



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 15, 2017 – 01:08 am GMT

PDB ID : 1M3K
Title : biosynthetic thiolase, inactive C89A mutant
Authors : Kursula, P.; Ojala, J.; Lambeir, A.-M.; Wierenga, R.K.
Deposited on : 2002-06-28
Resolution : 1.70 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

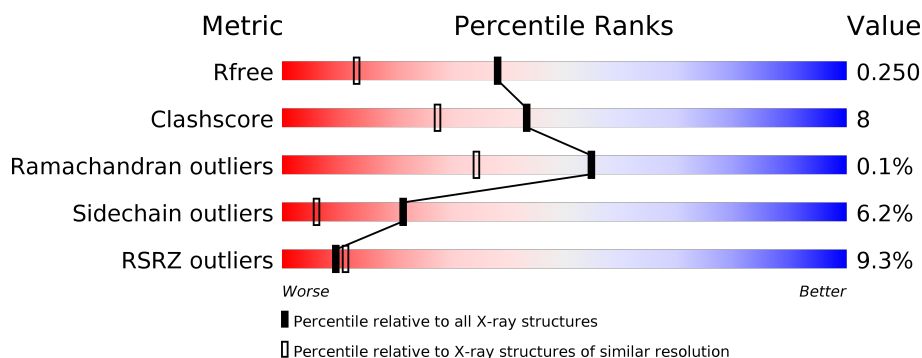
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.70 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	3453 (1.70-1.70)
Clashscore	112137	3876 (1.70-1.70)
Ramachandran outliers	110173	3815 (1.70-1.70)
Sidechain outliers	110143	3815 (1.70-1.70)
RSRZ outliers	101464	3491 (1.70-1.70)

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	392	<div> <div>2%</div> <div>85%</div> <div>13%</div> <div>•</div> </div>
1	B	392	<div> <div>2%</div> <div>87%</div> <div>12%</div> <div>•</div> </div>
1	C	392	<div> <div>11%</div> <div>84%</div> <div>16%</div> <div>•</div> </div>
1	D	392	<div> <div>23%</div> <div>78%</div> <div>21%</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 crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	GOL	B	6393	-	-	-	X

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 12527 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 Acetyl-CoA acetyltransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	392	Total	C	N	O	S	0	1	0
			2834	1759	512	543	20			
1	B	392	Total	C	N	O	S	0	1	0
			2834	1759	512	543	20			
1	C	392	Total	C	N	O	S	0	1	0
			2834	1759	512	543	20			
1	D	392	Total	C	N	O	S	0	1	0
			2834	1759	512	543	20			

There are 12 discrepancies between the modelled and reference sequences:

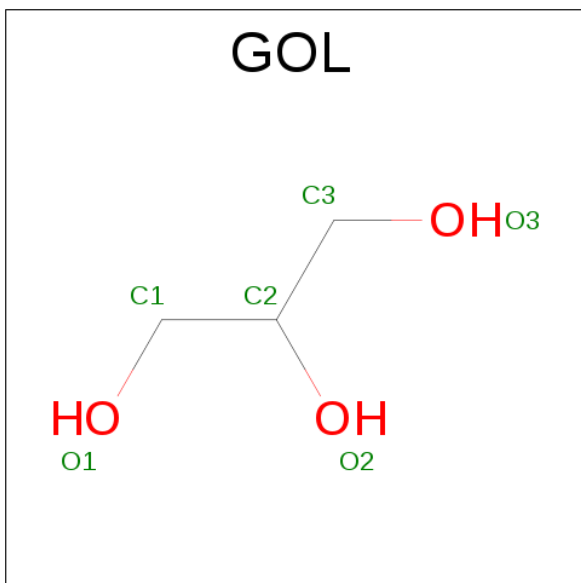
Chain	Residue	Modelled	Actual	Comment	Reference
A	10	ALA	-	INSERTION	UNP P07097
A	89	ALA	CYS	ENGINEERED	UNP P07097
A	129	ARG	ALA	CONFLICT	UNP P07097
B	10	ALA	-	INSERTION	UNP P07097
B	89	ALA	CYS	ENGINEERED	UNP P07097
B	129	ARG	ALA	CONFLICT	UNP P07097
C	10	ALA	-	INSERTION	UNP P07097
C	89	ALA	CYS	ENGINEERED	UNP P07097
C	129	ARG	ALA	CONFLICT	UNP P07097
D	10	ALA	-	INSERTION	UNP P07097
D	89	ALA	CYS	ENGINEERED	UNP P07097
D	129	ARG	ALA	CONFLICT	UNP P07097

- 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	A	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		

