



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 07:59 PM UTC

PDB ID : 2P7J / pdb_00002p7j
Title : Crystal structure of the domain of putative sensory box/GGDEF family protein from *Vibrio parahaemolyticus*
Authors : Wu, R.; James, A.; Joachimiak, A.; Midwest Center for Structural Genomics (MCSG)
Deposited on : 2007-03-20
Resolution : 2.25 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

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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	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

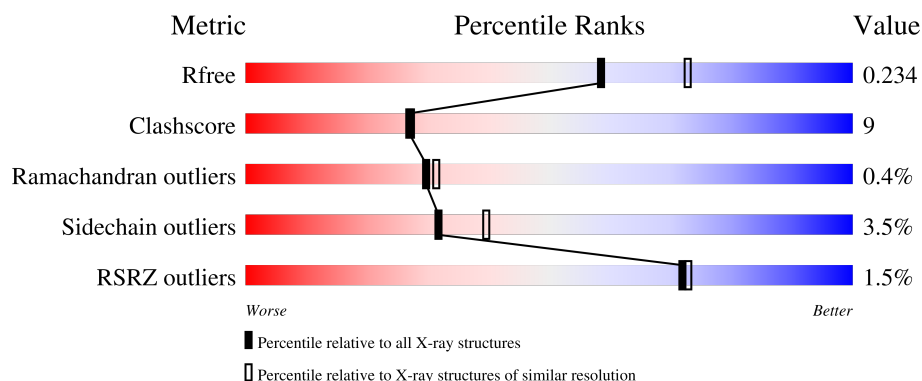
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.25 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}	180053	1898 (2.26-2.26)
Clashscore	190562	2005 (2.26-2.26)
Ramachandran outliers	187476	1965 (2.26-2.26)
Sidechain outliers	187428	1966 (2.26-2.26)
RSRZ outliers	180081	1898 (2.26-2.26)

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	287	% 79% 11% • 8%
1	B	287	2% 79% 12% • 5%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 4836 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 sensory box/GGDEF family protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	265	Total	C	N	O	Se	0	7	0
			2219	1408	378	430	3			
1	B	274	Total	C	N	O	Se	0	6	0
			2281	1444	387	446	4			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	ASN	-	cloning artifact	UNP Q87SR8
A	67	MSE	MET	modified residue	UNP Q87SR8
A	155	MSE	MET	modified residue	UNP Q87SR8
A	224	MSE	MET	modified residue	UNP Q87SR8
B	0	ASN	-	cloning artifact	UNP Q87SR8
B	67	MSE	MET	modified residue	UNP Q87SR8
B	155	MSE	MET	modified residue	UNP Q87SR8
B	224	MSE	MET	modified residue	UNP Q87SR8

- Molecule 2 is SULFATE ION (CCD ID: SO4) (formula: O₄S).

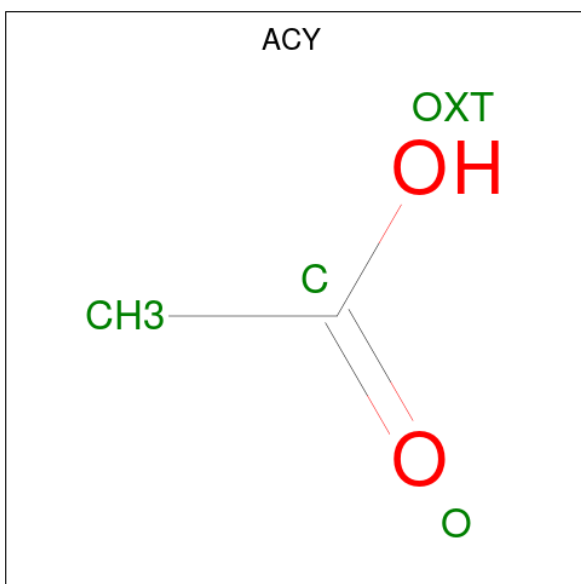


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		

- Molecule 3 is SODIUM ION (CCD ID: NA) (formula: Na).

