



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 29, 2017 – 11:01 PM EDT

PDB ID : 3NBW
Title : X-ray structure of ketohexokinase in complex with a pyrazole compound
Authors : Abad, M.C.; Gibbs, A.C.; Spurlino, J.C.
Deposited on : unknown
Resolution : 2.34 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 : rb-20030345
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) : rb-20030345

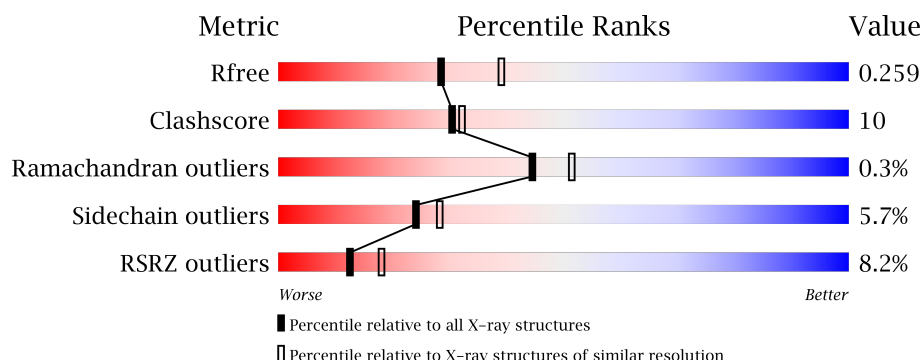
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.34 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	1570 (2.36-2.32)
Clashscore	112137	1673 (2.36-2.32)
Ramachandran outliers	110173	1654 (2.36-2.32)
Sidechain outliers	110143	1655 (2.36-2.32)
RSRZ outliers	101464	1576 (2.36-2.32)

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	313	<div> <div>11%</div> <div> <div></div> <div>70%</div> <div>21%</div> <div>• 5%</div> </div> </div>
1	B	313	<div> <div>5%</div> <div> <div></div> <div>80%</div> <div>15%</div> <div>• •</div> </div> </div>

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	GOL	A	299	-	-	-	X

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 4730 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 Ketohexokinase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	296	Total	C	N	O	S	0	0	0
			2259	1414	405	428	12			
1	B	301	Total	C	N	O	S	0	0	0
			2296	1438	413	433	12			

There are 38 discrepancies between the modelled and reference sequences:

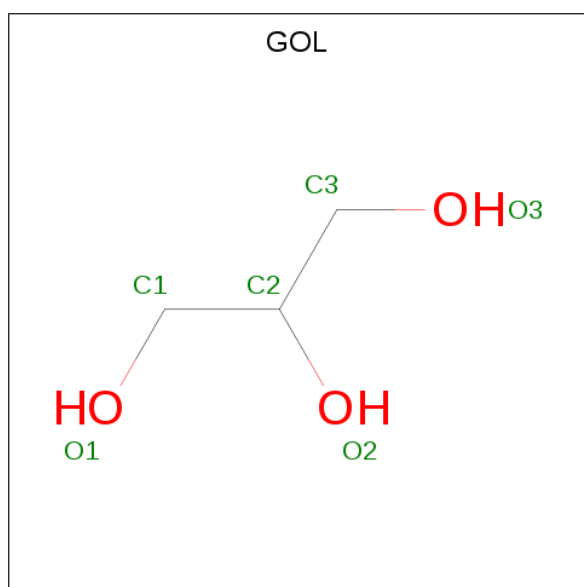
Chain	Residue	Modelled	Actual	Comment	Reference
A	-14	MET	-	EXPRESSION TAG	UNP P50053-2
A	-13	GLY	-	EXPRESSION TAG	UNP P50053-2
A	-12	SER	-	EXPRESSION TAG	UNP P50053-2
A	-11	SER	-	EXPRESSION TAG	UNP P50053-2
A	-10	HIS	-	EXPRESSION TAG	UNP P50053-2
A	-9	HIS	-	EXPRESSION TAG	UNP P50053-2
A	-8	HIS	-	EXPRESSION TAG	UNP P50053-2
A	-7	HIS	-	EXPRESSION TAG	UNP P50053-2
A	-6	HIS	-	EXPRESSION TAG	UNP P50053-2
A	-5	HIS	-	EXPRESSION TAG	UNP P50053-2
A	-4	SER	-	EXPRESSION TAG	UNP P50053-2
A	-3	SER	-	EXPRESSION TAG	UNP P50053-2
A	-2	GLY	-	EXPRESSION TAG	UNP P50053-2
A	-1	LEU	-	EXPRESSION TAG	UNP P50053-2
A	0	VAL	-	EXPRESSION TAG	UNP P50053-2
A	1	PRO	-	EXPRESSION TAG	UNP P50053-2
A	2	ARG	-	EXPRESSION TAG	UNP P50053-2
A	3	GLY	-	EXPRESSION TAG	UNP P50053-2
A	4	SER	-	EXPRESSION TAG	UNP P50053-2
B	-14	MET	-	EXPRESSION TAG	UNP P50053-2
B	-13	GLY	-	EXPRESSION TAG	UNP P50053-2
B	-12	SER	-	EXPRESSION TAG	UNP P50053-2
B	-11	SER	-	EXPRESSION TAG	UNP P50053-2
B	-10	HIS	-	EXPRESSION TAG	UNP P50053-2
B	-9	HIS	-	EXPRESSION TAG	UNP P50053-2