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



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

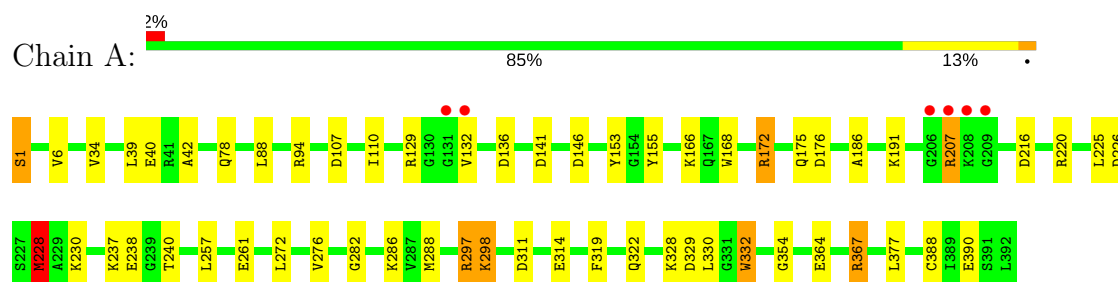
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	416	Total	O	0	0
			416	416		
4	B	425	Total	O	0	0
			425	425		
4	C	152	Total	O	0	0
			152	152		
4	D	166	Total	O	0	0
			166	166		

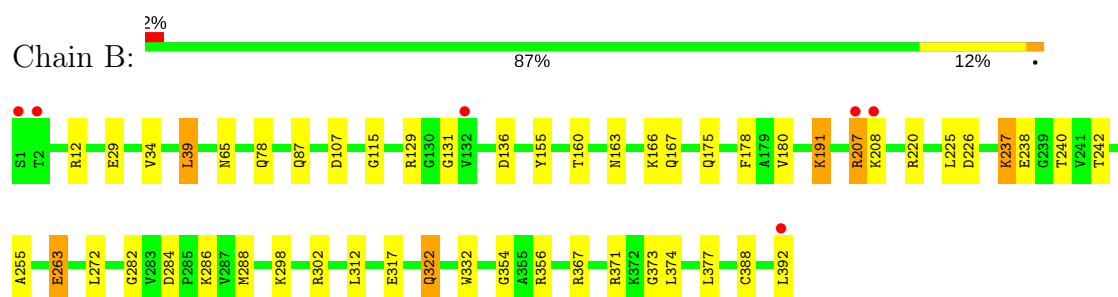
3 Residue-property plots [i](#)

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.

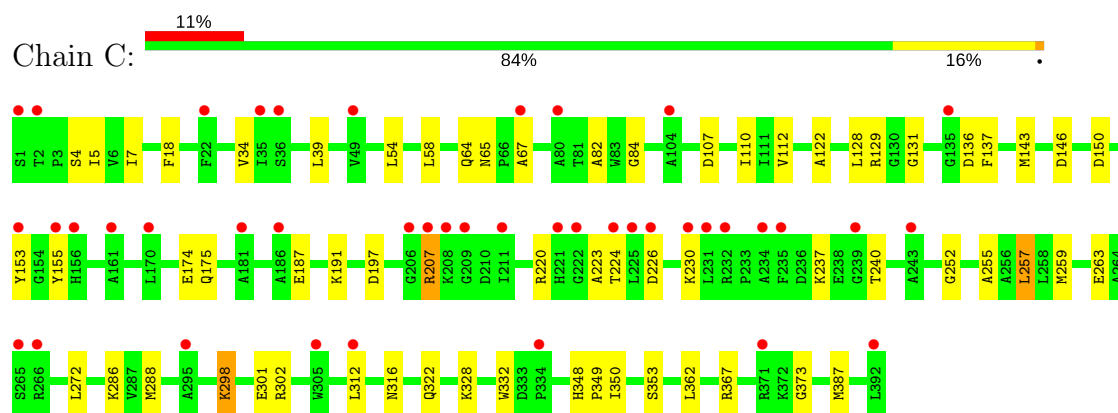
- Molecule 1: Acetyl-CoA acetyltransferase



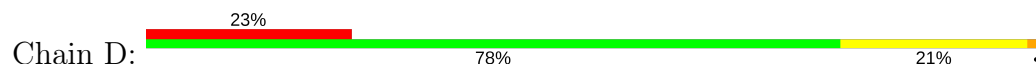
- Molecule 1: Acetyl-CoA acetyltransferase

