



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 13, 2017 – 08:53 pm GMT

PDB ID : 2Y3X
Title : Catalytic domain of mouse 2',3'-cyclic nucleotide 3'- phosphodiesterase, complexed with sulfate
Authors : Myllykoski, M.; Kursula, P.
Deposited on : 2011-01-04
Resolution : 2.10 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 : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : 1.9-1692
EDS : trunk28620
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
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) : recalc28949

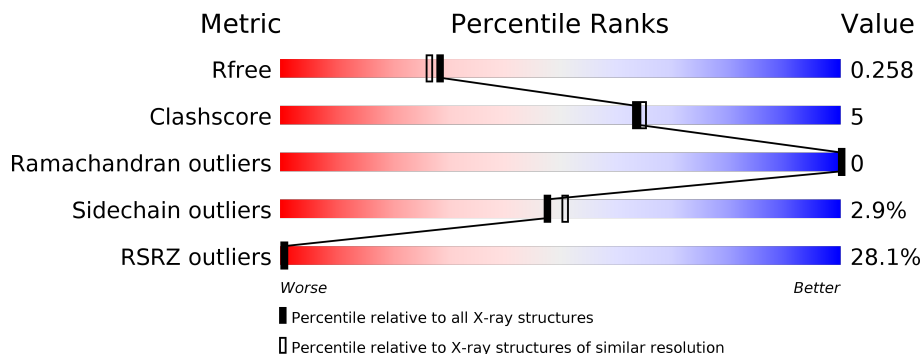
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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}	100719	4243 (2.10-2.10)
Clashscore	112137	4788 (2.10-2.10)
Ramachandran outliers	110173	4740 (2.10-2.10)
Sidechain outliers	110143	4741 (2.10-2.10)
RSRZ outliers	101464	4275 (2.10-2.10)

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 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	221	<div> <div>3%</div> <div>86%</div> <div>10%</div> <div>• •</div> </div>
1	B	221	<div> <div>3%</div> <div>89%</div> <div>8%</div> <div>• •</div> </div>
1	E	221	<div> <div>76%</div> <div>81%</div> <div>11%</div> <div>• 5%</div> </div>

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 5198 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.

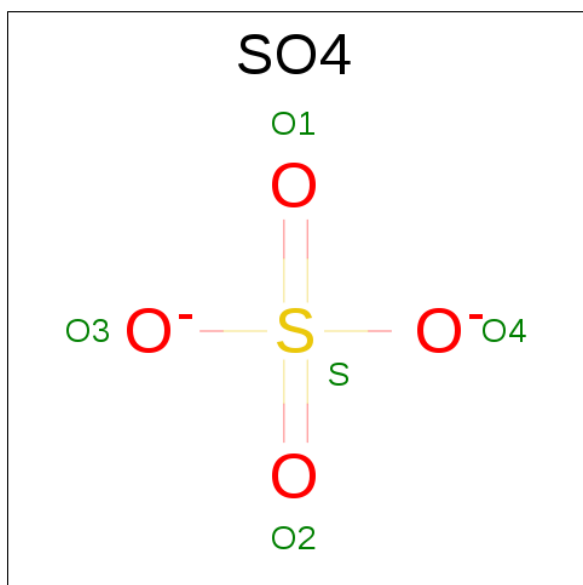
- Molecule 1 is a protein called 2', 3'-CYCLIC-NUCLEOTIDE 3'-PHOSPHODIESTERASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	215	Total	C	N	O	S	0	0	0
			1671	1078	281	307	5			
1	B	215	Total	C	N	O	S	0	0	0
			1672	1079	281	307	5			
1	E	210	Total	C	N	O	S	0	0	0
			1634	1056	275	298	5			

There are 3 discrepancies between the modelled and reference sequences:

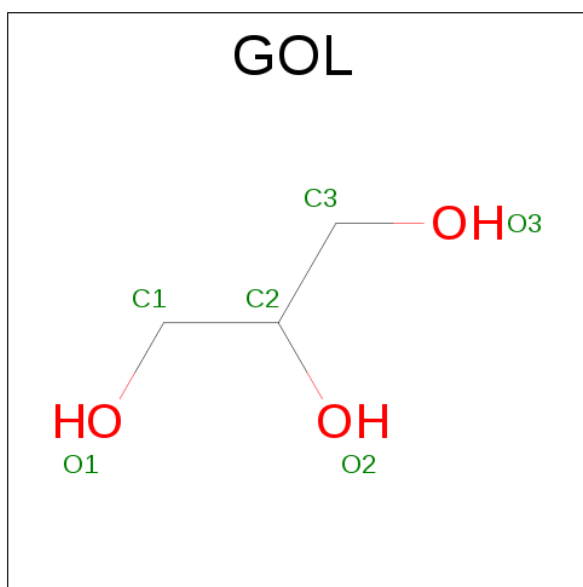
Chain	Residue	Modelled	Actual	Comment	Reference
A	158	GLY	-	EXPRESSION TAG	UNP P16330
B	158	GLY	-	EXPRESSION TAG	UNP P16330
E	158	GLY	-	EXPRESSION TAG	UNP P16330

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



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

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	B	1	Total C O 6 3 3	0	0
3	B	1	Total C O 6 3 3	0	0

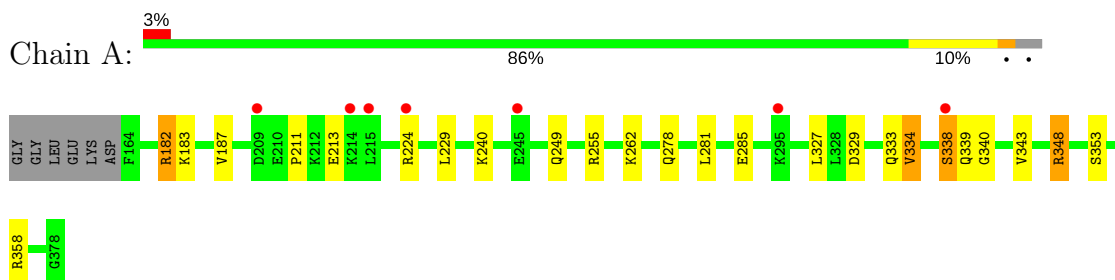
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	58	Total 58	O 58	0	0
4	B	96	Total 96	O 96	0	0
4	E	5	Total 5	O 5	0	0

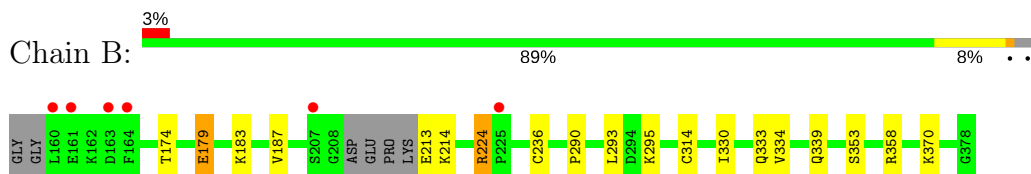
3 Residue-property plots [i](#)