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-8	HIS	-	EXPRESSION TAG	UNP P50053-2
B	-7	HIS	-	EXPRESSION TAG	UNP P50053-2
B	-6	HIS	-	EXPRESSION TAG	UNP P50053-2
B	-5	HIS	-	EXPRESSION TAG	UNP P50053-2
B	-4	SER	-	EXPRESSION TAG	UNP P50053-2
B	-3	SER	-	EXPRESSION TAG	UNP P50053-2
B	-2B	GLY	-	EXPRESSION TAG	UNP P50053-2
B	-1A	LEU	-	EXPRESSION TAG	UNP P50053-2
B	0	VAL	-	EXPRESSION TAG	UNP P50053-2
B	1	PRO	-	EXPRESSION TAG	UNP P50053-2
B	2	ARG	-	EXPRESSION TAG	UNP P50053-2
B	3	GLY	-	EXPRESSION TAG	UNP P50053-2
B	4	SER	-	EXPRESSION TAG	UNP P50053-2

- Molecule 2 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



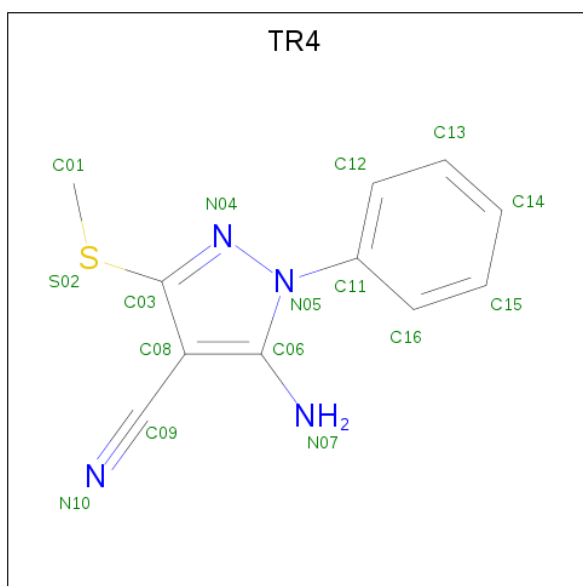
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			6	3	3		

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



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

- Molecule 4 is 5-amino-3-(methylsulfanyl)-1-phenyl-1H-pyrazole-4-carbonitrile (three-letter code: TR4) (formula: C₁₁H₁₀N₄S).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	S	0	0
			16	11	4	1		
4	B	1	Total	C	N	S	0	0
			16	11	4	1		

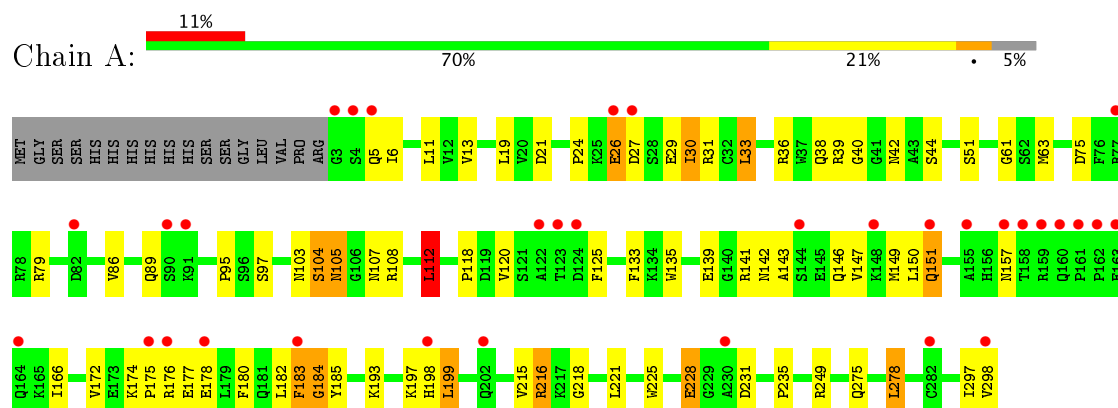
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	38	Total	O	0	0
			38	38		
5	B	84	Total	O	0	0
			84	84		