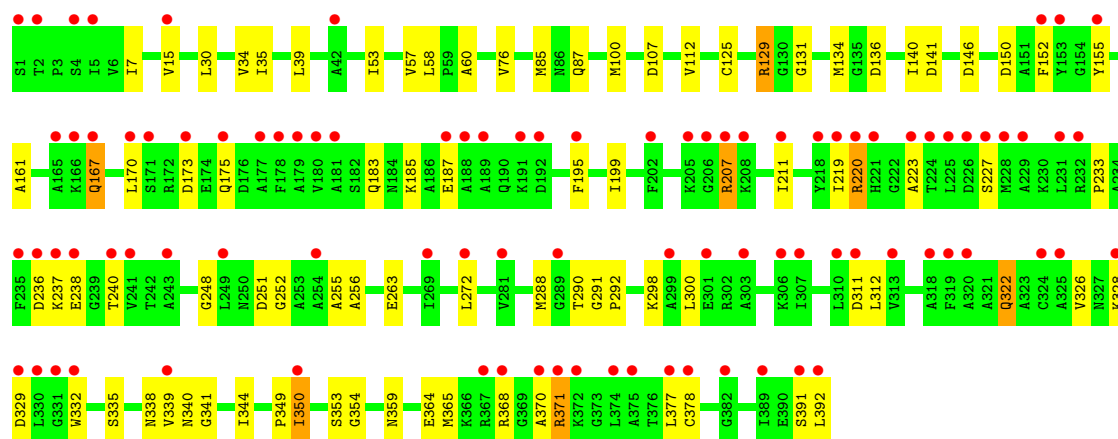


- Molecule 1: Acetyl-CoA acetyltransferase



- Molecule 1: Acetyl-CoA acetyltransferase





4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	84.37Å 79.20Å 148.86Å 90.00° 92.32° 90.00°	Depositor
Resolution (Å)	20.00 – 1.70 19.84 – 1.70	Depositor EDS
% Data completeness (in resolution range)	90.1 (20.00-1.70) 81.4 (19.84-1.70)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.08	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.91 (at 1.70Å)	Xtriage
Refinement program	REFMAC 5.1.19	Depositor
R, R_{free}	0.199 , 0.243 0.211 , 0.250	Depositor DCC
R_{free} test set	8981 reflections (4.86%)	DCC
Wilson B-factor (Å ²)	17.8	Xtriage
Anisotropy	0.440	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 50.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.37$, $\langle L^2 \rangle = 0.19$	Xtriage
Estimated twinning fraction	0.155 for h,-k,-l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	12527	wwPDB-VP
Average B, all atoms (Å ²)	16.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.86% 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 [i](#)

5.1 Standard geometry [i](#)

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	1.06	6/2880 (0.2%)	1.05	11/3890 (0.3%)
1	B	1.03	3/2880 (0.1%)	1.06	9/3890 (0.2%)
1	C	0.61	0/2880	0.83	7/3890 (0.2%)
1	D	0.56	0/2880	0.79	5/3890 (0.1%)
All	All	0.85	9/11520 (0.1%)	0.94	32/15560 (0.2%)

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	317	GLU	CD-OE1	6.37	1.32	1.25
1	A	314	GLU	CD-OE1	6.01	1.32	1.25
1	A	94	ARG	CZ-NH1	-5.66	1.25	1.33
1	B	115	GLY	CA-C	-5.52	1.43	1.51
1	B	178	PHE	CE2-CZ	5.45	1.47	1.37
1	A	34	VAL	CB-CG1	-5.40	1.41	1.52
1	A	319	PHE	CE2-CZ	5.36	1.47	1.37
1	A	186	ALA	CA-CB	-5.13	1.41	1.52
1	A	42	ALA	CA-CB	-5.04	1.41	1.52

All (32) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	367	ARG	NE-CZ-NH1	9.85	125.22	120.30
1	B	367	ARG	NE-CZ-NH2	-9.83	115.39	120.30
1	A	107	ASP	CB-CG-OD2	8.45	125.90	118.30
1	A	141	ASP	CB-CG-OD2	7.88	125.39	118.30
1	B	107	ASP	CB-CG-OD2	7.82	125.34	118.30
1	D	146	ASP	CB-CG-OD2	7.30	124.87	118.30
1	D	136	ASP	CB-CG-OD2	7.01	124.61	118.30
1	A	311	ASP	CB-CG-OD2	7.00	124.60	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	228	MET	CG-SD-CE	6.61	110.78	100.20
1	B	12	ARG	NE-CZ-NH2	-6.57	117.01	120.30
1	C	146	ASP	CB-CG-OD2	6.38	124.04	118.30
1	A	146	ASP	CB-CG-OD2	6.21	123.88	118.30
1	D	329	ASP	CB-CG-OD2	5.98	123.69	118.30
1	B	284	ASP	CB-CG-OD2	5.94	123.65	118.30
1	C	150	ASP	CB-CG-OD2	5.92	123.62	118.30
1	A	226	ASP	CB-CG-OD2	5.91	123.62	118.30
1	A	94	ARG	NE-CZ-NH2	5.74	123.17	120.30
1	A	297	ARG	NE-CZ-NH1	5.71	123.15	120.30
1	B	136	ASP	CB-CG-OD2	5.66	123.39	118.30
1	C	302	ARG	NE-CZ-NH1	5.52	123.06	120.30
1	D	173	ASP	CB-CG-OD2	5.48	123.23	118.30
1	C	197	ASP	CB-CG-OD2	5.33	123.10	118.30
1	D	107	ASP	CB-CG-OD2	5.32	123.09	118.30
1	C	107	ASP	CB-CG-OD2	5.29	123.07	118.30
1	A	176	ASP	CB-CG-OD2	5.26	123.04	118.30
1	B	39	LEU	CA-CB-CG	5.23	127.34	115.30
1	C	367	ARG	NE-CZ-NH1	5.12	122.86	120.30
1	A	216	ASP	CB-CG-OD2	5.11	122.89	118.30
1	B	302	ARG	NE-CZ-NH1	5.11	122.85	120.30
1	A	172	ARG	NE-CZ-NH1	5.06	122.83	120.30
1	B	129	ARG	NE-CZ-NH2	-5.05	117.78	120.30
1	C	136	ASP	CB-CG-OD1	5.03	122.82	118.30

There are no chirality outliers.

There are no planarity outliers.

