



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 08:19 AM GMT

PDB ID : 3E4B
Title : Crystal structure of AlgK from Pseudomonas fluorescens WCS374r
Authors : Keiski, C.-L.; Harwich, M.; Jain, S.; Neculai, A.M.; Yip, P.; Robinson, H.; Whitney, J.C.; Burrows, L.L.; Ohman, D.E.; Howell, P.L.
Deposited on : 2008-08-11
Resolution : 2.50 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 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
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) : trunk26865

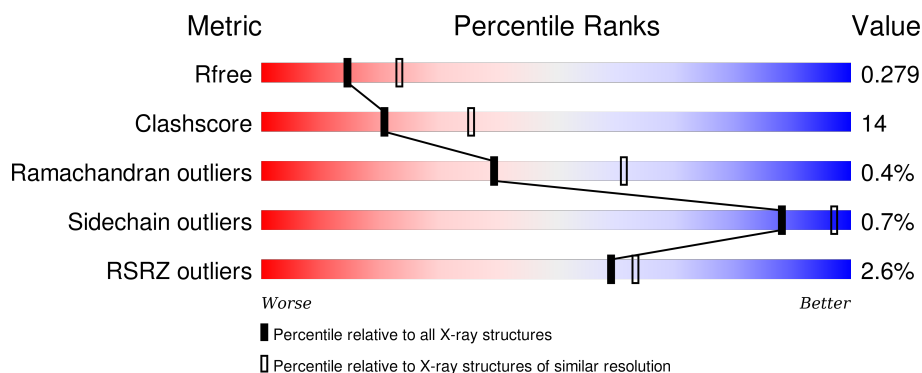
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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}	91344	3553 (2.50-2.50)
Clashscore	102246	4242 (2.50-2.50)
Ramachandran outliers	100387	4156 (2.50-2.50)
Sidechain outliers	100360	4158 (2.50-2.50)
RSRZ outliers	91569	3562 (2.50-2.50)

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	452	
1	B	452	
1	C	452	
1	D	452	

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
3	GOL	C	455	-	-	-	X

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 12341 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 AlgK.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	395	Total	C	N	O	S	0	0	0
			2988	1877	526	579	6			
1	B	405	Total	C	N	O	S	0	0	0
			3045	1915	530	594	6			
1	C	405	Total	C	N	O	S	0	0	0
			3057	1918	533	600	6			
1	D	316	Total	C	N	O	S	0	0	0
			2371	1493	407	466	5			

- Molecule 2 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	1	Total	Cl	0	0
			1	1		
2	A	1	Total	Cl	0	0
			1	1		
2	C	1	Total	Cl	0	0
			1	1		

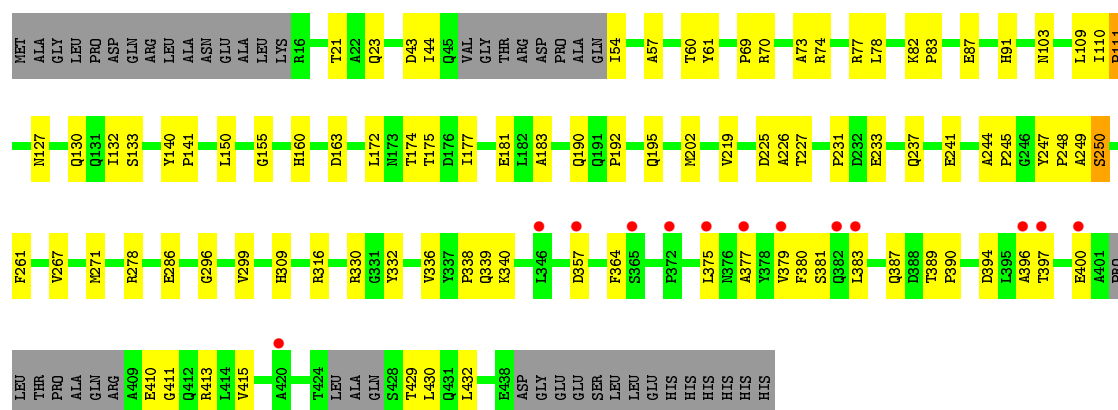
- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