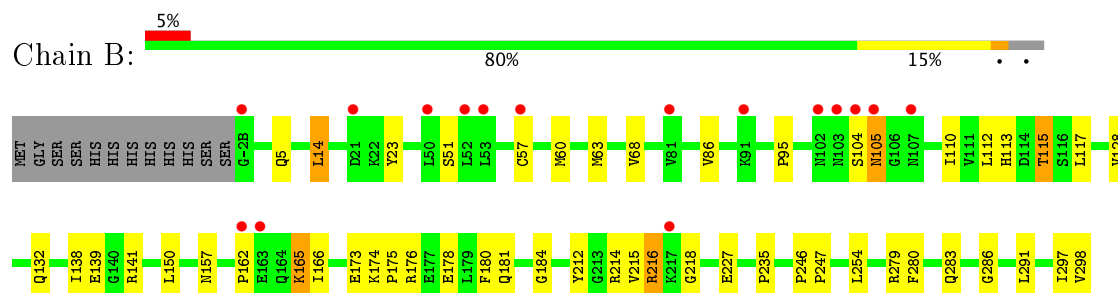
3 Residue-property plots [i](#)

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: Ketohexokinase



• Molecule 1: Ketohexokinase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	82.70 Å 85.63 Å 136.60 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	31.72 – 2.34 44.86 – 2.34	Depositor EDS
% Data completeness (in resolution range)	92.7 (31.72-2.34) 92.6 (44.86-2.34)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.01 (at 2.34 Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.5_2)	Depositor
R, R_{free}	0.225 , 0.274 0.205 , 0.259	Depositor DCC
R_{free} test set	1969 reflections (5.11%)	DCC
Wilson B-factor (Å ²)	47.1	Xtriage
Anisotropy	0.162	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 40.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.52$, $\langle L^2 \rangle = 0.35$	Xtriage
Estimated twinning fraction	0.001 for k,h,-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	4730	wwPDB-VP
Average B, all atoms (Å ²)	53.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.86% 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, TR4

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	0.42	0/2301	0.58	2/3111 (0.1%)
1	B	0.47	1/2339 (0.0%)	0.60	0/3163
All	All	0.45	1/4640 (0.0%)	0.59	2/6274 (0.0%)

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	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	57	CYS	CB-SG	-5.21	1.73	1.81

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	112	LEU	CA-CB-CG	5.56	128.09	115.30
1	A	184	GLY	N-CA-C	-5.53	99.27	113.10

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	104	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	2259	0	2237	60	0
1	B	2296	0	2283	37	0
2	A	6	0	8	0	0
3	A	5	0	0	0	0
3	B	10	0	0	0	0
4	A	16	0	10	0	0
4	B	16	0	10	2	0
5	A	38	0	0	0	0
5	B	84	0	0	3	0
All	All	4730	0	4548	96	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 10.