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	2834	0	2842	31	0
1	B	2834	0	2842	48	0
1	C	2834	0	2842	39	0
1	D	2834	0	2842	58	0
2	A	10	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	10	0	0	0	0
3	A	6	0	7	2	0
3	B	6	0	8	0	0
4	A	416	0	0	17	0
4	B	425	0	0	29	1
4	C	152	0	0	18	0
4	D	166	0	0	36	0
All	All	12527	0	11383	174	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 8.

All (174) 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:225:LEU:HG	4:A:9889:HOH:O	1.51	1.08
1:A:228:MET:SD	4:A:488:HOH:O	2.19	1.00
1:C:353:SER:HA	4:C:505:HOH:O	1.63	0.96
1:A:225:LEU:HD21	4:A:523:HOH:O	1.67	0.95
1:B:371:ARG:HD3	4:B:476:HOH:O	1.69	0.92
4:C:483:HOH:O	1:D:87:GLN:HA	1.70	0.89
1:C:65:ASN:ND2	4:C:483:HOH:O	2.06	0.87
1:D:183:GLN:HG2	4:D:539:HOH:O	1.75	0.85
1:D:252:GLY:HA3	4:D:515:HOH:O	1.75	0.84
4:A:432:HOH:O	1:B:65:ASN:HB2	1.77	0.84
1:B:163:ASN:ND2	4:B:416:HOH:O	2.12	0.83
1:D:141:ASP:HA	4:D:446:HOH:O	1.79	0.82
1:D:125:CYS:SG	4:D:431:HOH:O	2.37	0.81
1:B:191:LYS:HB3	1:B:191:LYS:NZ	1.97	0.80
1:D:185:LYS:O	4:D:409:HOH:O	2.01	0.79
4:A:9993:HOH:O	1:C:131:GLY:HA3	1.82	0.78
1:D:152:PHE:CE2	4:D:503:HOH:O	2.37	0.77
1:A:6:VAL:HG11	4:A:530:HOH:O	1.84	0.76
1:C:110:ILE:HG22	4:C:528:HOH:O	1.86	0.76
1:C:67:ALA:HB1	4:C:524:HOH:O	1.86	0.75
1:D:150:ASP:HB2	4:D:494:HOH:O	1.86	0.73
1:B:160:THR:HA	4:B:416:HOH:O	1.89	0.71
1:B:388:CYS:HA	4:B:444:HOH:O	1.90	0.71
1:D:251:ASP:O	4:D:551:HOH:O	2.07	0.71
1:B:322:GLN:HB3	4:B:524:HOH:O	1.90	0.71
1:D:57:VAL:HG21	1:D:350:ILE:HG22	1.74	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:223:ALA:HB3	4:D:487:HOH:O	1.91	0.70
1:C:143:MET:HB2	4:C:399:HOH:O	1.91	0.69
1:A:207:ARG:H	1:A:207:ARG:HD3	1.56	0.69
1:D:53:ILE:HG22	4:D:460:HOH:O	1.93	0.68
1:D:370:ALA:HB1	4:D:538:HOH:O	1.94	0.68
1:D:290:THR:HA	4:D:502:HOH:O	1.93	0.67
1:C:58:LEU:HD13	4:C:399:HOH:O	1.93	0.67
1:D:344:ILE:HG22	4:D:539:HOH:O	1.96	0.65
1:B:388:CYS:SG	4:B:444:HOH:O	2.55	0.65
1:D:340:ASN:ND2	1:D:364:GLU:OE1	2.23	0.64
1:B:191:LYS:HZ3	1:B:191:LYS:HB3	1.62	0.64
1:D:7:ILE:HG23	1:D:256:ALA:HB1	1.81	0.63
1:C:82:ALA:HB1	4:C:524:HOH:O	1.97	0.63
1:C:252:GLY:HA2	4:C:459:HOH:O	2.00	0.62
1:B:87:GLN:C	4:B:9970:HOH:O	2.38	0.61
1:B:191:LYS:NZ	1:B:191:LYS:CB	2.64	0.60
1:D:30:LEU:HD11	4:D:543:HOH:O	2.00	0.60
1:D:15:VAL:HG13	4:D:551:HOH:O	2.01	0.60
1:D:170:LEU:HB3	4:D:496:HOH:O	2.02	0.60
1:B:191:LYS:HB3	4:B:475:HOH:O	2.02	0.59
1:A:228:MET:HG3	4:A:9831:HOH:O	2.02	0.59
1:A:129:ARG:O	4:A:9993:HOH:O	2.16	0.58
3:A:5393:GOL:C1	4:A:511:HOH:O	2.25	0.58
1:B:374:LEU:HB2	4:B:444:HOH:O	2.02	0.58
1:D:57:VAL:HG21	1:D:350:ILE:CG2	2.32	0.58
1:B:166:LYS:HG3	4:B:480:HOH:O	2.03	0.58