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

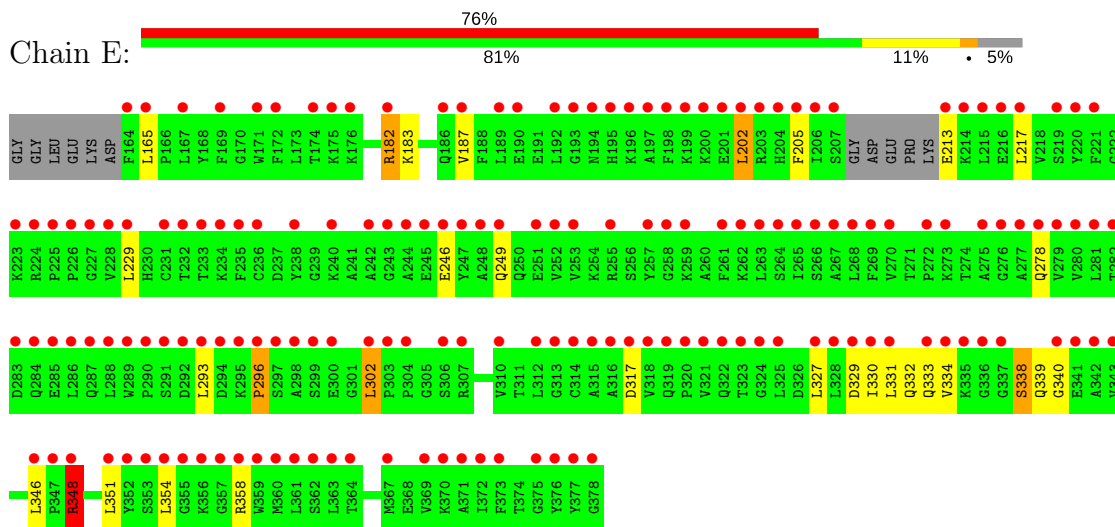
- Molecule 1: 2', 3'-CYCLIC-NUCLEOTIDE 3'-PHOSPHODIESTERASE



- Molecule 1: 2', 3'-CYCLIC-NUCLEOTIDE 3'-PHOSPHODIESTERASE



- Molecule 1: 2', 3'-CYCLIC-NUCLEOTIDE 3'-PHOSPHODIESTERASE



4 Data and refinement statistics

Property	Value	Source
Space group	P 31	Depositor
Cell constants a, b, c, α , β , γ	82.43Å 82.43Å 86.31Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	71.40 – 2.10 32.98 – 2.10	Depositor EDS
% Data completeness (in resolution range)	99.8 (71.40-2.10) 99.8 (32.98-2.10)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.57 (at 2.10Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.190 , 0.228 0.226 , 0.258	Depositor DCC
R_{free} test set	1980 reflections (5.18%)	DCC
Wilson B-factor (Å ²)	39.8	Xtriage
Anisotropy	0.308	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 28.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.42$, $\langle L^2 \rangle = 0.25$	Xtriage
Estimated twinning fraction	0.068 for -h,-k,l 0.085 for h,-h-k,-l 0.159 for -k,-h,-l	Xtriage
Reported twinning fraction	0.788 for H, K, L 0.212 for -H, H+K, -L	Depositor
Outliers	0 of 38236 reflections	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	5198	wwPDB-VP
Average B, all atoms (Å ²)	71.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.23% 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: GOL, 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	0.74	0/1710	0.92	3/2303 (0.1%)
1	B	0.99	3/1709 (0.2%)	0.85	0/2299
1	E	0.39	0/1671	0.80	3/2249 (0.1%)
All	All	0.75	3/5090 (0.1%)	0.86	6/6851 (0.1%)

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	E	0	2
All	All	0	4

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	314	CYS	CB-SG	-9.27	1.66	1.82
1	B	179	GLU	CG-CD	5.41	1.60	1.51
1	B	236	CYS	CB-SG	-5.33	1.73	1.81

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	348	ARG	NE-CZ-NH2	-20.06	110.27	120.30
1	E	348	ARG	NE-CZ-NH2	-19.00	110.80	120.30
1	A	348	ARG	NE-CZ-NH1	15.96	128.28	120.30
1	E	348	ARG	NE-CZ-NH1	15.20	127.90	120.30
1	A	348	ARG	CD-NE-CZ	9.40	136.76	123.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	348	ARG	CD-NE-CZ	8.67	135.74	123.60

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	340	GLY	Peptide
1	A	348	ARG	Sidechain
1	E	340	GLY	Peptide
1	E	348	ARG	Sidechain

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	1671	0	1694	17	1
1	B	1672	0	1697	16	0
1	E	1634	0	1660	21	1
2	A	25	0	0	0	0
2	B	25	0	0	0	0
3	B	12	0	16	4	0
4	A	58	0	0	0	0
4	B	96	0	0	4	0
4	E	5	0	0	1	0
All	All	5198	0	5067	49	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 5.