All (96) 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:105:ASN:HD22	1:A:107:ASN:H	1.04	1.02
1:A:105:ASN:ND2	1:A:107:ASN:H	1.72	0.86
1:B:157:ASN:HD21	1:B:166:ILE:H	1.21	0.86
1:A:105:ASN:HD21	1:A:107:ASN:CG	1.81	0.84
1:B:162:PRO:HA	1:B:165:LYS:HD3	1.63	0.81
1:A:193:LYS:HE2	1:A:197:LYS:HE3	1.64	0.80
1:B:132:GLN:HB2	5:B:303:HOH:O	1.87	0.74
1:A:183:PHE:N	1:A:184:GLY:HA3	2.02	0.74
1:A:143:ALA:HB3	1:A:178:GLU:HG2	1.69	0.73
1:A:147:VAL:O	1:A:151:GLN:HG2	1.89	0.73
1:A:157:ASN:HD21	1:A:166:ILE:H	1.36	0.71
1:A:24:PRO:HG3	1:A:30:ILE:HD11	1.73	0.70
1:A:104:SER:O	1:A:105:ASN:HB2	1.92	0.69
1:A:105:ASN:HD22	1:A:107:ASN:N	1.86	0.69
1:A:105:ASN:HD21	1:A:107:ASN:CB	2.04	0.69
1:A:36:ARG:HE	1:A:38:GLN:NE2	1.93	0.67
1:B:157:ASN:ND2	1:B:166:ILE:H	1.93	0.67
1:B:60:MET:CE	1:B:128:VAL:HG21	2.26	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:97:SER:HB3	1:A:112:LEU:HA	1.77	0.65
1:A:63:MET:HE2	1:A:86:VAL:HG21	1.78	0.65
1:A:89:GLN:HG3	1:A:118:PRO:HD2	1.78	0.64
1:B:5:GLN:HE22	1:B:132:GLN:HE21	1.46	0.62
1:B:184:GLY:O	1:B:216:ARG:HG2	2.00	0.62
1:B:176:ARG:HH11	1:B:178:GLU:HG3	1.66	0.61
1:A:105:ASN:ND2	1:A:107:ASN:CB	2.64	0.61
1:A:36:ARG:HE	1:A:38:GLN:HE21	1.48	0.60
1:B:95:PRO:HD3	1:B:117:LEU:HD22	1.85	0.58
1:A:105:ASN:HD21	1:A:107:ASN:ND2	2.01	0.58
1:A:105:ASN:ND2	1:A:107:ASN:HB2	2.19	0.58
1:B:60:MET:HE2	1:B:128:VAL:HG21	1.86	0.58
1:B:178:GLU:O	1:B:181:GLN:HG2	2.04	0.57
1:A:36:ARG:HH21	1:A:38:GLN:HE22	1.53	0.57
1:B:5:GLN:NE2	1:B:132:GLN:HE21	2.03	0.57
1:A:142:ASN:O	1:A:146:GLN:HG3	2.05	0.56
1:B:115:THR:O	1:B:115:THR:HG23	2.05	0.56
1:B:280:PHE:HA	1:B:283:GLN:HE21	1.70	0.55
1:A:150:LEU:HD13	1:A:185:TYR:HB2	1.89	0.55
1:A:26:GLU:HG2	1:B:23:TYR:CG	2.42	0.54
1:A:105:ASN:HD21	1:A:107:ASN:HB2	1.73	0.54
1:B:298:VAL:HA	5:B:372:HOH:O	2.08	0.53
1:B:104:SER:O	1:B:105:ASN:HB3	2.09	0.53
1:A:21:ASP:HB3	1:A:33:LEU:HD21	1.90	0.52
1:A:105:ASN:ND2	1:A:107:ASN:N	2.52	0.52
1:B:60:MET:HE1	1:B:128:VAL:HG21	1.92	0.52
1:B:297:ILE:O	1:B:298:VAL:OXT	2.28	0.52
1:A:193:LYS:HE2	1:A:197:LYS:CE	2.36	0.51
1:B:174:LYS:HE2	5:B:343:HOH:O	2.11	0.51
1:A:125:PHE:CD2	1:A:149:MET:HB3	2.44	0.50
1:B:247:PRO:HG3	1:B:286:GLY:O	2.12	0.50
1:A:6:ILE:HG23	1:A:135:TRP:HB3	1.92	0.50
1:B:212:TYR:O	1:B:215:VAL:HG22	2.12	0.50
1:A:40:GLY:O	1:A:44:SER:HB3	2.13	0.49
1:A:79:ARG:HH11	1:A:79:ARG:HG3	1.77	0.49
1:A:11:LEU:HD21	1:A:141:ARG:CD	2.43	0.48
1:A:297:ILE:HG13	1:A:298:VAL:HG13	1.96	0.48
1:A:105:ASN:ND2	1:A:107:ASN:CG	2.60	0.47
1:A:157:ASN:ND2	1:A:166:ILE:H	2.09	0.47
1:B:110:ILE:HG22	1:B:112:LEU:HD23	1.95	0.47
1:B:176:ARG:HH11	1:B:178:GLU:CG	2.27	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:218:GLY:HA2	1:A:235:PRO:HG3	1.95	0.47
4:B:301:TR4:H16	4:B:301:TR4:HN07	1.80	0.47
1:A:176:ARG:HH21	1:A:176:ARG:HG3	1.80	0.47
1:B:110:ILE:CG2	1:B:112:LEU:HD23	2.44	0.47
1:B:180:PHE:HB3	1:B:214:ARG:NH1	2.29	0.46
1:A:197:LYS:C	1:A:199:LEU:H	2.20	0.46
1:A:42:ASN:HB2	1:A:139:GLU:CD	2.37	0.45
1:A:26:GLU:O	1:A:27:ASP:CB	2.65	0.44
1:A:63:MET:CE	1:A:86:VAL:HG21	2.47	0.44
1:B:279:ARG:O	1:B:283:GLN:HG3	2.17	0.44
1:A:19:LEU:HD11	1:A:103:ASN:HD22	1.83	0.43
1:A:13:VAL:HG22	1:A:95:PRO:HB2	1.99	0.43
1:A:39:ARG:NE	1:A:75:ASP:OD2	2.50	0.43
1:B:246:PRO:HA	1:B:247:PRO:HD3	1.91	0.43
1:A:5:GLN:HE21	1:A:133:PHE:HE1	1.65	0.43
1:B:139:GLU:O	1:B:141:ARG:HG3	2.19	0.43
1:A:278:LEU:HD23	1:A:278:LEU:HA	1.86	0.42
1:B:218:GLY:HA2	1:B:235:PRO:HG3	2.00	0.42
1:A:174:LYS:HA	1:A:175:PRO:HD3	1.84	0.42
1:A:11:LEU:HD21	1:A:141:ARG:HD3	2.01	0.42
1:A:29:GLU:HG3	1:B:112:LEU:HD11	2.00	0.42
1:A:31:ARG:HG3	1:B:113:HIS:O	2.19	0.42
1:A:174:LYS:O	1:A:176:ARG:N	2.49	0.42
1:A:216:ARG:NH1	1:A:216:ARG:HG2	2.34	0.41
1:A:79:ARG:HH11	1:A:79:ARG:CG	2.33	0.41
1:A:180:PHE:N	1:A:180:PHE:CD2	2.87	0.41
1:A:61:GLY:HA2	1:A:120:VAL:HG11	2.03	0.41
1:A:151:GLN:HG2	1:A:151:GLN:H	1.53	0.41
1:B:138:ILE:HD12	1:B:150:LEU:HD21	2.03	0.41
1:B:63:MET:CE	1:B:86:VAL:HG21	2.51	0.41
1:A:172:VAL:HG11	1:A:183:PHE:HE1	1.85	0.41
1:A:225:TRP:HB3	1:A:228:GLU:HB3	2.03	0.40
1:B:174:LYS:HA	1:B:175:PRO:HD3	1.90	0.40
4:B:301:TR4:C16	4:B:301:TR4:HN07	2.34	0.40
1:B:180:PHE:HB3	1:B:214:ARG:HH12	1.85	0.40
1:B:14:LEU:HD23	1:B:68:VAL:HG13	2.03	0.40
1:A:183:PHE:O	1:A:215:VAL:HG12	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	294/313 (94%)	280 (95%)	13 (4%)	1 (0%)	44	51
1	B	299/313 (96%)	293 (98%)	5 (2%)	1 (0%)	44	51
All	All	593/626 (95%)	573 (97%)	18 (3%)	2 (0%)	44	51