1:D:233:PRO:HB2	1:D:236:ASP:O	2.04	0.57
1:A:88:LEU:HG	4:A:432:HOH:O	2.04	0.57
1:A:298:LYS:HE3	2:A:9722:SO4:O3	2.05	0.57
1:D:220:ARG:NH1	4:D:479:HOH:O	2.37	0.57
1:B:175:GLN:HE22	1:B:240:THR:CG2	2.18	0.57
1:B:29:GLU:HG2	4:B:497:HOH:O	2.05	0.57
1:D:85:MET:HG3	4:D:460:HOH:O	2.04	0.56
1:A:172:ARG:NH1	4:A:501:HOH:O	2.38	0.56
1:B:34:VAL:HG12	1:B:255:ALA:HB3	1.87	0.56
1:D:338:ASN:HB3	1:D:341:GLY:O	2.05	0.55
1:A:168:TRP:CH2	1:A:329:ASP:HB2	2.41	0.55
1:D:392:LEU:HG	4:D:500:HOH:O	2.06	0.55
1:D:251:ASP:C	4:D:551:HOH:O	2.46	0.54
1:B:29:GLU:CG	4:B:497:HOH:O	2.54	0.54
1:A:207:ARG:H	1:A:207:ARG:CD	2.20	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:191:LYS:HD2	4:B:475:HOH:O	2.08	0.53
1:C:349:PRO:HG2	4:C:505:HOH:O	2.09	0.53
1:B:191:LYS:HB3	1:B:191:LYS:HZ2	1.73	0.53
1:C:129:ARG:CG	4:C:509:HOH:O	2.57	0.53
1:A:168:TRP:HH2	1:A:329:ASP:HB2	1.75	0.52
1:B:374:LEU:CB	4:B:444:HOH:O	2.58	0.52
1:D:140:ILE:HG22	4:D:431:HOH:O	2.10	0.52
1:C:257:LEU:CD1	1:C:259:MET:CE	2.87	0.52
1:B:87:GLN:HA	4:B:9970:HOH:O	2.09	0.52
1:C:175:GLN:HE22	1:C:240:THR:HG21	1.74	0.52
1:B:240:THR:C	4:B:510:HOH:O	2.47	0.52
1:C:257:LEU:CD1	1:C:259:MET:HE2	2.39	0.52
1:D:349:PRO:HB3	4:D:551:HOH:O	2.09	0.51
1:C:122:ALA:HA	4:C:514:HOH:O	2.11	0.51
1:B:242:THR:CG2	4:B:510:HOH:O	2.59	0.50
1:B:242:THR:HG23	4:B:510:HOH:O	2.12	0.50
1:B:312:LEU:HB3	4:B:479:HOH:O	2.11	0.50
1:B:87:GLN:CA	4:B:9970:HOH:O	2.59	0.50
1:B:225:LEU:HB2	4:B:515:HOH:O	2.11	0.50
1:D:15:VAL:HG22	4:D:515:HOH:O	2.11	0.50
1:D:60:ALA:O	4:D:519:HOH:O	2.20	0.50
1:A:228:MET:CE	4:A:488:HOH:O	2.54	0.49
1:A:40:GLU:HG3	4:A:9951:HOH:O	2.12	0.49
1:B:175:GLN:HE22	1:B:240:THR:HG23	1.76	0.49
1:A:276:VAL:CG2	1:A:388:CYS:HB2	2.42	0.49
1:B:226:ASP:HB3	4:B:509:HOH:O	2.12	0.49
1:B:180:VAL:HG11	4:B:515:HOH:O	2.12	0.49
1:C:129:ARG:HG2	4:C:509:HOH:O	2.13	0.48
1:C:7:ILE:HD13	1:C:362:LEU:HD11	1.94	0.48
1:A:282:GLY:HA3	1:B:78:GLN:O	2.13	0.48
1:B:263:GLU:OE1	4:B:9846:HOH:O	2.20	0.48
1:A:166:LYS:HB3	4:A:489:HOH:O	2.13	0.48
1:D:291:GLY:N	1:D:292:PRO:CD	2.76	0.48
1:B:286:LYS:NZ	4:B:9815:HOH:O	2.28	0.47
1:B:34:VAL:CG1	1:B:255:ALA:HB3	2.43	0.47
1:B:374:LEU:C	1:B:374:LEU:HD23	2.35	0.47
1:B:207:ARG:HD3	1:B:207:ARG:N	2.29	0.47
1:C:112:VAL:HG22	1:C:257:LEU:HD23	1.96	0.47
1:C:54:LEU:O	1:C:84:GLY:HA2	2.14	0.47
1:D:140:ILE:HB	4:D:431:HOH:O	2.15	0.47
1:A:237:LYS:HD3	1:A:237:LYS:N	2.30	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:131:GLY:HA2	1:D:131:GLY:HA2	1.97	0.47
1:B:208:LYS:NZ	4:B:468:HOH:O	2.48	0.47
1:C:64:GLN:O	1:C:65:ASN:C	2.54	0.47
1:D:34:VAL:CG1	1:D:255:ALA:HB3	2.45	0.47
1:C:223:ALA:HB1	4:C:523:HOH:O	2.16	0.46
1:D:219:ILE:HD11	4:D:510:HOH:O	2.15	0.46