All (49) 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:329:ASP:OD2	1:A:358:ARG:NH1	2.11	0.82
1:A:334:VAL:HG23	1:A:339:GLN:HB3	1.62	0.81
1:E:334:VAL:HG12	1:E:339:GLN:HB3	1.61	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:329:ASP:OD2	1:E:358:ARG:NH1	2.18	0.76
3:B:1380:GOL:H11	4:B:2069:HOH:O	1.87	0.74
1:A:182:ARG:HH12	1:A:229:LEU:HD21	1.52	0.73
1:A:333:GLN:OE1	1:A:358:ARG:NH2	2.29	0.66
1:B:333:GLN:HG3	1:B:358:ARG:HH12	1.59	0.66
1:E:182:ARG:HH12	1:E:229:LEU:HD21	1.61	0.65
3:B:1380:GOL:C1	4:B:2069:HOH:O	2.46	0.64
1:A:211:PRO:O	1:A:213:GLU:HG2	2.00	0.61
1:E:333:GLN:OE1	1:E:358:ARG:NH2	2.33	0.60
1:B:224:ARG:HB2	4:B:2066:HOH:O	2.03	0.58
1:A:278:GLN:HG3	1:A:327:LEU:HD21	1.86	0.58
1:E:213:GLU:OE1	4:E:2002:HOH:O	2.17	0.57
1:E:331:LEU:HA	1:E:334:VAL:HG22	1.85	0.57
1:B:183:LYS:HE2	1:B:187:VAL:CG2	2.33	0.57
1:B:333:GLN:HG3	1:B:358:ARG:NH1	2.20	0.55
1:B:290:PRO:HG2	1:B:293:LEU:HD21	1.89	0.55
1:A:255:ARG:HD3	1:E:296:PRO:CG	2.37	0.54
1:E:333:GLN:HE21	1:E:338:SER:HB3	1.74	0.53
1:A:255:ARG:HG3	1:E:296:PRO:HB2	1.91	0.52
1:A:333:GLN:HE21	1:A:338:SER:HB3	1.75	0.52
1:B:330:ILE:O	1:B:334:VAL:HG23	2.10	0.52
1:B:183:LYS:HD3	4:B:2007:HOH:O	2.10	0.51
1:E:278:GLN:HG3	1:E:327:LEU:HD21	1.92	0.51
1:A:262:LYS:NZ	1:E:246:GLU:HB3	2.27	0.50
1:B:183:LYS:HE2	1:B:187:VAL:HG21	1.93	0.50
1:B:183:LYS:CE	1:B:187:VAL:HG21	2.42	0.49
1:B:370:LYS:HD2	3:B:1379:GOL:H11	1.96	0.48
1:A:182:ARG:NH1	1:A:229:LEU:HD21	2.25	0.47
1:A:255:ARG:HD3	1:E:296:PRO:HG3	1.97	0.47
1:E:330:ILE:HG23	1:E:354:LEU:HD13	1.96	0.46
1:E:302:LEU:HD22	1:E:332:GLN:NE2	2.31	0.46
1:E:183:LYS:O	1:E:187:VAL:HG23	2.16	0.46
1:A:182:ARG:NH1	1:A:224:ARG:HH11	2.14	0.45
1:B:213:GLU:OE2	1:E:317:ASP:HA	2.15	0.45
1:A:343:VAL:HG11	1:A:353:SER:HB2	1.98	0.45
1:B:183:LYS:HE2	1:B:187:VAL:HG23	1.99	0.44
1:A:183:LYS:O	1:A:187:VAL:HG23	2.17	0.44
1:B:179:GLU:OE1	1:B:179:GLU:HA	2.18	0.44
1:A:262:LYS:HZ1	1:E:246:GLU:HB3	1.83	0.43
1:A:281:LEU:HD22	1:A:285:GLU:HB3	2.01	0.43
1:B:214:LYS:HE2	1:E:317:ASP:OD2	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:339:GLN:HA	1:E:354:LEU:HD23	2.00	0.43
1:E:346:LEU:HD11	1:E:351:LEU:HD22	2.02	0.42
1:B:174:THR:OG1	3:B:1379:GOL:H12	2.21	0.41
1:B:339:GLN:NE2	1:B:353:SER:HB3	2.35	0.41
1:E:202:LEU:HD13	1:E:217:LEU:HD21	2.04	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:240:LYS:NZ	1:E:205:PHE:O[3_664]	2.00	0.20

