Full wwPDB X-ray Structure Validation Report (i)

Aug 22, 2023 – 10:14 PM EDT

PDB ID	:	3E2F
Title	:	Crystal structure of mouse kynurenine aminotransferase III, PLP-bound form
Authors	:	Han, Q.; Robinson, R.; Cai, T.; Tagle, D.A.; Li, J.
Deposited on	:	2008-08-05
Resolution	:	2.59 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
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references (i)) were used in the production of this report:

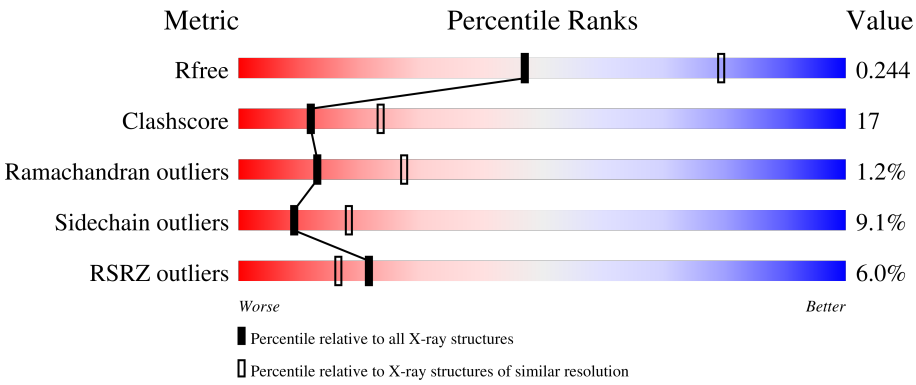
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.59 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}	130704	3163 (2.60-2.60)
Clashscore	141614	3518 (2.60-2.60)
Ramachandran outliers	138981	3455 (2.60-2.60)
Sidechain outliers	138945	3455 (2.60-2.60)
RSRZ outliers	127900	3104 (2.60-2.60)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=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	410	5% 66% 29% 5%
1	B	410	7% 66% 27% 6% •

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
1	LLP	A	281	-	X	-	-
2	GOL	A	456	-	X	X	-
2	GOL	A	457	-	-	X	-

2 Entry composition (i)

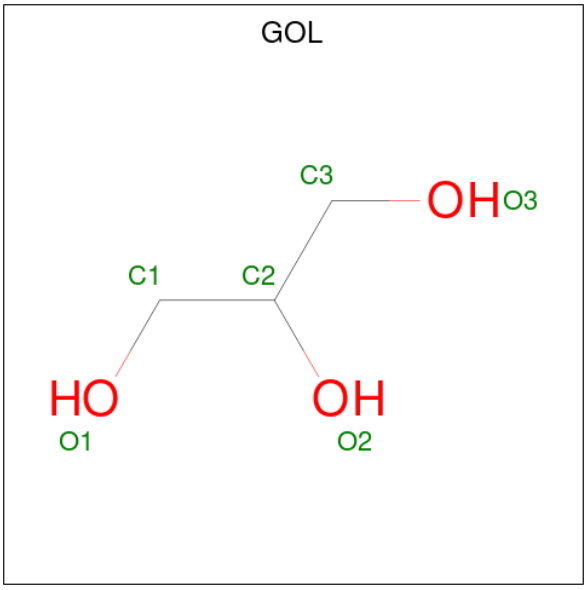
There are 3 unique types of molecules in this entry. The entry contains 6736 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Kynurenine-oxoglutarate transaminase 3.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	P	S			
1	A	410	3268	2108	537	604	1	18	0	0	0
1	B	410	3268	2108	537	604	1	18	0	0	0

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



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

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

- Molecule 3 is water.

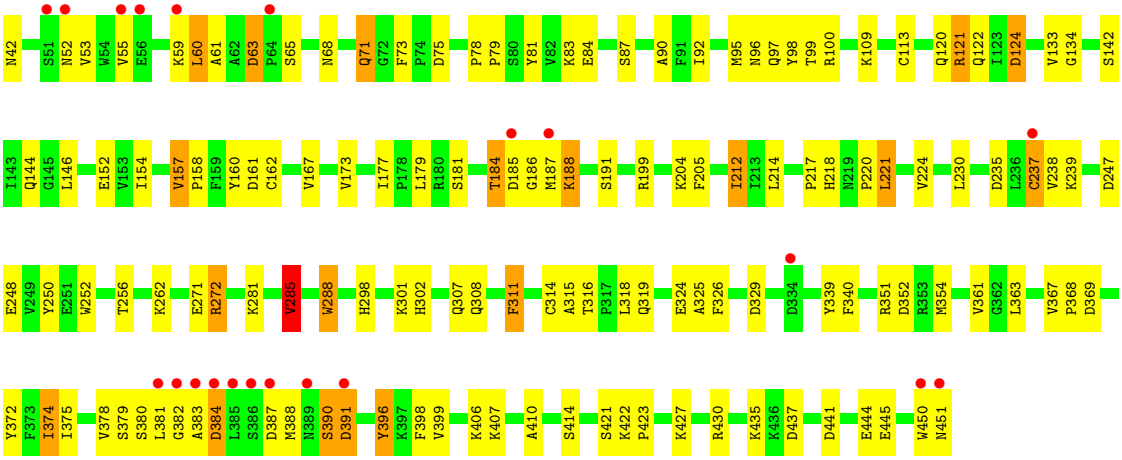
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
3	A	61	61	61	0	0
			Total	O		
3	B	79	79	79	0	0