4:A:9993:HOH:O	1:C:131:GLY:CA	2.52	0.46
1:A:110:ILE:HG23	1:A:257:LEU:HD21	1.98	0.46
1:B:191:LYS:HZ2	1:B:191:LYS:CB	2.27	0.46
1:D:248:GLY:HA2	4:D:474:HOH:O	2.16	0.46
1:B:356:ARG:HD2	1:B:356:ARG:C	2.37	0.46
1:C:129:ARG:HG3	4:C:509:HOH:O	2.16	0.45
1:C:174:GLU:OE2	1:C:328:LYS:NZ	2.39	0.45
1:A:330:LEU:HD12	1:A:332:TRP:CZ2	2.51	0.45
1:A:261:GLU:HG3	4:A:530:HOH:O	2.17	0.45
1:B:237:LYS:N	1:B:237:LYS:HD2	2.31	0.45
1:A:225:LEU:HD23	1:A:225:LEU:C	2.37	0.45
1:D:322:GLN:O	1:D:326:VAL:HG23	2.16	0.45
1:D:58:LEU:HB3	4:D:441:HOH:O	2.16	0.45
1:D:167:GLN:HB3	4:D:397:HOH:O	2.17	0.45
1:B:373:GLY:CA	4:B:479:HOH:O	2.65	0.44
1:C:34:VAL:HG12	1:C:255:ALA:HB3	1.99	0.44
1:C:128:LEU:HD21	1:C:137:PHE:CZ	2.52	0.44
1:C:4:SER:C	1:C:5:ILE:HD13	2.37	0.44
1:D:211:ILE:HB	4:D:554:HOH:O	2.17	0.44
1:A:354:GLY:HA2	1:A:377:LEU:HD11	2.00	0.44
1:C:175:GLN:HE22	1:C:240:THR:CG2	2.30	0.44
1:D:76:VAL:HG23	4:D:540:HOH:O	2.16	0.44
1:A:364:GLU:OE1	1:A:367:ARG:HD2	2.18	0.44
1:A:1:SER:O	1:A:1:SER:OG	2.29	0.43
1:D:207:ARG:HD3	1:D:207:ARG:N	2.33	0.43
1:D:175:GLN:NE2	1:D:240:THR:OG1	2.51	0.43
1:D:335:SER:HA	4:D:526:HOH:O	2.18	0.43
1:D:335:SER:O	1:D:339:VAL:HG12	2.19	0.43
1:C:153:TYR:CE2	1:C:286:LYS:HD3	2.53	0.43
1:D:312:LEU:HD13	1:D:368:ARG:HD2	2.00	0.43
1:B:392:LEU:HD23	4:B:471:HOH:O	2.18	0.43
1:D:326:VAL:HG22	4:D:502:HOH:O	2.18	0.43
1:D:292:PRO:HD3	1:D:378:CYS:HB3	2.01	0.43
1:D:300:LEU:HD22	4:D:427:HOH:O	2.19	0.42
1:C:257:LEU:HD13	1:C:259:MET:HE2	1.99	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:365:MET:CE	1:D:371:ARG:O	2.67	0.42
1:A:276:VAL:HG11	1:A:390:GLU:HB2	2.01	0.42
1:C:316:ASN:HD21	1:C:348:HIS:CE1	2.37	0.42
1:D:195:PHE:HB3	1:D:199:ILE:HD12	2.02	0.42
1:A:175:GLN:HE22	1:A:240:THR:CG2	2.33	0.42
1:C:226:ASP:O	1:C:230:LYS:HG3	2.19	0.42
1:C:312:LEU:O	1:C:373:GLY:HA2	2.20	0.42
1:A:297:ARG:NE	4:A:9987:HOH:O	2.53	0.41
1:D:354:GLY:HA2	1:D:377:LEU:HD21	2.02	0.41
1:A:78:GLN:O	1:B:282:GLY:HA3	2.20	0.41
1:D:35:ILE:HG12	1:D:112:VAL:HG11	2.02	0.41
1:C:18:PHE:CZ	1:D:129:ARG:HD3	2.56	0.41
1:D:328:LYS:HA	4:D:520:HOH:O	2.20	0.41
1:D:100:MET:SD	1:D:100:MET:C	2.98	0.41
1:C:387:MET:HB2	4:C:497:HOH:O	2.21	0.41
1:B:312:LEU:CB	4:B:479:HOH:O	2.68	0.41
1:B:354:GLY:HA2	1:B:377:LEU:HD11	2.03	0.41
1:C:298:LYS:HD3	1:C:301:GLU:OE1	2.21	0.40
1:C:207:ARG:HG2	4:C:517:HOH:O	2.20	0.40
1:C:65:ASN:CG	4:C:483:HOH:O	2.52	0.40
1:A:153:TYR:CE2	1:A:286:LYS:HG3	2.56	0.40
1:C:257:LEU:HD11	1:C:259:MET:CE	2.51	0.40
1:B:175:GLN:HE22	1:B:240:THR:HG21	1.86	0.40
1:D:161:ALA:HB2	4:D:415:HOH:O	2.21	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)
4:B:437:HOH:O	4:B:9890:HOH:O[2_555]	2.19	0.01