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	213/221 (96%)	210 (99%)	3 (1%)	0	100	100
1	B	211/221 (96%)	203 (96%)	8 (4%)	0	100	100
1	E	206/221 (93%)	202 (98%)	4 (2%)	0	100	100
All	All	630/663 (95%)	615 (98%)	15 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	176/180 (98%)	172 (98%)	4 (2%)	56	60
1	B	176/180 (98%)	174 (99%)	2 (1%)	78	83
1	E	172/180 (96%)	163 (95%)	9 (5%)	27	24
All	All	524/540 (97%)	509 (97%)	15 (3%)	48	51

All (15) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	182	ARG
1	A	249	GLN
1	A	334	VAL
1	A	338	SER
1	B	224	ARG
1	B	295	LYS
1	E	165	LEU
1	E	182	ARG
1	E	202	LEU
1	E	249	GLN
1	E	293	LEU
1	E	296	PRO
1	E	302	LEU
1	E	338	SER
1	E	348	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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

12 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	A	1379	-	4,4,4	0.16	0	6,6,6	0.55	0
2	SO4	A	1380	-	4,4,4	0.47	0	6,6,6	0.92	0
2	SO4	A	1381	-	4,4,4	0.16	0	6,6,6	0.23	0
2	SO4	A	1382	-	4,4,4	0.13	0	6,6,6	0.14	0
2	SO4	A	1383	-	4,4,4	0.13	0	6,6,6	0.20	0
3	GOL	B	1379	-	5,5,5	0.41	0	5,5,5	0.41	0
3	GOL	B	1380	-	5,5,5	0.36	0	5,5,5	0.87	0
2	SO4	B	1381	-	4,4,4	0.18	0	6,6,6	0.18	0
2	SO4	B	1382	-	4,4,4	0.39	0	6,6,6	0.55	0
2	SO4	B	1383	-	4,4,4	0.15	0	6,6,6	0.38	0
2	SO4	B	1384	-	4,4,4	0.14	0	6,6,6	0.17	0
2	SO4	B	1385	-	4,4,4	0.14	0	6,6,6	0.18	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	A	1379	-	-	0/0/0/0	0/0/0/0
2	SO4	A	1380	-	-	0/0/0/0	0/0/0/0
2	SO4	A	1381	-	-	0/0/0/0	0/0/0/0
2	SO4	A	1382	-	-	0/0/0/0	0/0/0/0
2	SO4	A	1383	-	-	0/0/0/0	0/0/0/0
3	GOL	B	1379	-	-	0/4/4/4	0/0/0/0
3	GOL	B	1380	-	-	0/4/4/4	0/0/0/0
2	SO4	B	1381	-	-	0/0/0/0	0/0/0/0
2	SO4	B	1382	-	-	0/0/0/0	0/0/0/0
2	SO4	B	1383	-	-	0/0/0/0	0/0/0/0
2	SO4	B	1384	-	-	0/0/0/0	0/0/0/0
2	SO4	B	1385	-	-	0/0/0/0	0/0/0/0

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 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	1379	GOL	2	0
3	B	1380	GOL	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 ⓘ

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	215/221 (97%)	0.62	7 (3%)	47 54	31, 50, 75, 87	0
1	B	215/221 (97%)	0.52	6 (2%)	53 60	24, 39, 67, 88	0
1	E	210/221 (95%)	4.44	167 (79%)	0 0	92, 124, 164, 186	0
All	All	640/663 (96%)	1.84	180 (28%)	1 1	24, 54, 149, 186	0