3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density (RSRZ > 2). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

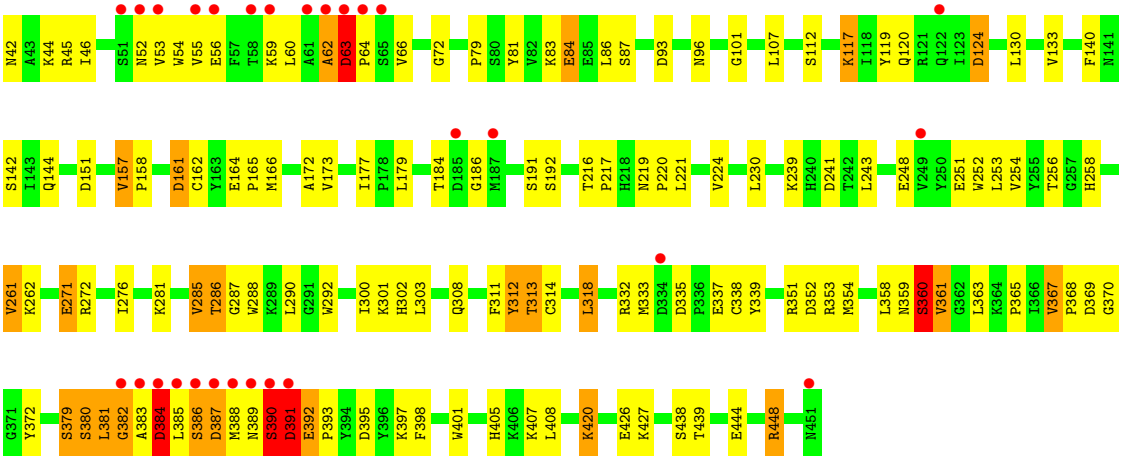
• Molecule 1: Kynurenine-oxoglutarate transaminase 3

Chain A:



• Molecule 1: Kynurenine-oxoglutarate transaminase 3

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α, β, γ	91.82Å 91.82Å 233.65Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.21 – 2.59 29.21 – 2.59	Depositor EDS
% Data completeness (in resolution range)	91.0 (29.21-2.59) 91.0 (29.21-2.59)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.27 (at 2.61Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.193 , 0.246 0.193 , 0.244	Depositor DCC
R_{free} test set	1476 reflections (5.08%)	wwPDB-VP
Wilson B-factor (Å^2)	36.5	Xtriage
Anisotropy	0.236	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.39 , 52.9	EDS
L-test for twinning[2]	$< \|L\| > = 0.51$, $< L^2 > = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	6736	wwPDB-VP
Average B, all atoms (Å^2)	30.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.68% of the height of the origin peak. No significant pseudotranslation is detected.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ 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: LLP, GOL

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	1.18	2/3331 (0.1%)	1.05	9/4525 (0.2%)
1	B	1.12	3/3331 (0.1%)	1.02	7/4525 (0.2%)
All	All	1.15	5/6662 (0.1%)	1.04	16/9050 (0.2%)

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	1	6
1	B	1	9
All	All	2	15

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	396	TYR	CD2-CE2	5.62	1.47	1.39
1	B	251	GLU	CD-OE1	5.48	1.31	1.25
1	A	311	PHE	CB-CG	-5.46	1.42	1.51
1	B	314	CYS	CB-SG	-5.26	1.73	1.81
1	B	271	GLU	CG-CD	5.16	1.59	1.51

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	352	ASP	CB-CG-OD2	5.98	123.69	118.30
1	A	199	ARG	NE-CZ-NH1	5.72	123.16	120.30
1	A	230	LEU	CB-CG-CD2	-5.30	102.00	111.00
1	A	124	ASP	CB-CG-OD2	5.26	123.03	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	63	ASP	CB-CG-OD2	5.25	123.02	118.30
1	B	63	ASP	CB-CG-OD2	5.24	123.02	118.30
1	B	391	ASP	CB-CG-OD2	5.23	123.01	118.30
1	A	384	ASP	CB-CG-OD2	5.22	123.00	118.30
1	B	387	ASP	CB-CG-OD2	5.22	123.00	118.30
1	B	384	ASP	CB-CG-OD2	5.21	122.99	118.30
1	B	124	ASP	CB-CG-OD2	5.20	122.98	118.30
1	A	391	ASP	CB-CG-OD2	5.20	122.98	118.30
1	A	352	ASP	CB-CG-OD2	5.18	122.96	118.30
1	A	288	TRP	CA-CB-CG	-5.08	104.05	113.70
1	B	161	ASP	CB-CG-OD2	5.08	122.87	118.30
1	A	437	ASP	CB-CG-OD2	-5.03	113.77	118.30