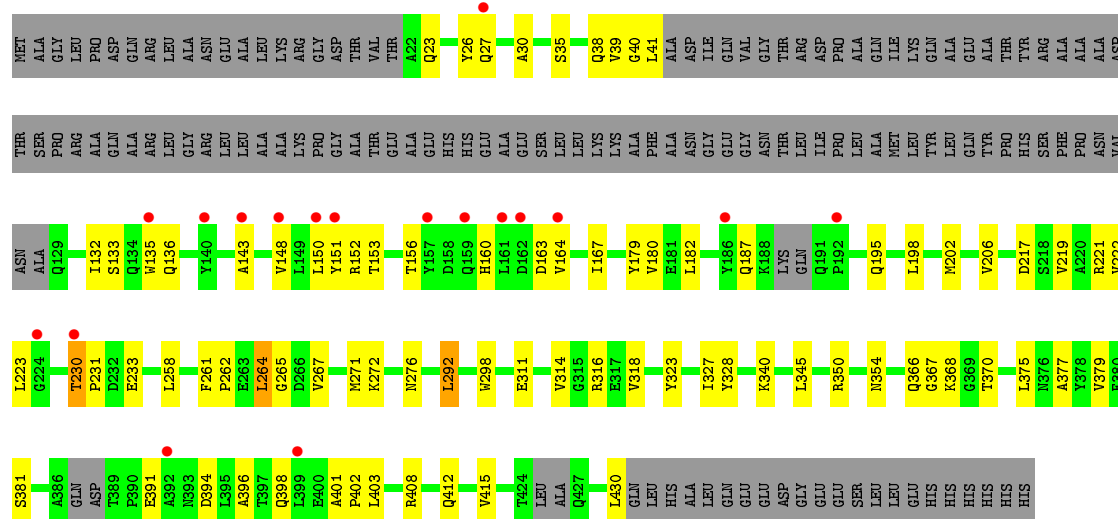
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	B	1	Total	C	O	0	0
			6	3	3		
3	C	1	Total	C	O	0	0
			6	3	3		
3	C	1	Total	C	O	0	0
			6	3	3		
3	D	1	Total	C	O	0	0
			6	3	3		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	197	Total	O	0	0
			197	197		
4	B	222	Total	O	0	0
			222	222		
4	C	302	Total	O	0	0
			302	302		
4	D	132	Total	O	0	0
			132	132		



● Molecule 1: AlgK



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	79.09Å 107.82Å 119.03Å 90.00° 96.97° 90.00°	Depositor
Resolution (Å)	49.05 – 2.50 49.05 – 2.50	Depositor EDS
% Data completeness (in resolution range)	99.8 (49.05-2.50) 100.0 (49.05-2.50)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.05 (at 2.51Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.220 , 0.280 0.220 , 0.279	Depositor DCC
R_{free} test set	3540 reflections (5.16%)	DCC
Wilson B-factor (Å ²)	41.9	Xtriage
Anisotropy	0.218	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 63.8	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 68663 reflections	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	12341	wwPDB-VP
Average B, all atoms (Å ²)	48.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.10% 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, 0.375 respectively for untwinned datasets, and 0.333, 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, CL

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	0.46	0/3039	0.66	0/4129
1	B	0.50	0/3100	0.67	1/4217 (0.0%)
1	C	0.53	0/3111	0.68	0/4230
1	D	0.50	0/2411	0.70	2/3277 (0.1%)
All	All	0.50	0/11661	0.68	3/15853 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	292	LEU	CA-CB-CG	5.51	127.98	115.30
1	B	215	ARG	CG-CD-NE	-5.28	100.72	111.80
1	D	264	LEU	CA-CB-CG	5.00	126.80	115.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2988	0	2888	83	0
1	B	3045	0	2896	85	0
1	C	3057	0	2913	96	0
1	D	2371	0	2243	65	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
3	B	6	0	8	0	0
3	C	12	0	16	0	0
3	D	6	0	8	0	0
4	A	197	0	0	7	0
4	B	222	0	0	7	0
4	C	302	0	0	6	0
4	D	132	0	0	3	0
All	All	12341	0	10972	324	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 14.