All (180) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	207	SER	17.4
1	E	291	SER	14.3
1	E	203	ARG	14.0
1	E	204	HIS	12.1
1	E	206	ILE	11.2
1	E	318	VAL	10.6
1	E	214	LYS	10.6
1	E	224	ARG	10.2
1	E	234	LYS	10.1
1	E	200	LYS	10.0
1	E	202	LEU	9.9
1	E	315	ALA	9.9
1	E	248	ALA	9.8
1	E	331	LEU	9.5
1	E	317	ASP	9.3
1	E	319	GLN	9.2
1	E	198	PHE	9.1
1	E	330	ILE	9.1
1	E	195	HIS	8.9
1	E	289	TRP	8.8
1	E	360	MET	8.7
1	E	164	PHE	8.3
1	E	295	LYS	8.1

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Mol	Chain	Res	Type	RSRZ
1	E	377	TYR	8.0
1	E	247	TYR	8.0
1	E	288	LEU	8.0
1	B	160	LEU	7.8
1	E	223	LYS	7.6
1	E	205	PHE	7.6
1	E	225	PRO	7.5
1	E	336	GLY	7.5
1	E	298	ALA	7.4
1	E	263	LEU	7.3
1	E	217	LEU	7.3
1	E	286	LEU	7.3
1	E	253	VAL	7.2
1	E	251	GLU	7.2
1	E	294	ASP	7.1
1	E	303	PRO	7.1
1	E	293	LEU	7.0
1	E	371	ALA	7.0
1	E	213	GLU	6.9
1	E	270	VAL	6.9
1	E	348	ARG	6.8
1	E	235	PHE	6.6
1	E	238	TYR	6.6
1	E	297	SER	6.6
1	E	340	GLY	6.5
1	E	323	THR	6.4
1	E	165	LEU	6.3
1	E	199	LYS	6.3
1	E	281	LEU	6.2
1	E	378	GLY	6.2
1	E	359	TRP	6.2
1	E	357	GLY	6.1
1	E	287	GLN	6.1
1	E	313	GLY	6.0
1	E	171	TRP	6.0
1	E	322	GLN	5.9
1	E	375	GLY	5.8
1	E	276	GLY	5.8
1	E	306	SER	5.6
1	E	259	LYS	5.6
1	E	172	PHE	5.5
1	E	376	TYR	5.4

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Mol	Chain	Res	Type	RSRZ
1	E	316	ALA	5.4
1	A	338	SER	5.4
1	E	337	GLY	5.4
1	E	220	TYR	5.4
1	E	354	LEU	5.3
1	E	245	GLU	5.3
1	E	342	ALA	5.3
1	E	279	VAL	5.1
1	B	225	PRO	5.1
1	E	261	PHE	5.1
1	E	192	LEU	5.1
1	B	164	PHE	5.0
1	E	175	LYS	5.0
1	E	310	VAL	4.9
1	E	233	THR	4.9
1	E	304	PRO	4.9
1	E	290	PRO	4.9
1	E	283	ASP	4.9
1	E	364	THR	4.8
1	E	215	LEU	4.8
1	E	346	LEU	4.8
1	E	355	GLY	4.8
1	E	280	VAL	4.7
1	E	320	PRO	4.4
1	E	335	LYS	4.3
1	E	356	LYS	4.3
1	E	169	PHE	4.3
1	E	244	ALA	4.2
1	E	373	PHE	4.2
1	E	243	GLY	4.2
1	E	334	VAL	4.1
1	E	307	ARG	4.1
1	E	312	LEU	4.1
1	E	240	LYS	4.1
1	E	242	ALA	4.1
1	E	201	GLU	4.0
1	E	328	LEU	3.9
1	E	370	LYS	3.9
1	E	321	VAL	3.8
1	E	363	LEU	3.8
1	E	299	SER	3.8
1	E	324	GLY	3.7