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	391/392 (100%)	378 (97%)	13 (3%)	0	100	100
1	B	391/392 (100%)	380 (97%)	11 (3%)	0	100	100
1	C	391/392 (100%)	374 (96%)	16 (4%)	1 (0%)	44	25
1	D	391/392 (100%)	371 (95%)	19 (5%)	1 (0%)	44	25
All	All	1564/1568 (100%)	1503 (96%)	59 (4%)	2 (0%)	55	34

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	350	ILE
1	C	350	ILE

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	279/278 (100%)	261 (94%)	18 (6%)	20	5
1	B	279/278 (100%)	265 (95%)	14 (5%)	28	10
1	C	279/278 (100%)	264 (95%)	15 (5%)	26	9
1	D	279/278 (100%)	257 (92%)	22 (8%)	14	3
All	All	1116/1112 (100%)	1047 (94%)	69 (6%)	21	6

All (69) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	SER
1	A	39	LEU
1	A	132	VAL
1	A	136	ASP
1	A	155	TYR
1	A	191	LYS
1	A	207	ARG

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Mol	Chain	Res	Type
1	A	220	ARG
1	A	228	MET
1	A	230	LYS
1	A	238	GLU
1	A	272	LEU
1	A	288	MET
1	A	298	LYS
1	A	322	GLN
1	A	328	LYS
1	A	332	TRP
1	A	367	ARG
1	B	39	LEU
1	B	155	TYR
1	B	167	GLN
1	B	191	LYS
1	B	207	ARG
1	B	220	ARG
1	B	237	LYS
1	B	238	GLU
1	B	263	GLU
1	B	272	LEU
1	B	288	MET
1	B	298	LYS
1	B	322	GLN
1	B	332	TRP
1	C	39	LEU
1	C	155	TYR
1	C	187	GLU
1	C	191	LYS
1	C	207	ARG
1	C	220	ARG
1	C	224	THR
1	C	237	LYS
1	C	257	LEU
1	C	263	GLU
1	C	272	LEU
1	C	288	MET
1	C	298	LYS
1	C	322	GLN
1	C	332	TRP
1	D	39	LEU
1	D	129	ARG

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Mol	Chain	Res	Type
1	D	134	MET
1	D	155	TYR
1	D	167	GLN
1	D	187	GLU
1	D	207	ARG
1	D	220	ARG
1	D	227	SER
1	D	237	LYS
1	D	238	GLU
1	D	263	GLU
1	D	272	LEU
1	D	288	MET
1	D	298	LYS
1	D	311	ASP
1	D	322	GLN
1	D	332	TRP
1	D	353	SER
1	D	359	ASN
1	D	371	ARG
1	D	391	SER

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	78	GLN
1	A	175	GLN
1	A	184	ASN
1	B	175	GLN
1	B	184	ASN
1	C	175	GLN
1	C	184	ASN
1	C	316	ASN
1	D	78	GLN
1	D	175	GLN
1	D	184	ASN
1	D	316	ASN

5.3.3 RNA ⓘ

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	$\# Z > 2$
3	GOL	A	5393	-	5,5,5	1.09	1 (20%)	5,5,5	1.15	0
2	SO4	A	9720	-	4,4,4	0.09	0	6,6,6	0.40	0
2	SO4	A	9722	-	4,4,4	0.16	0	6,6,6	0.56	0
3	GOL	B	6393	-	5,5,5	0.24	0	5,5,5	0.94	0
2	SO4	B	9719	-	4,4,4	0.19	0	6,6,6	0.23	0
2	SO4	B	9721	-	4,4,4	0.18	0	6,6,6	0.20	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
3	GOL	A	5393	-	-	0/4/4/4	0/0/0/0
2	SO4	A	9720	-	-	0/0/0/0	0/0/0/0
2	SO4	A	9722	-	-	0/0/0/0	0/0/0/0
3	GOL	B	6393	-	-	0/4/4/4	0/0/0/0
2	SO4	B	9719	-	-	0/0/0/0	0/0/0/0
2	SO4	B	9721	-	-	0/0/0/0	0/0/0/0

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	5393	GOL	O3-C3	-2.24	1.32	1.42

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
3	A	5393	GOL	2	0
2	A	9722	SO4	1	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	392/392 (100%)	-0.10	6 (1%) 74 78	5, 10, 25, 48	0
1	B	392/392 (100%)	-0.09	6 (1%) 74 78	5, 10, 25, 51	0
1	C	392/392 (100%)	0.83	42 (10%) 7 8	3, 13, 26, 40	0
1	D	392/392 (100%)	1.42	92 (23%) 1 1	2, 15, 27, 39	0
All	All	1568/1568 (100%)	0.52	146 (9%) 9 11	2, 12, 26, 51	0

All (146) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	170	LEU	9.2
1	C	1	SER	9.1
1	D	1	SER	8.2
1	D	229	ALA	8.0
1	D	2	THR	7.3
1	D	232	ARG	6.6
1	D	392	LEU	6.6
1	D	228	MET	6.3
1	B	207	ARG	6.0
1	D	231	LEU	5.6
1	D	237	LYS	5.6
1	C	104	ALA	5.5
1	D	188	ALA	5.5
1	D	235	PHE	5.4
1	C	225	LEU	5.3
1	C	208	LYS	5.2
1	A	208	LYS	5.2
1	D	226	ASP	5.1
1	D	328	LYS	5.0
1	D	208	LYS	4.8
1	C	2	THR	4.8