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

- Molecule 4 is ACETIC ACID (CCD ID: ACY) (formula: C₂H₄O₂).



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

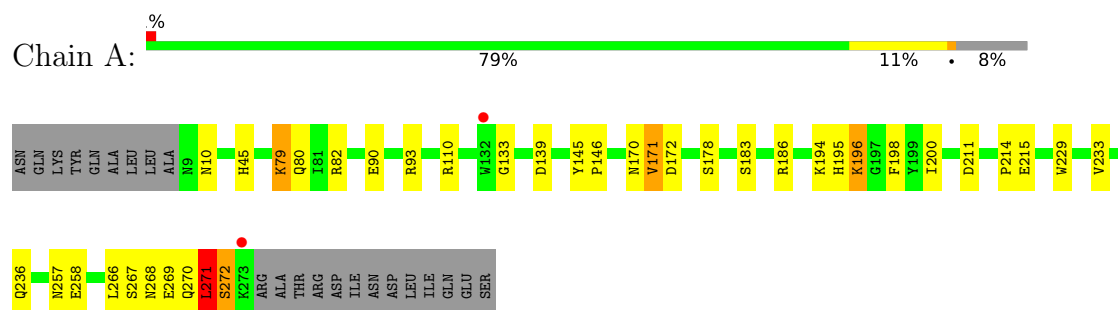
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	172	Total	O	0	0
			172	172		
5	B	149	Total	O	0	0
			149	149		

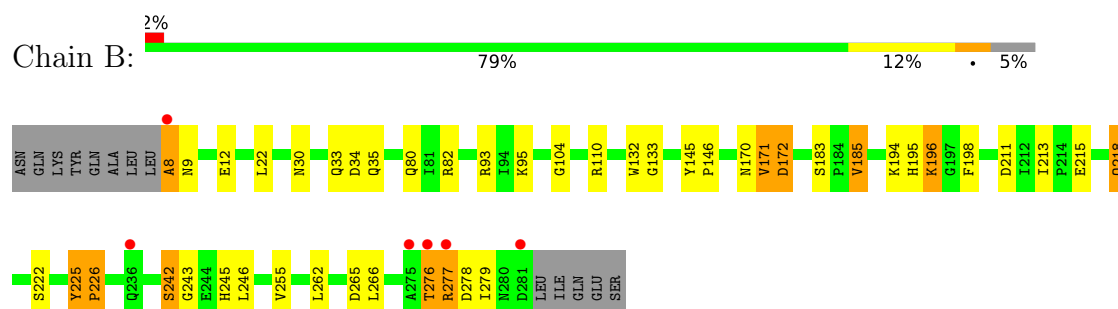
3 Residue-property plots

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: Putative sensory box/GGDEF family protein



- Molecule 1: Putative sensory box/GGDEF family protein



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	72.98Å 81.60Å 121.85Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	38.69 – 2.25 38.69 – 2.25	Depositor EDS
% Data completeness (in resolution range)	99.0 (38.69-2.25) 98.9 (38.69-2.25)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	6.84 (at 2.24Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.193 , 0.239 (Not available) , 0.234	Depositor DCC
R_{free} test set	1746 reflections (4.96%)	wwPDB-VP
Wilson B-factor (Å ²)	40.0	Xtriage
Anisotropy	0.028	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 41.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	4836	wwPDB-VP
Average B, all atoms (Å ²)	42.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.89% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ACY, 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	0.80	1/2263 (0.0%)	0.97	7/3058 (0.2%)
1	B	0.82	1/2325 (0.0%)	1.00	10/3142 (0.3%)
All	All	0.81	2/4588 (0.0%)	0.99	17/6200 (0.3%)

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	2
1	B	0	2
All	All	0	4

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	185	VAL	CA-CB	5.69	1.61	1.54
1	A	271	LEU	CA-C	5.13	1.59	1.52