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	256	THR	CB
1	B	286	THR	CB

All (15) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	121	ARG	Peptide
1	A	237	CYS	Peptide
1	A	383	ALA	Peptide
1	A	388	MET	Peptide
1	A	390	SER	Peptide
1	A	391	ASP	Peptide
1	B	380	SER	Peptide
1	B	381	LEU	Peptide
1	B	382	GLY	Peptide
1	B	383	ALA	Peptide
1	B	384	ASP	Peptide
1	B	390	SER	Peptide
1	B	391	ASP	Peptide
1	B	392	GLU	Peptide
1	B	62	ALA	Peptide

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	3268	0	3236	110	0
1	B	3268	0	3235	139	0
2	A	36	0	47	11	0
2	B	24	0	32	3	0
3	A	61	0	0	3	0
3	B	79	0	0	1	0
All	All	6736	0	6550	228	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 17.

All (228) 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:52:ASN:OD1	1:A:55:VAL:HG13	1.35	1.23
1:B:66:VAL:HG13	1:B:407:LYS:O	1.51	1.11
2:A:456:GOL:H31	2:A:457:GOL:O1	1.49	1.10
2:A:456:GOL:C3	2:A:457:GOL:O1	1.99	1.09
1:A:97:GLN:NE2	1:B:286:THR:HB	1.81	0.96
1:B:389:ASN:O	1:B:390:SER:HB2	1.64	0.95
1:A:78:PRO:HG2	1:A:83:LYS:HD2	1.47	0.95
1:A:96:ASN:HD22	1:B:288:TRP:HE1	0.97	0.95
1:A:430:ARG:HH22	2:A:456:GOL:H11	1.28	0.95
1:B:448:ARG:HG3	1:B:448:ARG:HH11	1.34	0.93
1:B:311:PHE:HB2	3:B:502:HOH:O	1.70	0.90
1:B:184:THR:HG23	1:B:186:GLY:H	1.38	0.86
1:A:288:TRP:HE1	1:B:96:ASN:HD22	1.21	0.85
1:B:392:GLU:HB2	1:B:393:PRO:CD	2.07	0.85
1:A:184:THR:HG23	1:A:186:GLY:H	1.43	0.82
1:A:52:ASN:OD1	1:A:55:VAL:CG1	2.25	0.81
1:A:96:ASN:ND2	1:B:288:TRP:HE1	1.77	0.81
1:B:56:GLU:HA	1:B:59:LYS:HE3	1.64	0.80
1:B:285:VAL:O	1:B:285:VAL:CG1	2.30	0.80
1:A:285:VAL:CG1	1:A:285:VAL:O	2.30	0.79
2:A:456:GOL:H32	2:A:457:GOL:O1	1.82	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:448:ARG:HG3	1:B:448:ARG:NH1	1.94	0.77
1:A:42:ASN:HB3	1:B:302:HIS:CE1	2.20	0.77
1:B:380:SER:O	1:B:381:LEU:HD23	1.87	0.75
1:A:221:LEU:HD12	1:A:375:ILE:HD12	1.67	0.75
1:A:184:THR:CG2	1:A:186:GLY:H	2.00	0.73
1:A:324:GLU:HA	1:A:324:GLU:OE2	1.87	0.72
1:B:63:ASP:N	1:B:64:PRO:HD3	2.05	0.71
1:A:99:THR:HG23	1:A:100:ARG:N	2.06	0.71
1:B:62:ALA:O	1:B:64:PRO:CD	2.39	0.70
1:A:97:GLN:HE22	1:B:286:THR:HB	1.56	0.70
1:A:97:GLN:NE2	1:A:97:GLN:HA	2.07	0.70
1:B:392:GLU:CB	1:B:393:PRO:CD	2.68	0.70
1:A:382:GLY:O	1:A:384:ASP:HB2	1.92	0.70
1:A:95:MET:O	1:A:316:THR:HB	1.90	0.70
1:B:312:TYR:CD1	1:B:313:THR:HG22	2.27	0.69
1:B:285:VAL:O	1:B:285:VAL:HG13	1.92	0.69
1:A:71:GLN:OE1	1:A:73:PHE:HB2	1.92	0.69
1:A:98:TYR:N	1:B:286:THR:OG1	2.25	0.69
1:B:62:ALA:O	1:B:64:PRO:HD2	1.92	0.69
1:B:285:VAL:HG13	1:B:288:TRP:CG	2.28	0.68
1:A:97:GLN:HE21	1:B:286:THR:HB	1.57	0.67
1:B:392:GLU:HB2	1:B:393:PRO:HD2	1.77	0.67
1:B:191:SER:OG	1:B:368:PRO:HA	1.93	0.67
1:A:285:VAL:O	1:A:285:VAL:HG13	1.93	0.67