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Mol	Chain	Res	Type	RSRZ
1	D	207	ARG	4.6
1	C	232	ARG	4.5
1	D	240	THR	4.5
1	C	211	ILE	4.4
1	D	224	THR	4.3
1	C	186	ALA	4.2
1	C	243	ALA	4.2
1	D	332	TRP	4.2
1	D	225	LEU	4.2
1	D	221	HIS	4.1
1	C	206	GLY	4.1
1	D	227	SER	4.0
1	D	219	ILE	4.0
1	D	325	ALA	4.0
1	D	167	GLN	3.9
1	C	231	LEU	3.9
1	D	371	ARG	3.9
1	D	152	PHE	3.9
1	D	238	GLU	3.8
1	B	1	SER	3.8
1	A	132	VAL	3.7
1	C	36	SER	3.6
1	A	209	GLY	3.6
1	D	206	GLY	3.6
1	C	221	HIS	3.6
1	D	377	LEU	3.6
1	D	223	ALA	3.6
1	D	382	GLY	3.6
1	B	392	LEU	3.5
1	D	236	ASP	3.4
1	D	330	LEU	3.4
1	D	339	VAL	3.3
1	D	269	ILE	3.3
1	D	220	ARG	3.2
1	D	306	LYS	3.2
1	D	173	ASP	3.2
1	C	67	ALA	3.2
1	C	234	ALA	3.2
1	C	80	ALA	3.2
1	D	324	CYS	3.2
1	D	378	CYS	3.2
1	C	153	TYR	3.2

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Mol	Chain	Res	Type	RSRZ
1	D	310	LEU	3.1
1	D	180	VAL	3.1
1	D	281	VAL	3.1
1	D	375	ALA	3.1
1	D	153	TYR	3.0
1	A	206	GLY	2.9
1	D	331	GLY	2.9
1	D	195	PHE	2.9
1	D	313	VAL	2.9
1	B	208	LYS	2.9
1	D	5	ILE	2.9
1	D	181	ALA	2.9
1	D	189	ALA	2.8
1	D	350	ILE	2.8
1	B	132	VAL	2.8
1	C	392	LEU	2.8
1	D	391	SER	2.8
1	A	131	GLY	2.7
1	D	155	TYR	2.7
1	D	178	PHE	2.7
1	C	226	ASP	2.7
1	C	209	GLY	2.7
1	C	334	PRO	2.7
1	D	307	ILE	2.7
1	C	235	PHE	2.7
1	D	303	ALA	2.6
1	C	135	GLY	2.6
1	D	289	GLY	2.6
1	D	15	VAL	2.6
1	C	224	THR	2.6
1	C	207	ARG	2.6
1	C	371	ARG	2.6
1	C	239	GLY	2.6
1	A	207	ARG	2.6
1	D	191	LYS	2.6
1	D	301	GLU	2.6
1	D	311	ASP	2.6
1	D	367	ARG	2.5
1	D	254	ALA	2.5
1	D	192	ASP	2.5
1	C	230	LYS	2.5
1	D	241	VAL	2.5

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Mol	Chain	Res	Type	RSRZ
1	D	299	ALA	2.4
1	C	312	LEU	2.4
1	D	165	ALA	2.4
1	D	389	ILE	2.4
1	D	175	GLN	2.4
1	D	368	ARG	2.4
1	C	49	VAL	2.4
1	D	329	ASP	2.3
1	D	166	LYS	2.3
1	D	374	LEU	2.3
1	D	370	ALA	2.3
1	C	222	GLY	2.3
1	D	171	SER	2.3
1	D	319	PHE	2.3
1	D	42	ALA	2.2
1	D	177	ALA	2.2
1	D	211	ILE	2.2
1	D	4	SER	2.2
1	C	35	ILE	2.2
1	C	22	PHE	2.2
1	C	156	HIS	2.2
1	C	295	ALA	2.2
1	C	266	ARG	2.2
1	D	249	LEU	2.2
1	D	318	ALA	2.2
1	C	265	SER	2.1
1	D	202	PHE	2.1
1	C	170	LEU	2.1
1	C	181	ALA	2.1
1	D	272	LEU	2.1
1	C	161	ALA	2.1
1	D	372	LYS	2.1
1	B	2	THR	2.1
1	C	155	TYR	2.1
1	C	305	TRP	2.1
1	D	179	ALA	2.1
1	D	243	ALA	2.1
1	D	187	GLU	2.1
1	D	320	ALA	2.0
1	D	205	LYS	2.0
1	D	218	TYR	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 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
3	GOL	B	6393	6/6	0.93	0.11	2.10	9,24,30,31	0
3	GOL	A	5393	6/6	0.91	0.10	0.62	17,23,28,28	0
2	SO4	B	9719	5/5	0.98	0.07	-	67,67,68,69	0
2	SO4	A	9722	5/5	0.94	0.15	-	65,65,68,69	0
2	SO4	B	9721	5/5	0.97	0.08	-	42,45,51,54	0
2	SO4	A	9720	5/5	0.98	0.10	-	44,49,52,55	0

6.5 Other polymers [i](#)

There are no such residues in this entry.