All (324) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:202:MET:HE3	1:B:219:VAL:HG21	1.30	1.09
1:B:202:MET:CE	1:B:219:VAL:HG21	2.02	0.90
1:C:387:GLN:HG2	1:C:389:THR:HG23	1.52	0.90
1:A:191:GLN:HB3	1:A:194:GLN:OE1	1.72	0.89
1:C:330:ARG:HB3	1:C:330:ARG:HH11	1.39	0.85
1:C:233:GLU:HG2	1:C:261:PHE:CD1	2.13	0.84
1:A:303:ALA:HB1	1:A:333:LEU:HD23	1.59	0.83
1:B:191:GLN:HB3	1:B:194:GLN:OE1	1.76	0.83
1:C:336:VAL:O	1:C:338:PRO:HD3	1.78	0.83
1:C:60:THR:HG23	1:C:61:TYR:H	1.43	0.83
1:B:60:THR:HB	4:B:716:HOH:O	1.77	0.83
1:C:202:MET:CE	1:C:219:VAL:HG21	2.10	0.82
1:B:274:LEU:O	1:B:278:ARG:HG3	1.78	0.82
1:D:391:GLU:H	1:D:391:GLU:CD	1.84	0.80
1:D:148:VAL:HG22	1:D:164:VAL:HG22	1.63	0.79
1:B:233:GLU:HG2	1:B:261:PHE:CD1	2.20	0.77
1:B:367:GLY:HA2	1:B:370:THR:O	1.83	0.77
1:C:74:ARG:NH1	1:C:74:ARG:HB2	2.00	0.77
1:C:54:ILE:HG12	1:C:54:ILE:O	1.84	0.76
1:C:430:LEU:HB3	1:C:432:LEU:HD11	1.66	0.76
1:C:202:MET:HE3	1:C:219:VAL:HG21	1.67	0.75
1:C:390:PRO:O	1:C:394:ASP:HB2	1.87	0.75
1:A:214:GLN:HG2	1:A:214:GLN:O	1.88	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:226:ALA:HA	1:C:231:PRO:HG3	1.71	0.73
1:D:233:GLU:HB2	1:D:264:LEU:CD2	2.19	0.72
1:B:175:THR:HG22	1:B:177:ILE:HG22	1.72	0.72
1:D:202:MET:HE2	1:D:219:VAL:HG21	1.71	0.72
1:B:57:ALA:O	1:B:60:THR:HG22	1.90	0.71
1:B:26:TYR:CE1	1:B:41:LEU:HD11	2.25	0.71
1:B:311:GLU:O	1:B:314:VAL:HG22	1.91	0.71
1:A:335:LYS:HG2	1:A:336:VAL:H	1.54	0.71
1:B:278:ARG:HH11	1:B:278:ARG:HB3	1.54	0.71
1:B:225:ASP:OD1	1:B:227:THR:HB	1.91	0.70
1:A:331:GLY:HA3	1:A:336:VAL:HG22	1.71	0.70
1:B:26:TYR:CZ	1:B:41:LEU:HD11	2.27	0.69
1:C:339:GLN:HG3	1:C:340:LYS:H	1.56	0.69
1:D:233:GLU:HB2	1:D:264:LEU:HD23	1.73	0.69
1:A:369:GLY:C	1:B:436:GLN:HG3	2.11	0.69
1:A:22:ALA:HA	1:A:118:GLN:HE21	1.58	0.69
1:D:272:LYS:HE2	1:D:276:ASN:HD21	1.59	0.68
1:B:385:LYS:HA	1:B:392:ALA:HB1	1.74	0.68
1:C:183:ALA:HA	1:C:195:GLN:HE22	1.58	0.67
1:B:44:ILE:CG2	1:B:78:LEU:HD13	2.24	0.67
1:C:432:LEU:HD12	1:C:432:LEU:N	2.10	0.67
1:B:186:TYR:HB3	1:B:195:GLN:HG2	1.74	0.67
1:B:109:LEU:HD21	1:B:135:TRP:CE3	2.29	0.67
1:A:353:GLN:HE21	1:A:355:SER:HB2	1.59	0.66
1:A:299:VAL:HB	1:A:300:PRO:HD2	1.78	0.66
1:A:330:ARG:HD2	1:A:332:TYR:CZ	2.30	0.66
1:B:286:GLU:OE1	1:B:309:HIS:HD2	1.80	0.65
1:A:411:GLY:HA2	1:A:414:LEU:HD12	1.77	0.65
1:B:233:GLU:HG2	1:B:261:PHE:CG	2.31	0.65
1:C:87:GLU:HG2	1:C:91:HIS:CE1	2.32	0.65
1:A:413:ARG:HH11	1:A:413:ARG:HG2	1.62	0.64
1:B:160:HIS:HD2	1:B:163:ASP:OD2	1.80	0.64
1:D:318:VAL:HG23	4:D:704:HOH:O	1.98	0.64
1:C:57:ALA:HA	1:C:60:THR:HG22	1.79	0.64
1:C:375:LEU:O	1:C:379:VAL:HG23	1.98	0.64
1:C:60:THR:HG23	1:C:61:TYR:N	2.12	0.64
1:D:264:LEU:HD12	1:D:264:LEU:O	1.98	0.63
1:A:92:GLU:O	1:A:96:LEU:HG	1.99	0.63
1:C:411:GLY:O	1:C:415:VAL:HG23	1.98	0.63
1:B:190:GLN:O	1:B:192:PRO:HD3	1.99	0.63
1:C:364:PHE:HB2	1:C:377:ALA:HB2	1.81	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:330:ARG:HB3	1:C:330:ARG:NH1	2.10	0.62
