99	0.44
1:B:231:LYS:HZ1	1:B:249:GLN:HE21	1.66	0.44
1:A:267:LYS:HB3	1:A:267:LYS:HE3	1.87	0.43
1:A:46:MSE:HE1	1:A:123:MSE:SE	2.68	0.43
1:A:202:ASN:HD22	1:B:234:ILE:HG12	1.84	0.43
1:A:298:GLU:O	1:A:299:HIS:CB	2.67	0.43
1:B:264:ILE:H	1:B:264:ILE:HG12	1.52	0.43
1:A:50:LEU:HA	1:A:50:LEU:HD12	1.72	0.43
1:B:170:PRO:O	1:B:174:GLU:HG2	2.18	0.43
1:B:177:LEU:O	1:B:178:PRO:C	2.56	0.42
1:A:191:PRO:O	1:A:194:SER:HB2	2.20	0.42
1:B:149:PRO:HD2	1:B:165:MSE:O	2.19	0.42
1:A:48:ARG:HG2	1:A:52:GLU:OE2	2.20	0.42
1:A:200:LEU:O	1:A:204:MSE:HE3	2.20	0.42
1:A:138:LEU:HB3	1:A:143:ILE:HB	2.02	0.42
1:A:250:ARG:NH2	1:A:259:ARG:HG3	2.36	0.41
1:B:59:VAL:HB	1:B:77:ILE:HD12	2.03	0.41
1:B:315:SER:O	1:B:317:ASN:N	2.54	0.41
1:B:257:ALA:HA	1:B:258:PRO:HD3	1.87	0.41
1:B:173:PHE:CE1	1:B:188:HIS:HB2	2.55	0.40
1:B:50:LEU:HD11	1:B:179:LEU:CD1	2.47	0.40
1:A:82:ARG:HG3	1:A:82:ARG:H	1.59	0.40
1:B:153:GLY:C	1:B:155:VAL:N	2.75	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	286/320 (89%)	274 (96%)	10 (4%)	2 (1%)	22	17
1	B	281/320 (88%)	269 (96%)	10 (4%)	2 (1%)	22	17
All	All	567/640 (89%)	543 (96%)	20 (4%)	4 (1%)	22	17

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	254	ARG
1	B	316	ARG
1	A	226	ASP
1	B	103	ASP

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	197/225 (88%)	187 (95%)	10 (5%)	24	21
1	B	191/225 (85%)	180 (94%)	11 (6%)	20	17
All	All	388/450 (86%)	367 (95%)	21 (5%)	22	19

All (21) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	44	LEU
1	A	62	ARG

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Mol	Chain	Res	Type
1	A	82	ARG
1	A	126	ILE
1	A	155	VAL
1	A	226	ASP
1	A	259	ARG
1	A	267	LYS
1	A	277	GLN
1	A	316	ARG
1	B	37	LEU
1	B	93	SER
1	B	96	GLU
1	B	155	VAL
1	B	159	GLN
1	B	164	ILE
1	B	177	LEU
1	B	197	LEU
1	B	234	ILE
1	B	264	ILE
1	B	285	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	192	HIS
1	A	196	GLN
1	A	202	ASN
1	A	245	GLN
1	A	247	HIS
1	A	249	GLN
1	A	265	GLN
1	A	277	GLN
1	A	306	GLN
1	B	145	HIS
1	B	196	GLN
1	B	247	HIS
1	B	249	GLN
1	B	265	GLN
1	B	306	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](#)

2 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	401	-	4,4,4	0.23	0	6,6,6	0.29	0
2	SO4	A	401	-	4,4,4	0.18	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.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	401	SO4	1	0
2	A	401	SO4	2	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	278/320 (86%)	0.12	1 (0%) 92 93	20, 39, 52, 60	0
1	B	275/320 (85%)	0.20	3 (1%) 80 84	23, 43, 54, 60	0
All	All	553/640 (86%)	0.16	4 (0%) 87 89	20, 41, 54, 60	0

All (4) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	116	PRO	2.3
1	A	225	ALA	2.1
1	B	117	GLY	2.1
1	B	107	ALA	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	401	5/5	0.99	0.09	43,44,47,47	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	SO4	B	401	5/5	0.99	0.12	52,52,53,56	0

6.5 Other polymers [i](#)

There are no such residues in this entry.