1:A:363:LEU:HD21	1:A:381:LEU:HD22	1.77	0.67
1:B:389:ASN:O	1:B:390:SER:CB	2.41	0.66
1:A:185:ASP:OD2	1:A:187:MET:N	2.29	0.65
1:B:107:LEU:O	1:B:107:LEU:HD12	1.96	0.65
1:A:217:PRO:HG2	1:A:250:TYR:O	1.96	0.65
1:B:392:GLU:CB	1:B:393:PRO:HD3	2.25	0.65
1:B:448:ARG:HH11	1:B:448:ARG:CG	2.10	0.65
1:B:63:ASP:CG	1:B:63:ASP:O	2.33	0.64
1:B:363:LEU:O	1:B:365:PRO:HD3	1.98	0.64
1:A:97:GLN:NE2	1:B:286:THR:H	1.95	0.64
1:A:97:GLN:HE22	1:B:286:THR:H	1.46	0.64
1:A:298:HIS:HA	1:A:301:LYS:HE2	1.80	0.63
1:B:335:ASP:HB3	1:B:337:GLU:OE1	1.99	0.63
1:B:390:SER:O	1:B:397:LYS:HE3	1.98	0.63
1:B:241:ASP:OD1	1:B:272:ARG:NH2	2.32	0.62
1:A:315:ALA:O	1:A:319:GLN:HG3	1.99	0.62
1:A:430:ARG:NH2	2:A:456:GOL:H11	2.08	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:122:GLN:NE2	3:A:514:HOH:O	2.30	0.61
1:B:380:SER:C	1:B:381:LEU:HD23	2.19	0.61
1:A:185:ASP:OD2	1:A:186:GLY:N	2.34	0.61
1:B:332:ARG:O	1:B:338:CYS:HB2	2.00	0.61
1:A:399:VAL:HG11	1:A:410:ALA:O	2.00	0.61
1:A:285:VAL:HG13	1:A:288:TRP:CG	2.36	0.61
1:B:381:LEU:HD23	1:B:381:LEU:N	2.16	0.60
1:A:311:PHE:CD2	1:B:311:PHE:CZ	2.89	0.60
1:B:361:VAL:HG23	1:B:361:VAL:O	2.02	0.60
1:A:248:GLU:OE1	1:A:262:LYS:HG2	2.02	0.60
1:B:120:GLN:OE1	1:B:120:GLN:HA	2.02	0.59
1:B:117:LYS:HE2	1:B:333:MET:HE3	1.84	0.59
1:A:224:VAL:HG23	1:A:369:ASP:HB2	1.85	0.59
1:A:133:VAL:HG21	1:B:133:VAL:HG21	1.83	0.59
1:A:288:TRP:CD1	1:A:288:TRP:N	2.69	0.59
1:B:151:ASP:O	1:B:172:ALA:HB1	2.01	0.59
1:A:98:TYR:CE2	1:B:286:THR:HG22	2.38	0.59
1:A:152:GLU:HG2	1:A:173:VAL:HG22	1.85	0.58
1:A:61:ALA:HB1	1:A:68:ASN:ND2	2.18	0.58
1:B:359:ASN:O	1:B:361:VAL:N	2.36	0.58
1:B:62:ALA:C	1:B:64:PRO:HD3	2.23	0.58
1:B:60:LEU:N	1:B:60:LEU:HD12	2.19	0.58
1:A:396:TYR:HE1	1:A:414:SER:OG	1.87	0.57
2:A:456:GOL:C3	2:A:457:GOL:C1	2.82	0.57
1:A:142:SER:O	1:A:146:LEU:HB2	2.04	0.57
1:A:302:HIS:CE1	1:B:42:ASN:HB3	2.40	0.56
1:A:95:MET:CE	1:A:95:MET:HA	2.36	0.56
1:B:62:ALA:O	1:B:64:PRO:HD3	2.04	0.56
1:A:363:LEU:HD22	1:A:378:VAL:HG12	1.87	0.56
1:B:390:SER:O	1:B:397:LYS:CE	2.53	0.56
2:A:456:GOL:H32	2:A:457:GOL:C1	2.36	0.56
1:B:81:TYR:HA	1:B:84:GLU:HB2	1.88	0.56
1:B:162:CYS:O	1:B:166:MET:HB2	2.06	0.56
1:B:66:VAL:HG13	1:B:407:LYS:C	2.23	0.55
1:A:187:MET:HB3	1:A:188:LYS:HG3	1.89	0.55
1:B:66:VAL:HG22	1:B:407:LYS:HB3	1.88	0.55
1:B:117:LYS:HE2	1:B:333:MET:CE	2.37	0.54
1:A:154:ILE:HB	1:A:212:ILE:HG13	1.90	0.54
1:A:221:LEU:HD12	1:A:375:ILE:CD1	2.36	0.54
1:B:290:LEU:HD11	1:B:318:LEU:HB3	1.90	0.54
1:A:285:VAL:O	1:A:285:VAL:HG12	2.08	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:161:ASP:OD1	2:A:457:GOL:H2	2.08	0.53
1:B:140:PHE:CZ	1:B:144:GLN:HG3	2.42	0.53
1:B:420:LYS:HD2	1:B:420:LYS:N	2.23	0.53
1:A:97:GLN:NE2	1:B:286:THR:CB	2.65	0.53