1:C:233:GLU:HG2	1:C:261:PHE:CG	2.34	0.62
1:A:240:LEU:HB2	1:A:254:LEU:HD21	1.80	0.62
1:D:156:THR:HB	1:D:160:HIS:HE1	1.64	0.62
1:C:202:MET:HE1	1:C:219:VAL:HG21	1.82	0.61
1:C:247:TYR:O	1:C:250:SER:HB2	1.99	0.61
1:D:40:GLY:O	1:D:41:LEU:CB	2.48	0.61
1:C:57:ALA:O	1:C:60:THR:HG22	2.00	0.61
1:A:225:ASP:OD1	1:A:227:THR:HB	2.01	0.61
1:C:339:GLN:CG	1:C:340:LYS:H	2.14	0.60
1:A:291:LYS:O	1:A:295:GLU:HG2	2.01	0.60
1:D:202:MET:CE	1:D:219:VAL:HG21	2.31	0.60
1:B:291:LYS:HE3	1:B:323:TYR:OH	2.02	0.60
1:C:225:ASP:OD1	1:C:227:THR:HB	2.02	0.60
1:B:108:THR:C	1:B:111:PRO:HD2	2.21	0.59
1:B:208:ARG:HG2	1:B:208:ARG:HH11	1.67	0.59
1:B:32:LEU:HD21	1:B:152:ARG:CZ	2.32	0.59
1:A:335:LYS:HG2	1:A:336:VAL:N	2.18	0.59
1:C:387:GLN:HG2	1:C:389:THR:CG2	2.27	0.58
1:B:283:PRO:HD2	4:B:598:HOH:O	2.04	0.58
1:C:127:ASN:HB3	1:C:130:GLN:HB2	1.86	0.58
1:B:188:LYS:NZ	4:B:652:HOH:O	2.36	0.57
1:B:278:ARG:NH1	1:B:278:ARG:HB3	2.19	0.57
1:A:269:GLN:O	1:A:272:LYS:N	2.35	0.57
1:D:156:THR:HB	1:D:160:HIS:CE1	2.39	0.57
1:C:190:GLN:O	1:C:192:PRO:HD3	2.05	0.57
1:A:28:GLN:HB3	4:A:524:HOH:O	2.04	0.57
1:A:291:LYS:HE3	1:A:323:TYR:OH	2.04	0.57
1:B:299:VAL:HG22	1:B:300:PRO:HD2	1.87	0.57
1:B:57:ALA:O	1:B:60:THR:CG2	2.52	0.57
1:B:289:LEU:HD23	1:B:309:HIS:CD2	2.40	0.57
1:D:202:MET:HE1	1:D:219:VAL:HG11	1.85	0.57
1:A:186:TYR:CB	1:A:195:GLN:HG2	2.35	0.56
1:A:186:TYR:HB3	1:A:195:GLN:HG2	1.87	0.56
1:D:187:GLN:NE2	1:D:230:THR:O	2.39	0.56
1:D:153:THR:HG22	4:D:763:HOH:O	2.06	0.56
1:C:233:GLU:HG2	1:C:261:PHE:CE1	2.40	0.56
1:A:394:ASP:HB3	4:A:585:HOH:O	2.06	0.56
1:B:330:ARG:CZ	1:B:332:TYR:OH	2.54	0.55
1:C:330:ARG:NH1	1:C:332:TYR:CE1	2.75	0.55
1:D:35:SER:HG	1:D:38:GLN:CD	2.10	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:136:GLN:HG3	1:A:143:ALA:HB1	1.89	0.55
1:D:202:MET:O	1:D:206:VAL:HG23	2.07	0.55
1:B:377:ALA:HB1	1:B:399:LEU:HD13	1.88	0.55
1:C:155:GLY:HA2	4:C:609:HOH:O	2.06	0.55
1:B:296:GLY:HA2	1:B:299:VAL:O	2.07	0.55
1:C:110:ILE:HB	1:C:111:PRO:HD3	1.88	0.54
1:A:289:LEU:HD22	1:A:309:HIS:ND1	2.22	0.54
1:C:57:ALA:CA	1:C:60:THR:HG22	2.37	0.54
1:B:39:VAL:HG23	1:B:41:LEU:HD13	1.88	0.54
1:A:269:GLN:OE1	1:A:269:GLN:HA	2.08	0.54
1:A:283:PRO:HG3	1:A:316:ARG:CZ	2.37	0.54
1:C:57:ALA:O	1:C:60:THR:CG2	2.55	0.54
1:C:74:ARG:HH11	1:C:74:ARG:HB2	1.71	0.54
1:B:14:LEU:HD12	1:B:14:LEU:H	1.73	0.54
1:B:131:GLN:O	1:B:134:GLN:HB3	2.08	0.54
1:A:281:ASP:O	1:A:283:PRO:HD3	2.07	0.54
1:C:174:THR:HG23	4:C:720:HOH:O	2.08	0.54
1:D:375:LEU:O	1:D:379:VAL:HG23	2.08	0.54
1:A:331:GLY:CA	1:A:336:VAL:HG22	2.36	0.53
1:B:154:GLN:O	1:B:156:THR:HG23	2.07	0.53
1:A:289:LEU:O	1:A:289:LEU:HD23	2.09	0.53
1:A:326:GLN:OE1	1:A:326:GLN:HA	2.07	0.53
1:D:182:LEU:HB3	1:D:198:LEU:HD22	1.91	0.53
1:A:289:LEU:C	1:A:289:LEU:HD23	2.29	0.53
1:C:73:ALA:HB1	1:C:77:ARG:HH12	1.74	0.53
1:B:375:LEU:O	1:B:379:VAL:HG23	2.09	0.53