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	271	LEU	N-CA-C	11.24	127.13	113.41
1	B	226	PRO	N-CA-C	-10.12	100.61	114.27
1	B	172	ASP	N-CA-C	-9.91	87.78	107.69
1	A	172	ASP	N-CA-C	-9.67	88.25	107.69
1	B	242	SER	N-CA-C	8.18	123.62	112.90
1	B	225	TYR	N-CA-C	8.15	122.83	109.79
1	A	195	HIS	CA-C-N	6.58	129.76	120.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	195	HIS	C-N-CA	6.58	129.76	120.28
1	B	8	ALA	CA-C-N	5.75	132.05	121.70
1	B	8	ALA	C-N-CA	5.75	132.05	121.70
1	A	271	LEU	CA-C-N	5.55	131.69	121.70
1	A	271	LEU	C-N-CA	5.55	131.69	121.70
1	A	171	VAL	CB-CA-C	-5.54	103.62	111.21
1	B	171	VAL	CB-CA-C	-5.18	104.12	111.21
1	B	104	GLY	CA-C-N	5.08	125.06	120.03
1	B	104	GLY	C-N-CA	5.08	125.06	120.03
1	B	276	THR	N-CA-C	5.05	116.35	109.18

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	171	VAL	Peptide
1	A	271	LEU	Peptide
1	B	171	VAL	Peptide
1	B	225	TYR	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	2219	0	2165	32	1
1	B	2281	0	2220	55	1
2	A	5	0	0	0	0
2	B	5	0	0	0	0
3	B	1	0	0	0	0
4	B	4	0	3	0	0
5	A	172	0	0	7	0
5	B	149	0	0	14	0
All	All	4836	0	4388	82	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 9.