1:A:237:CYS:O	1:A:272:ARG:HD3	2.08	0.53
1:A:315:ALA:HA	1:B:287:GLY:O	2.09	0.53
1:B:360:SER:OG	1:B:361:VAL:HG13	2.08	0.53
1:B:312:TYR:CD1	1:B:313:THR:CG2	2.91	0.52
1:B:124:ASP:C	1:B:124:ASP:OD2	2.48	0.52
1:B:216:THR:HA	1:B:217:PRO:C	2.30	0.52
1:A:311:PHE:HD2	1:B:311:PHE:CZ	2.28	0.52
1:B:63:ASP:N	1:B:64:PRO:CD	2.73	0.52
1:B:312:TYR:HD1	1:B:313:THR:CG2	2.23	0.52
1:B:337:GLU:OE1	1:B:337:GLU:N	2.43	0.51
1:A:237:CYS:O	1:A:272:ARG:CD	2.58	0.51
1:B:285:VAL:HG13	1:B:288:TRP:HB2	1.91	0.51
1:B:52:ASN:O	1:B:55:VAL:HG12	2.10	0.51
1:A:368:PRO:HD3	1:A:374:ILE:HD12	1.91	0.51
1:B:285:VAL:CG1	1:B:288:TRP:CG	2.93	0.51
1:B:382:GLY:C	1:B:384:ASP:OD2	2.48	0.51
1:A:95:MET:HA	1:A:95:MET:HE2	1.92	0.51
1:A:288:TRP:N	1:A:288:TRP:HD1	2.09	0.50
1:A:217:PRO:HB2	1:A:250:TYR:HB2	1.92	0.50
2:A:456:GOL:H31	2:A:457:GOL:C1	2.40	0.50
1:B:224:VAL:HG23	1:B:369:ASP:HB2	1.93	0.50
1:B:258:HIS:CD2	1:B:369:ASP:HB3	2.47	0.50
1:B:248:GLU:OE1	1:B:262:LYS:HG2	2.12	0.50
1:A:90:ALA:O	1:B:83:LYS:HG2	2.11	0.50
1:A:441:ASP:O	1:A:444:GLU:HB3	2.12	0.50
1:B:285:VAL:O	1:B:285:VAL:HG12	2.09	0.50
1:B:63:ASP:O	1:B:63:ASP:OD1	2.30	0.49
1:B:252:TRP:CZ3	2:B:458:GOL:H2	2.46	0.49
1:A:181:SER:O	2:A:458:GOL:O3	2.30	0.49
1:A:351:ARG:HD2	1:A:368:PRO:HG2	1.95	0.49
1:B:359:ASN:O	1:B:360:SER:C	2.49	0.49
1:B:56:GLU:O	1:B:59:LYS:HB2	2.11	0.49
1:A:124:ASP:OD2	1:A:124:ASP:C	2.50	0.49
1:A:87:SER:OG	1:B:87:SER:OG	2.26	0.49
1:B:101:GLY:HA2	1:B:313:THR:HB	1.94	0.49
1:A:122:GLN:HA	3:A:498:HOH:O	2.12	0.49
1:A:361:VAL:HG23	1:A:363:LEU:HG	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:98:TYR:CZ	1:B:286:THR:HG22	2.48	0.48
1:B:353:ARG:HH11	1:B:444:GLU:HG3	1.79	0.48
1:A:83:LYS:HE3	1:B:93:ASP:OD2	2.14	0.48
1:A:422:LYS:N	1:A:423:PRO:HD3	2.29	0.48
1:A:298:HIS:HA	1:A:301:LYS:CE	2.44	0.48
1:A:52:ASN:O	1:A:55:VAL:HG22	2.13	0.48
1:B:130:LEU:CD2	1:B:303:LEU:HB3	2.44	0.48
1:B:391:ASP:OD1	1:B:391:ASP:O	2.32	0.47
1:A:252:TRP:CE3	1:A:340:PHE:HB3	2.50	0.47
1:A:81:TYR:HA	1:A:84:GLU:HG3	1.96	0.47
1:A:406:LYS:O	1:A:407:LYS:HB2	2.14	0.47
1:B:130:LEU:HD23	1:B:303:LEU:HB3	1.97	0.47
1:B:290:LEU:CD1	1:B:318:LEU:HB3	2.44	0.47
1:A:318:LEU:HD11	1:B:318:LEU:HD22	1.96	0.47
1:B:230:LEU:HD12	1:B:261:VAL:HG22	1.97	0.47
1:B:253:LEU:O	1:B:370:GLY:HA2	2.14	0.47
1:B:161:ASP:OD2	2:B:456:GOL:H11	2.15	0.46
1:A:177:ILE:HB	1:A:204:LYS:HE3	1.96	0.46
1:B:119:TYR:O	1:B:120:GLN:HB2	2.15	0.46
1:A:157:VAL:HG23	1:A:158:PRO:HA	1.97	0.46
1:B:54:TRP:CH2	2:B:457:GOL:H12	2.51	0.46
1:A:144:GLN:O	1:B:45:ARG:NH1	2.46	0.46
1:B:276:ILE:HA	1:B:292:TRP:O	2.16	0.46
1:B:408:LEU:HD12	1:B:408:LEU:HA	1.72	0.46
1:B:164:GLU:HB3	1:B:165:PRO:HD3	1.98	0.46
1:B:351:ARG:HD2	1:B:368:PRO:HD2	1.98	0.45