1:D:316:ARG:HG3	1:D:316:ARG:HH11	1.73	0.53
1:A:280:ALA:O	1:A:281:ASP:HB3	2.07	0.53
1:B:360:ILE:O	1:B:363:LEU:HB3	2.09	0.53
1:A:408:ARG:HD3	4:A:560:HOH:O	2.09	0.52
1:B:247:TYR:O	1:B:250:SER:HB2	2.09	0.52
1:B:44:ILE:O	1:B:44:ILE:HG22	2.09	0.52
1:C:109:LEU:O	1:C:109:LEU:HD23	2.09	0.52
1:A:175:THR:HG22	1:A:177:ILE:HG22	1.90	0.52
1:A:190:GLN:O	1:A:192:PRO:HD3	2.09	0.52
1:C:286:GLU:OE1	1:C:309:HIS:HD2	1.92	0.52
1:D:163:ASP:O	1:D:167:ILE:HG13	2.09	0.52
1:C:74:ARG:HH11	1:C:74:ARG:CB	2.23	0.52
1:B:86:THR:OG1	1:B:89:GLU:HG3	2.10	0.52
1:A:24:GLN:O	1:A:28:GLN:HG3	2.10	0.51
1:A:243:ILE:HB	4:A:646:HOH:O	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:289:LEU:HD21	1:A:293:TYR:CE2	2.45	0.51
1:A:110:ILE:HB	1:A:111:PRO:HD3	1.91	0.51
1:A:77:ARG:NH2	4:A:599:HOH:O	2.43	0.51
1:B:94:GLU:O	1:B:98:LYS:HG3	2.09	0.51
1:D:233:GLU:HB2	1:D:264:LEU:HD21	1.91	0.51
1:A:202:MET:O	1:A:206:VAL:HG23	2.11	0.51
1:B:44:ILE:HG22	1:B:78:LEU:HD13	1.92	0.51
1:D:367:GLY:HA2	1:D:370:THR:O	2.11	0.51
1:A:259:TYR:HE2	1:A:295:GLU:OE2	1.94	0.51
1:C:109:LEU:C	1:C:109:LEU:HD23	2.31	0.51
1:B:310:PHE:CE2	1:B:323:TYR:HB3	2.45	0.50
1:A:78:LEU:HD23	1:A:78:LEU:C	2.31	0.50
1:B:301:ALA:O	1:C:133:SER:OG	2.22	0.50
1:D:202:MET:HE2	1:D:219:VAL:CG2	2.41	0.50
1:D:132:ILE:HA	1:D:135:TRP:CE3	2.47	0.50
1:A:413:ARG:NH1	1:A:413:ARG:HG2	2.27	0.50
1:C:316:ARG:HH11	1:C:316:ARG:HG3	1.77	0.50
1:C:330:ARG:NH1	1:C:332:TYR:HE1	2.10	0.49
1:C:78:LEU:C	1:C:78:LEU:HD23	2.33	0.49
1:B:401:ALA:HB3	1:B:402:PRO:HD3	1.95	0.49
1:C:396:ALA:O	1:C:400:GLU:HG3	2.13	0.49
1:B:208:ARG:NH1	1:B:208:ARG:HG2	2.26	0.49
1:C:430:LEU:HB3	1:C:432:LEU:CD1	2.40	0.49
1:A:150:LEU:HD23	1:A:150:LEU:C	2.33	0.49
1:C:430:LEU:CB	1:C:432:LEU:HD11	2.41	0.49
1:C:175:THR:HG22	1:C:177:ILE:HG22	1.95	0.49
1:C:60:THR:CG2	1:C:61:TYR:H	2.20	0.48
1:B:38:GLN:NE2	1:B:177:ILE:HB	2.27	0.48
1:D:272:LYS:HE2	1:D:276:ASN:ND2	2.26	0.48
1:B:197:GLU:HA	1:B:197:GLU:OE1	2.14	0.48
1:D:258:LEU:HD11	1:D:265:GLY:HA3	1.95	0.48
1:A:401:ALA:HB3	1:A:402:PRO:HD3	1.95	0.48
1:B:396:ALA:O	1:B:400:GLU:HB2	2.14	0.48
1:D:39:VAL:HG23	1:D:40:GLY:N	2.28	0.48
1:B:24:GLN:O	1:B:28:GLN:HG3	2.13	0.48
1:D:354:ASN:N	1:D:354:ASN:OD1	2.47	0.48
1:D:366:GLN:O	1:D:368:LYS:HG2	2.13	0.48
1:D:403:LEU:O	1:D:408:ARG:NH2	2.38	0.48
1:C:57:ALA:HA	1:C:60:THR:CG2	2.44	0.48
1:D:30:ALA:HB2	4:D:699:HOH:O	2.14	0.48
1:B:130:GLN:HG3	4:B:660:HOH:O	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:57:ALA:C	1:C:60:THR:HG22	2.35	0.47
1:B:283:PRO:HG3	1:B:316:ARG:CZ	2.44	0.47
1:A:190:GLN:C	1:A:192:PRO:HD3	2.35	0.47
1:D:292:LEU:HD22	1:D:298:TRP:HB2	1.96	0.47
1:B:411:GLY:O	1:B:415:VAL:HG23	2.14	0.47
1:D:179:TYR:CD1	1:D:198:LEU:HD11	2.49	0.47
1:B:27:GLN:O	1:B:31:GLU:HG2	2.14	0.47
1:B:278:ARG:HD2	1:B:286:GLU:OE2	2.14	0.47
1:C:397:THR:O	1:C:400:GLU:HB2	2.15	0.47
1:B:436:GLN:HB2	4:B:773:HOH:O	2.14	0.47
1:A:305:ALA:O	1:A:308:ALA:HB3	2.14	0.47