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Mol	Chain	Res	Type	RSRZ
1	E	221	PHE	3.7
1	E	262	LYS	3.6
1	E	369	VAL	3.6
1	E	258	GLY	3.6
1	E	329	ASP	3.6
1	E	257	TYR	3.6
1	E	231	CYS	3.6
1	E	341	GLU	3.6
1	E	285	GLU	3.5
1	E	196	LYS	3.5
1	E	351	LEU	3.5
1	E	269	PHE	3.5
1	E	228	VAL	3.4
1	E	343	VAL	3.4
1	E	167	LEU	3.4
1	E	275	ALA	3.4
1	E	182	ARG	3.4
1	E	358	ARG	3.3
1	E	296	PRO	3.3
1	E	292	ASP	3.3
1	E	197	ALA	3.3
1	B	161	GLU	3.2
1	E	216	GLU	3.2
1	E	255	ARG	3.2
1	E	176	LYS	3.2
1	E	252	VAL	3.1
1	E	219	SER	3.0
1	E	227	GLY	2.9
1	E	361	LEU	2.9
1	E	268	LEU	2.9
1	E	352	TYR	2.9
1	A	214	LYS	2.9
1	E	277	ALA	2.9
1	E	362	SER	2.9
1	E	273	LYS	2.8
1	E	246	GLU	2.7
1	E	333	GLN	2.7
1	E	265	ILE	2.7
1	E	282	THR	2.7
1	E	174	THR	2.7
1	E	249	GLN	2.7
1	E	284	GLN	2.7

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Mol	Chain	Res	Type	RSRZ
1	E	367	MET	2.7
1	E	353	SER	2.6
1	E	272	PRO	2.6
1	E	327	LEU	2.6
1	E	267	ALA	2.6
1	E	226	PRO	2.6
1	A	209	ASP	2.6
1	B	163	ASP	2.5
1	E	266	SER	2.5
1	E	372	ILE	2.5
1	E	314	CYS	2.5
1	A	215	LEU	2.4
1	E	236	CYS	2.4
1	E	300	GLU	2.4
1	B	207	SER	2.4
1	E	278	GLN	2.4
1	E	302	LEU	2.4
1	E	190	GLU	2.4
1	A	224	ARG	2.3
1	E	187	VAL	2.3
1	E	229	LEU	2.3
1	E	347	PRO	2.3
1	A	245	GLU	2.2
1	E	264	SER	2.2
1	E	232	THR	2.1
1	E	194	ASN	2.1
1	A	295	LYS	2.1
1	E	325	LEU	2.1
1	E	189	LEU	2.1
1	E	193	GLY	2.1
1	E	186	GLN	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 ⓘ

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(Å ²)	Q<0.9
2	SO4	A	1381	5/5	0.72	0.21	0.71	100,101,101,103	0
2	SO4	A	1380	5/5	0.98	0.18	0.70	35,42,52,55	0
2	SO4	B	1383	5/5	0.89	0.15	0.12	78,80,83,86	0
3	GOL	B	1380	6/6	0.87	0.13	-0.21	43,50,54,59	0
2	SO4	A	1379	5/5	0.94	0.15	-0.31	67,67,71,71	0
2	SO4	B	1382	5/5	0.98	0.13	-0.38	44,48,53,55	0
3	GOL	B	1379	6/6	0.81	0.18	-0.56	66,70,73,74	0
2	SO4	B	1381	5/5	0.95	0.10	-0.81	71,74,77,78	0
2	SO4	A	1383	5/5	0.86	0.18	-	97,97,100,101	0
2	SO4	B	1384	5/5	0.92	0.10	-	92,94,96,96	0
2	SO4	A	1382	5/5	0.69	0.21	-	131,132,132,133	0
2	SO4	B	1385	5/5	0.90	0.21	-	84,87,89,90	0

6.5 Other polymers [i](#)

There are no such residues in this entry.