1:B:79:PRO:HG3	1:B:339:TYR:CE1	2.52	0.45
1:A:406:LYS:HD2	1:A:450:TRP:CD2	2.52	0.45
1:A:98:TYR:CE2	1:B:286:THR:CG2	3.00	0.45
1:B:395:ASP:HB3	1:B:426:GLU:O	2.17	0.45
1:A:422:LYS:N	1:A:423:PRO:CD	2.79	0.45
1:A:238:VAL:CG2	1:A:239:LYS:N	2.80	0.45
1:B:59:LYS:O	1:B:62:ALA:HB3	2.16	0.44
1:B:66:VAL:HG22	1:B:407:LYS:CA	2.47	0.44
1:B:254:VAL:O	1:B:254:VAL:HG23	2.16	0.44
1:A:398:PHE:CD2	1:A:398:PHE:C	2.89	0.44
1:B:66:VAL:HG22	1:B:407:LYS:CB	2.46	0.44
1:B:66:VAL:HG22	1:B:407:LYS:HA	1.98	0.44
1:A:92:ILE:O	1:A:95:MET:HB2	2.18	0.44
1:B:45:ARG:HG3	1:B:46:ILE:HG23	1.99	0.44
1:A:247:ASP:C	1:A:247:ASP:OD1	2.55	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:142:SER:HA	1:B:303:LEU:HD11	1.99	0.44
1:B:360:SER:OG	1:B:361:VAL:CG1	2.65	0.44
1:A:410:ALA:HB1	1:A:430:ARG:O	2.18	0.44
1:B:56:GLU:O	1:B:60:LEU:CD1	2.66	0.44
1:B:191:SER:HB2	1:B:369:ASP:OD2	2.18	0.44
1:A:406:LYS:HD2	1:A:450:TRP:CE2	2.52	0.43
1:B:157:VAL:HA	1:B:158:PRO:C	2.38	0.43
1:B:401:TRP:CD1	1:B:405:HIS:HD2	2.36	0.43
1:B:444:GLU:O	1:B:448:ARG:HB2	2.18	0.43
1:A:63:ASP:OD2	1:A:63:ASP:C	2.56	0.43
1:B:56:GLU:O	1:B:60:LEU:HD13	2.18	0.43
1:A:79:PRO:HG3	1:A:339:TYR:CZ	2.54	0.42
1:A:81:TYR:OH	1:A:329:ASP:OD2	2.26	0.42
1:B:285:VAL:HG13	1:B:288:TRP:CB	2.47	0.42
1:A:221:LEU:HD12	1:A:221:LEU:HA	1.77	0.42
1:B:386:SER:C	1:B:388:MET:N	2.72	0.42
1:A:184:THR:CG2	1:A:186:GLY:N	2.75	0.42
1:A:205:PHE:HE2	1:A:237:CYS:HG	1.65	0.42
1:A:272:ARG:NH1	3:A:482:HOH:O	2.52	0.42
1:B:300:ILE:O	1:B:301:LYS:C	2.58	0.42
1:B:86:LEU:HD22	1:B:288:TRP:CZ2	2.54	0.42
1:A:363:LEU:HA	1:A:363:LEU:HD23	1.71	0.42
1:A:325:ALA:O	1:A:326:PHE:C	2.57	0.41
1:B:177:ILE:O	1:B:177:ILE:HG23	2.19	0.41
1:B:354:MET:O	1:B:358:LEU:HG	2.19	0.41
1:A:218:HIS:HE1	1:A:220:PRO:HD2	1.84	0.41
1:A:314:CYS:HB2	1:A:319:GLN:NE2	2.35	0.41
1:A:97:GLN:HE21	1:B:286:THR:CB	2.27	0.41
1:B:359:ASN:C	1:B:361:VAL:N	2.72	0.41
1:B:179:LEU:HD23	1:B:179:LEU:HA	1.90	0.41
1:A:363:LEU:CD2	1:A:381:LEU:HD22	2.49	0.41
1:A:75:ASP:OD1	1:A:435:LYS:HA	2.21	0.40
1:A:160:TYR:CE1	2:A:456:GOL:H32	2.55	0.40
1:A:308:GLN:NE2	1:B:52:ASN:HB2	2.36	0.40
1:A:387:ASP:OD1	1:A:387:ASP:N	2.48	0.40
1:B:380:SER:O	1:B:380:SER:OG	2.31	0.40
1:A:379:SER:O	1:A:381:LEU:N	2.55	0.40
1:B:219:ASN:HA	1:B:220:PRO:HA	1.92	0.40
1:B:379:SER:HB3	1:B:427:LYS:HG3	2.02	0.40
1:A:78:PRO:HD2	1:B:93:ASP:OD2	2.21	0.40
1:B:398:PHE:CD2	1:B:398:PHE:C	2.95	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:107:LEU:HD12	1:B:107:LEU:C	2.39	0.40
1:B:367:VAL:HA	1:B:368:PRO:HD3	1.88	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	407/410 (99%)	373 (92%)	29 (7%)	5 (1%)	13	27
1	B	407/410 (99%)	379 (93%)	23 (6%)	5 (1%)	13	27
All	All	814/820 (99%)	752 (92%)	52 (6%)	10 (1%)	13	27