1:D:180:VAL:HG13	1:D:222:VAL:HG21	1.96	0.47
1:A:74:ARG:HB3	4:A:540:HOH:O	2.15	0.47
1:D:258:LEU:CD1	1:D:265:GLY:HA3	2.45	0.47
1:D:412:GLN:HG3	1:D:412:GLN:O	2.14	0.47
1:D:377:ALA:O	1:D:381:SER:HB2	2.15	0.47
1:A:332:TYR:C	1:A:334:GLY:H	2.19	0.46
1:A:367:GLY:HA2	1:A:370:THR:O	2.15	0.46
1:B:190:GLN:C	1:B:192:PRO:HD3	2.35	0.46
1:C:336:VAL:C	1:C:338:PRO:HD3	2.35	0.46
1:C:339:GLN:HG3	1:C:340:LYS:N	2.27	0.46
1:C:375:LEU:HD11	1:C:411:GLY:HA3	1.97	0.46
1:C:316:ARG:NH1	1:C:316:ARG:HG3	2.31	0.46
1:C:339:GLN:CG	1:C:340:LYS:N	2.78	0.46
1:C:61:TYR:CE1	1:C:74:ARG:HD2	2.51	0.46
1:C:202:MET:HE1	1:C:219:VAL:CG2	2.45	0.46
1:C:23:GLN:NE2	4:C:568:HOH:O	2.48	0.46
1:D:264:LEU:CD1	1:D:264:LEU:O	2.63	0.46
1:B:336:VAL:HG12	1:B:337:TYR:N	2.31	0.46
1:A:176:ASP:OD1	1:A:215:ARG:NE	2.48	0.46
1:A:326:GLN:HE22	1:A:329:ARG:HH21	1.64	0.46
1:A:243:ILE:CG2	1:A:247:TYR:HB3	2.46	0.46
1:A:287:LEU:HD21	1:A:319:ALA:HB3	1.98	0.46
1:C:267:VAL:O	1:C:271:MET:HG2	2.15	0.46
1:C:330:ARG:HH11	1:C:330:ARG:CB	2.20	0.45
1:C:377:ALA:O	1:C:381:SER:HB2	2.17	0.45
1:B:188:LYS:HE2	1:B:228:LEU:HD22	1.98	0.45
1:C:172:LEU:O	1:C:172:LEU:HD12	2.17	0.45
1:A:109:LEU:HD23	1:A:109:LEU:C	2.37	0.45
1:D:401:ALA:HB3	1:D:402:PRO:HD3	1.99	0.45
1:C:160:HIS:HD2	1:C:163:ASP:OD2	2.00	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:233:GLU:HG2	1:A:234:LYS:H	1.81	0.45
1:B:193:GLU:HG3	4:B:710:HOH:O	2.17	0.45
1:A:232:ASP:OD1	1:A:235:THR:OG1	2.32	0.45
1:D:160:HIS:HB3	1:D:163:ASP:HB2	1.99	0.45
1:C:21:THR:HG22	4:C:624:HOH:O	2.17	0.44
1:C:140:TYR:HA	1:C:141:PRO:HD2	1.85	0.44
1:B:278:ARG:CB	1:B:278:ARG:NH1	2.80	0.44
1:A:175:THR:HA	4:A:526:HOH:O	2.16	0.44
1:D:398:GLN:O	1:D:402:PRO:HD3	2.17	0.44
1:D:26:TYR:HB2	1:D:27:GLN:NE2	2.32	0.44
1:B:202:MET:CE	1:B:219:VAL:CG2	2.87	0.44
1:A:326:GLN:NE2	1:A:329:ARG:HH21	2.15	0.44
1:C:70:ARG:HG3	1:C:70:ARG:HH11	1.83	0.44
1:C:410:GLU:O	1:C:413:ARG:HB3	2.17	0.44
1:B:113:ALA:HB2	1:B:135:TRP:HZ3	1.82	0.44
1:D:323:TYR:O	1:D:327:ILE:HG13	2.18	0.44
1:C:429:THR:HG22	1:D:350:ARG:NH2	2.33	0.44
1:D:328:TYR:CD2	1:D:340:LYS:HB3	2.52	0.44
1:B:342:LEU:O	1:B:346:LEU:HB2	2.18	0.44
1:A:22:ALA:HA	1:A:118:GLN:NE2	2.31	0.44
1:C:160:HIS:HE1	4:C:696:HOH:O	1.99	0.44
1:C:380:PHE:HA	1:C:383:LEU:HB2	2.00	0.44
1:B:304:LYS:HB2	1:C:130:GLN:NE2	2.33	0.44
1:C:73:ALA:HB1	1:C:77:ARG:NH1	2.33	0.44
1:C:78:LEU:O	1:C:78:LEU:HD23	2.18	0.44
1:A:381:SER:HB3	1:A:399:LEU:HD12	2.00	0.44
1:B:108:THR:O	1:B:111:PRO:HD2	2.18	0.44
1:C:177:ILE:HG13	1:C:177:ILE:O	2.18	0.43
1:D:311:GLU:HA	1:D:314:VAL:HG23	2.00	0.43
1:C:244:ALA:N	1:C:245:PRO:CD	2.81	0.43
1:A:356:ALA:O	1:A:360:ILE:HG13	2.19	0.43
1:A:108:THR:C	1:A:111:PRO:HD2	2.38	0.43
1:A:233:GLU:HG2	1:A:234:LYS:N	2.33	0.43
1:C:357:ASP:HB2	4:C:764:HOH:O	2.18	0.43
1:A:404:THR:HG23	1:A:407:GLN:OE1	2.18	0.43
1:A:189:LYS:HB3	1:A:191:GLN:HG3	1.99	0.43
1:B:278:ARG:HD3	1:B:289:LEU:CD2	2.49	0.43