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	105	ASN
1	B	105	ASN

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	245/260 (94%)	226 (92%)	19 (8%)	15	15
1	B	249/260 (96%)	240 (96%)	9 (4%)	40	51
All	All	494/520 (95%)	466 (94%)	28 (6%)	24	28

All (28) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	26	GLU
1	A	30	ILE
1	A	33	LEU
1	A	51	SER

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Mol	Chain	Res	Type
1	A	108	ARG
1	A	112	LEU
1	A	151	GLN
1	A	177	GLU
1	A	182	LEU
1	A	183	PHE
1	A	198	HIS
1	A	199	LEU
1	A	216	ARG
1	A	221	LEU
1	A	228	GLU
1	A	231	ASP
1	A	249	ARG
1	A	275	GLN
1	A	278	LEU
1	B	14	LEU
1	B	51	SER
1	B	115	THR
1	B	165	LYS
1	B	173	GLU
1	B	216	ARG
1	B	227	GLU
1	B	254	LEU
1	B	291	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	5	GLN
1	A	35	GLN
1	A	38	GLN
1	A	103	ASN
1	A	105	ASN
1	A	157	ASN
1	A	202	GLN
1	B	5	GLN
1	B	103	ASN
1	B	107	ASN
1	B	157	ASN
1	B	198	HIS
1	B	283	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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