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	387	ASP
1	B	390	SER
1	A	60	LEU
1	B	360	SER
1	A	134	GLY
1	A	380	SER
1	A	285	VAL
1	A	235	ASP
1	B	312	TYR
1	B	72	GLY

5.3.2 Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	357/357 (100%)	324 (91%)	33 (9%)	9 17
1	B	357/357 (100%)	325 (91%)	32 (9%)	9 18
All	All	714/714 (100%)	649 (91%)	65 (9%)	9 18

All (65) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	53	VAL
1	A	59	LYS
1	A	60	LEU
1	A	65	SER
1	A	71	GLN
1	A	109	LYS
1	A	113	CYS
1	A	120	GLN
1	A	121	ARG
1	A	157	VAL
1	A	162	CYS
1	A	167	VAL
1	A	179	LEU
1	A	184	THR
1	A	188	LYS
1	A	191	SER
1	A	212	ILE
1	A	214	LEU
1	A	221	LEU
1	A	256	THR
1	A	271	GLU
1	A	272	ARG
1	A	285	VAL
1	A	307	GLN
1	A	354	MET
1	A	367	VAL
1	A	372	TYR
1	A	374	ILE
1	A	390	SER
1	A	421	SER
1	A	427	LYS
1	A	445	GLU
1	A	451	ASN

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Mol	Chain	Res	Type
1	B	44	LYS
1	B	53	VAL
1	B	63	ASP
1	B	84	GLU
1	B	112	SER
1	B	117	LYS
1	B	157	VAL
1	B	173	VAL
1	B	192	SER
1	B	221	LEU
1	B	239	LYS
1	B	243	LEU
1	B	256	THR
1	B	261	VAL
1	B	271	GLU
1	B	285	VAL
1	B	286	THR
1	B	308	GLN
1	B	313	THR
1	B	318	LEU
1	B	360	SER
1	B	361	VAL
1	B	367	VAL
1	B	372	TYR
1	B	379	SER
1	B	385	LEU
1	B	386	SER
1	B	390	SER
1	B	420	LYS
1	B	438	SER
1	B	439	THR
1	B	448	ARG

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

Mol	Chain	Res	Type
1	A	42	ASN
1	A	96	ASN
1	A	97	GLN
1	A	307	GLN
1	A	308	GLN
1	A	341	ASN

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Mol	Chain	Res	Type
1	A	451	ASN
1	B	42	ASN
1	B	94	ASN
1	B	96	ASN
1	B	97	GLN
1	B	359	ASN
1	B	405	HIS

5.3.3 RNA (i)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains (i)

2 non-standard protein/DNA/RNA residues 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	$\#\|Z\| > 2$
1	LLP	A	281	1	23,24,25	3.45	13 (56%)	25,32,34	3.43	14 (56%)
1	LLP	B	281	1	23,24,25	2.13	10 (43%)	25,32,34	2.08	7 (28%)

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
1	LLP	A	281	1	-	7/16/17/19	0/1/1/1
1	LLP	B	281	1	-	7/16/17/19	0/1/1/1