1:B:177:ILE:O	1:B:177:ILE:HG13	2.18	0.43
1:D:381:SER:OG	1:D:396:ALA:HA	2.19	0.43
1:A:353:GLN:NE2	1:A:355:SER:HB2	2.27	0.43
1:D:379:VAL:HG13	1:D:415:VAL:CG2	2.48	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:23:GLN:O	1:D:27:GLN:HG2	2.19	0.43
1:A:267:VAL:O	1:A:271:MET:HG2	2.18	0.43
1:A:331:GLY:HA2	1:A:335:LYS:O	2.19	0.43
1:C:278:ARG:HH11	1:C:278:ARG:HG2	1.83	0.43
1:C:60:THR:CG2	1:C:61:TYR:N	2.81	0.43
1:B:278:ARG:HD3	1:B:289:LEU:HD22	2.00	0.43
1:A:424:THR:O	1:A:424:THR:HG22	2.18	0.42
1:B:115:LEU:HA	4:B:606:HOH:O	2.17	0.42
1:A:110:ILE:N	1:A:111:PRO:CD	2.82	0.42
1:D:35:SER:HG	1:D:38:GLN:CG	2.32	0.42
1:C:69:PRO:HG2	1:C:103:ASN:ND2	2.34	0.42
1:C:82:LYS:HA	1:C:83:PRO:HD3	1.90	0.42
1:D:195:GLN:HA	1:D:195:GLN:OE1	2.20	0.42
1:A:222:VAL:O	1:A:228:LEU:HD12	2.20	0.42
1:A:126:VAL:HG12	1:A:127:ASN:N	2.35	0.42
1:B:54:ILE:HA	1:B:54:ILE:HD13	1.88	0.42
1:B:346:LEU:HD22	1:B:350:ARG:CZ	2.50	0.42
1:D:136:GLN:HB3	1:D:143:ALA:HB1	2.01	0.42
1:C:43:ASP:O	1:C:44:ILE:HG23	2.20	0.42
1:A:331:GLY:HA3	1:A:336:VAL:CG2	2.43	0.41
1:A:112:LEU:HD11	1:A:116:TYR:CZ	2.55	0.41
1:C:237:GLN:O	1:C:241:GLU:HG3	2.21	0.41
1:A:269:GLN:O	1:A:270:MET:C	2.58	0.41
1:D:261:PHE:O	1:D:262:PRO:C	2.58	0.41
1:B:397:THR:HA	1:B:400:GLU:HB3	2.01	0.41
1:D:187:GLN:OE1	1:D:223:LEU:HD22	2.20	0.41
1:B:244:ALA:N	1:B:245:PRO:CD	2.83	0.41
1:D:150:LEU:C	1:D:152:ARG:N	2.73	0.41
1:B:392:ALA:O	1:B:396:ALA:HB2	2.20	0.41
1:A:345:LEU:O	1:A:356:ALA:HB1	2.21	0.41
1:D:391:GLU:N	1:D:391:GLU:CD	2.64	0.41
1:B:150:LEU:C	1:B:150:LEU:HD23	2.40	0.41
1:D:345:LEU:HA	1:D:345:LEU:HD23	1.91	0.41
1:D:316:ARG:HG3	1:D:316:ARG:NH1	2.36	0.41
1:D:267:VAL:O	1:D:271:MET:HG2	2.21	0.41
1:C:296:GLY:HA2	1:C:299:VAL:O	2.20	0.41
1:C:339:GLN:HA	1:D:430:LEU:CB	2.51	0.41
1:B:376:ASN:HA	1:B:379:VAL:HG23	2.02	0.41
1:C:286:GLU:OE1	1:C:309:HIS:CD2	2.73	0.41
1:C:377:ALA:O	1:C:381:SER:CB	2.68	0.41
1:A:259:TYR:CE2	1:A:295:GLU:OE2	2.72	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:133:SER:HA	1:D:136:GLN:HG2	2.02	0.41
1:C:181:GLU:HA	1:C:181:GLU:OE1	2.21	0.41
1:A:339:GLN:O	1:A:343:ASP:HB2	2.21	0.41
1:B:267:VAL:O	1:B:271:MET:HG2	2.21	0.41
1:A:186:TYR:HB2	1:A:195:GLN:HG2	2.02	0.41
1:A:289:LEU:HD22	1:A:309:HIS:CE1	2.56	0.41
1:B:362:GLN:HA	1:B:365:SER:OG	2.21	0.41
1:C:248:PRO:C	1:C:250:SER:N	2.74	0.40
1:C:132:ILE:HD12	1:C:150:LEU:HD12	2.02	0.40
1:D:230:THR:HA	1:D:231:PRO:HD2	1.89	0.40
1:D:150:LEU:O	1:D:152:ARG:N	2.54	0.40
1:D:217:ASP:O	1:D:221:ARG:HG3	2.21	0.40
1:C:74:ARG:CZ	1:C:74:ARG:HB2	2.51	0.40
1:B:333:LEU:HA	1:B:333:LEU:HD23	1.87	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	387/452 (86%)	367 (95%)	20 (5%)	0	100	100
1	B	397/452 (88%)	380 (96%)	14 (4%)	3 (1%)	24	41
1	C	397/452 (88%)	372 (94%)	24 (6%)	1 (0%)	46	68
1	D	306/452 (68%)	287 (94%)	17 (6%)	2 (1%)	26	46
All	All	1487/1808 (82%)	1406 (95%)	75 (5%)	6 (0%)	39	61