All (82) 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:139[A]:ASP:OD1	5:A:646:HOH:O	1.90	0.88
1:B:35:GLN:OE1	5:B:730:HOH:O	1.91	0.87
1:B:33:GLN:HE21	1:B:255:VAL:H	1.22	0.85
1:B:132:TRP:HB3	5:B:724:HOH:O	1.77	0.84
1:B:196:LYS:HE3	1:B:198:PHE:HD2	1.43	0.83
1:B:33:GLN:NE2	1:B:255:VAL:H	1.79	0.78
1:A:110[A]:ARG:NH2	5:A:646:HOH:O	2.01	0.77
1:B:82:ARG:HH21	1:B:170:ASN:HD21	1.35	0.74
1:A:82:ARG:HH21	1:A:170:ASN:HD21	1.32	0.74
1:B:245:HIS:HD2	1:B:265:ASP:OD1	1.71	0.72
1:B:196:LYS:HE3	1:B:198:PHE:CD2	2.28	0.68
1:B:277:ARG:NH1	5:B:702:HOH:O	2.27	0.68
1:B:33:GLN:HE21	1:B:255:VAL:N	1.91	0.68
1:A:110[A]:ARG:NE	5:A:646:HOH:O	2.16	0.68
1:B:196:LYS:C	1:B:196:LYS:HD3	2.18	0.68
1:B:196:LYS:CE	1:B:198:PHE:HD2	2.07	0.66
1:A:268:ASN:O	1:A:272:SER:HB2	1.95	0.66
1:B:218:GLN:NE2	1:B:218:GLN:H	1.93	0.66
1:B:145:TYR:HA	1:B:146:PRO:C	2.22	0.65
1:B:276:THR:CG2	5:B:728:HOH:O	2.45	0.65
1:B:183:SER:HB2	5:B:640:HOH:O	1.97	0.64
1:B:195:HIS:HE1	5:B:639:HOH:O	1.82	0.62
1:B:277:ARG:HD3	1:B:279:ILE:H	1.64	0.62
1:A:110[A]:ARG:HH22	1:B:110:ARG:HH12	1.48	0.61
1:A:110[A]:ARG:NH2	1:B:110:ARG:HH22	1.98	0.61
1:B:196:LYS:HD2	1:B:196:LYS:H	1.65	0.60
1:B:213:ILE:HG22	1:B:215[A]:GLU:HG2	1.84	0.59
1:B:132:TRP:CB	5:B:724:HOH:O	2.43	0.59
1:A:186:ARG:HG2	5:A:642:HOH:O	2.02	0.57
1:B:198:PHE:CD2	1:B:211:ASP:HB3	2.40	0.57
1:B:80:GLN:NE2	1:B:93:ARG:HE	2.03	0.57
1:B:242:SER:CB	5:B:708:HOH:O	2.51	0.57
1:A:110[A]:ARG:HH22	1:B:110:ARG:HH22	1.55	0.54
1:B:277:ARG:HD3	1:B:279:ILE:HG22	1.88	0.54
1:B:196:LYS:C	1:B:196:LYS:CD	2.80	0.54
1:A:194:LYS:HD3	1:A:200:ILE:HD11	1.90	0.54
1:B:277:ARG:CD	1:B:279:ILE:HG22	2.38	0.54
1:B:218:GLN:H	1:B:218:GLN:HE21	1.57	0.53
1:A:236:GLN:HB3	5:A:628:HOH:O	2.08	0.52
1:B:33:GLN:HG3	1:B:255:VAL:HG22	1.91	0.52
1:B:242:SER:N	1:B:243:GLY:HA2	2.24	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:132:TRP:N	5:B:724:HOH:O	2.26	0.52
1:A:196:LYS:HG2	1:A:198:PHE:HD2	1.75	0.51
1:A:145:TYR:HA	1:A:146:PRO:C	2.36	0.50
1:B:245:HIS:CD2	1:B:265:ASP:OD1	2.58	0.50
1:A:80:GLN:NE2	1:A:93:ARG:HE	2.09	0.50
1:A:266:LEU:HA	1:A:270:GLN:OE1	2.12	0.50
1:B:213:ILE:HG22	1:B:215[A]:GLU:CG	2.41	0.50
1:B:279:ILE:O	1:B:279:ILE:HG13	2.13	0.49
1:B:12:GLU:H	1:B:12:GLU:CD	2.21	0.48
1:B:195:HIS:HD2	5:B:659:HOH:O	1.96	0.48
1:A:90:GLU:OE1	1:A:110[B]:ARG:NH1	2.47	0.47
1:A:82:ARG:HH21	1:A:170:ASN:ND2	2.08	0.47
1:B:8:ALA:HB3	1:B:9:ASN:HB2	1.96	0.47
1:B:194:LYS:HE3	5:B:663:HOH:O	2.14	0.47
1:B:276:THR:HG21	5:B:728:HOH:O	2.10	0.47
1:B:222:SER:O	1:B:226:PRO:HA	2.16	0.46
1:A:110[A]:ARG:HH22	1:B:110:ARG:NH1	2.12	0.46
1:A:267:SER:O	1:A:271:LEU:HB2	2.15	0.46
1:B:80:GLN:HE21	1:B:93:ARG:HE	1.63	0.45
1:B:218:GLN:HE21	1:B:218:GLN:N	2.14	0.45
1:A:79:LYS:HE2	1:A:79:LYS:HB2	1.34	0.45
1:A:196:LYS:CG	1:A:198:PHE:HD2	2.29	0.45
1:B:194:LYS:HE2	1:B:196:LYS:HE2	2.00	0.44
1:A:267:SER:OG	1:A:269:GLU:HG2	2.17	0.44
1:B:196:LYS:HZ2	1:B:196:LYS:HG2	1.39	0.44
1:A:269:GLU:O	1:A:272:SER:HB3	2.18	0.44
1:B:195:HIS:CE1	5:B:639:HOH:O	2.65	0.44
1:A:45:HIS:HD2	5:A:547:HOH:O	2.01	0.43
1:A:80:GLN:HE21	1:A:93:ARG:HE	1.65	0.43
1:A:139[A]:ASP:CG	5:A:646:HOH:O	2.46	0.43
1:A:229:TRP:O	1:A:233:VAL:HG23	2.18	0.43
1:A:82:ARG:NH2	1:A:170:ASN:HD21	2.07	0.43
1:B:196:LYS:HD2	1:B:196:LYS:N	2.33	0.42
1:B:22:LEU:HD22	1:B:262:LEU:HB3	2.02	0.42
1:B:215[A]:GLU:HG2	1:B:215[A]:GLU:H	1.63	0.42
1:A:110[A]:ARG:HH22	1:B:110:ARG:NH2	2.17	0.42
1:B:246:LEU:HD23	1:B:266:LEU:HD12	2.01	0.42
1:A:269:GLU:OE1	1:A:269:GLU:N	2.45	0.41
1:A:214:PRO:O	1:A:215:GLU:HB2	2.21	0.41
1:A:269:GLU:H	1:A:269:GLU:CD	2.27	0.41
1:B:242:SER:HB2	5:B:708:HOH:O	2.18	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)
1:A:186:ARG:NH2	1:B:34:ASP:OD2[4_455]	2.08	0.12