6 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	GOL	A	299	-	5,5,5	0.48	0	5,5,5	0.68	0
3	SO4	A	300	-	4,4,4	0.17	0	6,6,6	0.07	0
4	TR4	A	301	-	16,17,17	1.93	4 (25%)	10,23,23	1.50	1 (10%)
3	SO4	B	299	-	4,4,4	0.23	0	6,6,6	0.26	0
3	SO4	B	300	-	4,4,4	0.23	0	6,6,6	0.21	0
4	TR4	B	301	-	16,17,17	1.98	4 (25%)	10,23,23	1.68	1 (10%)

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	GOL	A	299	-	-	0/4/4/4	0/0/0/0
3	SO4	A	300	-	-	0/0/0/0	0/0/0/0
4	TR4	A	301	-	-	0/4/8/8	0/2/2/2
3	SO4	B	299	-	-	0/0/0/0	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	SO4	B	300	-	-	0/0/0/0	0/0/0/0
4	TR4	B	301	-	-	0/4/8/8	0/2/2/2

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	301	TR4	C08-C09	-3.43	1.38	1.44
4	A	301	TR4	C08-C09	-3.28	1.39	1.44
4	A	301	TR4	N04-N05	-3.18	1.33	1.39
4	A	301	TR4	C03-S02	-3.07	1.70	1.76
4	B	301	TR4	C03-S02	-2.38	1.72	1.76
4	B	301	TR4	N04-N05	-2.36	1.35	1.39
4	A	301	TR4	C08-C03	4.49	1.45	1.40
4	B	301	TR4	C08-C03	5.30	1.45	1.40

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	301	TR4	C12-C11-N05	-3.74	114.07	119.49
4	A	301	TR4	C01-S02-C03	3.56	105.54	101.75

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	301	TR4	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	296/313 (94%)	0.82	33 (11%) 6 10	36, 56, 81, 104	0
1	B	301/313 (96%)	0.54	16 (5%) 27 38	33, 44, 69, 92	0
All	All	597/626 (95%)	0.68	49 (8%) 12 18	33, 50, 78, 104	0

All (49) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	144	SER	5.2
1	A	91	LYS	4.8
1	A	163	GLU	4.5
1	A	161	PRO	4.3
1	B	104	SER	4.0
1	A	155	ALA	3.9
1	A	198	HIS	3.5
1	B	163	GLU	3.5
1	A	151	GLN	3.5
1	B	91	LYS	3.4
1	B	105	ASN	3.2
1	A	159	ARG	3.1
1	B	21	ASP	3.1
1	A	4	SER	3.0
1	B	102	ASN	2.8
1	A	148	LYS	2.8
1	A	162	PRO	2.7
1	A	123	THR	2.7
1	A	282	CYS	2.7
1	B	162	PRO	2.7
1	A	157	ASN	2.6
1	A	176	ARG	2.6
1	B	217	LYS	2.6
1	A	158	THR	2.6

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Mol	Chain	Res	Type	RSRZ
1	B	50	LEU	2.5
1	A	164	GLN	2.5
1	A	77	ARG	2.5
1	B	52	LEU	2.5
1	A	124	ASP	2.5
1	A	27	ASP	2.4
1	A	178	GLU	2.4
1	A	3	GLY	2.4
1	A	160	GLN	2.3
1	B	53	LEU	2.3
1	B	-2(B)	GLY	2.3
1	A	298	VAL	2.3
1	A	5	GLN	2.2
1	B	103	ASN	2.1
1	B	81	VAL	2.1
1	B	57	CYS	2.1
1	A	90	SER	2.1
1	A	175	PRO	2.1
1	A	122	ALA	2.1
1	A	183	PHE	2.1
1	A	202	GLN	2.1
1	A	230	ALA	2.1
1	A	26	GLU	2.1
1	B	107	ASN	2.0
1	A	82	ASP	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 ⓘ

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	GOL	A	299	6/6	0.67	0.22	3.59	50,58,64,68	0
4	TR4	B	301	16/16	0.93	0.14	-0.48	46,52,55,56	0
4	TR4	A	301	16/16	0.94	0.17	-1.02	52,56,58,58	0
3	SO4	A	300	5/5	0.99	0.12	-1.78	54,56,58,59	0
3	SO4	B	299	5/5	0.97	0.13	-1.79	53,64,66,74	0
3	SO4	B	300	5/5	0.96	0.09	-3.14	55,62,70,77	0

6.5 Other polymers [i](#)

There are no such residues in this entry.