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	85	ALA

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Mol	Chain	Res	Type
1	B	386	ALA
1	C	249	ALA
1	D	151	TYR
1	B	367	GLY
1	D	230	THR

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	287/351 (82%)	286 (100%)	1 (0%)	94	99
1	B	287/351 (82%)	283 (99%)	4 (1%)	74	91
1	C	292/351 (83%)	290 (99%)	2 (1%)	88	97
1	D	223/351 (64%)	222 (100%)	1 (0%)	93	98
All	All	1089/1404 (78%)	1081 (99%)	8 (1%)	88	97

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	215	ARG
1	B	215	ARG
1	B	250	SER
1	B	288	LEU
1	B	346	LEU
1	C	111	PRO
1	C	250	SER
1	D	394	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (25) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	25	ASN
1	A	118	GLN
1	A	154	GLN

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Mol	Chain	Res	Type
1	A	351	ASN
1	A	353	GLN
1	B	160	HIS
1	B	201	GLN
1	B	256	GLN
1	B	309	HIS
1	C	23	GLN
1	C	24	GLN
1	C	125	ASN
1	C	130	GLN
1	C	131	GLN
1	C	187	GLN
1	C	190	GLN
1	C	191	GLN
1	C	195	GLN
1	C	309	HIS
1	C	431	GLN
1	C	433	HIS
1	D	27	GLN
1	D	237	GLN
1	D	276	ASN
1	D	351	ASN

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 ⓘ

Of 7 ligands modelled in this entry, 3 are monoatomic - leaving 4 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	$\# Z > 2$
3	GOL	B	453	-	5,5,5	0.25	0	5,5,5	0.25	0
3	GOL	C	453	-	5,5,5	0.32	0	5,5,5	0.20	0
3	GOL	C	455	-	5,5,5	0.29	0	5,5,5	0.23	0
3	GOL	D	453	-	5,5,5	0.14	0	5,5,5	0.27	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	B	453	-	-	0/4/4/4	0/0/0/0
3	GOL	C	453	-	-	0/4/4/4	0/0/0/0
3	GOL	C	455	-	-	0/4/4/4	0/0/0/0
3	GOL	D	453	-	-	0/4/4/4	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.

No monomer is involved in short contacts.

5.7 Other polymers

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 ⓘ

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	395/452 (87%)	-0.07	1 (0%) 94 95	28, 50, 73, 83	0
1	B	405/452 (89%)	-0.07	7 (1%) 73 76	23, 44, 90, 99	0
1	C	405/452 (89%)	0.04	13 (3%) 51 56	17, 38, 80, 94	0
1	D	316/452 (69%)	0.13	18 (5%) 27 31	26, 52, 84, 95	0
All	All	1521/1808 (84%)	0.00	39 (2%) 59 63	17, 46, 81, 99	0

All (39) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	161	LEU	4.8
1	C	396	ALA	4.1
1	D	399	LEU	4.0
1	D	224	GLY	3.7
1	C	397	THR	3.7
1	D	143	ALA	3.6
1	C	357	ASP	3.6
1	D	157	TYR	3.4
1	D	140	TYR	3.4
1	B	399	LEU	3.4
1	B	396	ALA	3.3
1	C	372	PRO	3.3
1	B	395	LEU	3.3
1	B	397	THR	3.2
1	B	378	TYR	3.1
1	B	429	THR	3.0
1	A	430	LEU	2.7
1	C	379	VAL	2.7
1	C	365	SER	2.5
1	D	186	TYR	2.5
1	C	346	LEU	2.5

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Mol	Chain	Res	Type	RSRZ
1	C	383	LEU	2.4
1	C	382	GLN	2.4
1	D	230	THR	2.4
1	D	135	TRP	2.4
1	C	420	ALA	2.3
1	D	27	GLN	2.2
1	B	403	LEU	2.2
1	D	392	ALA	2.2
1	D	159	GLN	2.1
1	D	148	VAL	2.1
1	C	375	LEU	2.1
1	D	150	LEU	2.1
1	C	400	GLU	2.1
1	D	164	VAL	2.1
1	D	151	TYR	2.0
1	C	377	ALA	2.0
1	D	192	PRO	2.0
1	D	162	ASP	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(Å ²)	Q<0.9
3	GOL	C	455	6/6	0.78	0.24	3.47	71,72,72,73	0
3	GOL	D	453	6/6	0.88	0.23	-	70,70,71,72	0
3	GOL	C	453	6/6	0.96	0.16	-	50,52,53,55	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
3	GOL	B	453	6/6	0.90	0.23	-	60,61,62,64	0
2	CL	C	454	1/1	0.95	0.15	-	51,51,51,51	0
2	CL	B	454	1/1	0.93	0.14	-	82,82,82,82	0
2	CL	A	453	1/1	0.99	0.15	-	66,66,66,66	0

6.5 Other polymers [i](#)

There are no such residues in this entry.