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	270/287 (94%)	262 (97%)	7 (3%)	1 (0%)	30	31
1	B	277/287 (96%)	268 (97%)	8 (3%)	1 (0%)	30	31
All	All	547/574 (95%)	530 (97%)	15 (3%)	2 (0%)	30	31

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	133	GLY
1	A	133	GLY

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	248/258 (96%)	239 (96%)	9 (4%)	31	39
1	B	254/258 (98%)	246 (97%)	8 (3%)	35	44
All	All	502/516 (97%)	485 (97%)	17 (3%)	32	40

All (17) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	10	ASN
1	A	79	LYS
1	A	178	SER
1	A	183	SER
1	A	196	LYS
1	A	211	ASP
1	A	257	ASN
1	A	258	GLU
1	A	272	SER
1	B	30	ASN
1	B	95	LYS
1	B	172	ASP
1	B	185	VAL
1	B	196	LYS
1	B	218	GLN
1	B	277	ARG
1	B	278	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	10	ASN
1	A	74	ASN
1	A	75	GLN
1	A	80	GLN
1	A	122	GLN
1	A	170	ASN
1	A	195	HIS
1	A	245	HIS
1	A	257	ASN
1	B	9	ASN
1	B	20	HIS
1	B	33	GLN
1	B	80	GLN
1	B	122	GLN
1	B	170	ASN
1	B	181	ASN
1	B	218	GLN
1	B	245	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 oligosaccharides 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	$\# Z > 2$
4	ACY	B	601	-	3,3,3	0.76	0	3,3,3	1.03	0
2	SO4	A	501	-	4,4,4	0.31	0	6,6,6	0.19	0
2	SO4	B	502	-	4,4,4	0.36	0	6,6,6	0.14	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 ⓘ

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	262/287 (91%)	-0.04	2 (0%) 82 84	17, 39, 56, 71	7 (2%)
1	B	271/287 (94%)	0.08	6 (2%) 62 63	18, 40, 58, 69	6 (2%)
All	All	533/574 (92%)	0.02	8 (1%) 72 73	17, 40, 57, 71	13 (2%)

All (8) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	276	THR	6.2
1	B	281[A]	ASP	5.4
1	B	8	ALA	4.7
1	B	275	ALA	4.5
1	A	273	LYS	3.1
1	A	132	TRP	2.9
1	B	236	GLN	2.2
1	B	277	ARG	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 oligosaccharides 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
4	ACY	B	601	4/4	0.85	0.15	48,48,49,50	0
2	SO4	B	502	5/5	0.98	0.08	32,32,33,34	0
3	NA	B	401	1/1	0.99	0.08	25,25,25,25	0
2	SO4	A	501	5/5	0.99	0.08	32,32,34,36	0

6.5 Other polymers [i](#)

There are no such residues in this entry.