All (23) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	281	LLP	O3-C3	7.87	1.55	1.37
1	A	281	LLP	C2-N1	7.57	1.48	1.33
1	A	281	LLP	C4'-NZ	5.41	1.45	1.27
1	B	281	LLP	O3-C3	-4.35	1.26	1.37
1	A	281	LLP	C4-C3	4.00	1.46	1.40
1	A	281	LLP	CD-CE	3.59	1.64	1.51
1	A	281	LLP	C4-C4'	3.59	1.53	1.46
1	A	281	LLP	CE-NZ	3.49	1.54	1.46
1	B	281	LLP	C4-C4'	3.48	1.53	1.46
1	A	281	LLP	C5'-C5	-3.48	1.41	1.50
1	B	281	LLP	CE-NZ	3.44	1.54	1.46
1	B	281	LLP	C4'-NZ	3.16	1.37	1.27
1	A	281	LLP	C6-N1	3.13	1.41	1.34
1	A	281	LLP	C6-C5	2.91	1.43	1.37
1	A	281	LLP	C3-C2	2.87	1.43	1.40
1	A	281	LLP	P-OP4	-2.86	1.51	1.60
1	B	281	LLP	C2-N1	2.80	1.39	1.33
1	A	281	LLP	C4-C5	-2.78	1.38	1.42
1	B	281	LLP	CG-CB	2.74	1.63	1.52
1	B	281	LLP	P-OP3	-2.63	1.44	1.54
1	B	281	LLP	P-OP2	-2.49	1.45	1.54
1	B	281	LLP	C6-C5	2.27	1.42	1.37
1	B	281	LLP	CD-CE	2.05	1.58	1.51

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	281	LLP	C2'-C2-C3	-6.75	112.55	120.89
1	A	281	LLP	OP3-P-OP4	-6.58	89.23	106.73
1	A	281	LLP	O3-C3-C4	6.00	135.72	119.60
1	A	281	LLP	O3-C3-C2	-5.58	105.33	117.49
1	B	281	LLP	OP4-C5'-C5	5.07	119.02	109.35
1	B	281	LLP	C4-C4'-NZ	-4.91	101.78	124.31
1	A	281	LLP	OP4-C5'-C5	4.59	118.10	109.35
1	A	281	LLP	C4-C3-C2	-4.29	117.53	120.19
1	B	281	LLP	C4-C3-C2	-4.28	117.54	120.19
1	A	281	LLP	CD-CE-NZ	-4.23	100.56	110.93
1	A	281	LLP	CE-NZ-C4'	-4.12	106.25	118.90
1	A	281	LLP	C2'-C2-N1	3.86	125.20	117.67
1	B	281	LLP	C3-C4-C5	3.38	120.86	118.26
1	A	281	LLP	C3-C4-C5	3.34	120.83	118.26
1	A	281	LLP	OP3-P-OP2	2.93	118.83	107.64
1	B	281	LLP	O3-C3-C2	2.55	123.06	117.49

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	281	LLP	C4-C4'-NZ	-2.37	113.43	124.31
1	B	281	LLP	C5-C6-N1	-2.28	120.02	123.82
1	A	281	LLP	OP2-P-OP1	2.22	119.36	110.68
1	A	281	LLP	OP2-P-OP4	-2.18	100.93	106.73
1	B	281	LLP	OP3-P-OP2	2.14	115.81	107.64

There are no chirality outliers.

All (14) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	281	LLP	C5'-OP4-P-OP2
1	A	281	LLP	C5'-OP4-P-OP3
1	A	281	LLP	N-CA-CB-CG
1	B	281	LLP	C5-C4-C4'-NZ
1	B	281	LLP	C5'-OP4-P-OP1
1	B	281	LLP	C5'-OP4-P-OP2
1	B	281	LLP	C5'-OP4-P-OP3
1	A	281	LLP	C4-C4'-NZ-CE
1	B	281	LLP	C3-C4-C4'-NZ
1	A	281	LLP	C5'-OP4-P-OP1
1	A	281	LLP	CD-CE-NZ-C4'
1	B	281	LLP	CD-CE-NZ-C4'
1	B	281	LLP	CA-CB-CG-CD
1	A	281	LLP	C3-C4-C4'-NZ

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

10 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	B	456	-	5,5,5	0.50	0	5,5,5	0.94	0
2	GOL	B	458	-	5,5,5	0.72	0	5,5,5	1.12	1 (20%)
2	GOL	B	459	-	5,5,5	0.66	0	5,5,5	0.68	0
2	GOL	A	457	-	5,5,5	0.17	0	5,5,5	0.74	0
2	GOL	A	458	-	5,5,5	0.54	0	5,5,5	0.96	0
2	GOL	A	461	-	5,5,5	0.40	0	5,5,5	0.36	0
2	GOL	A	456	-	5,5,5	2.82	1 (20%)	5,5,5	1.48	2 (40%)
2	GOL	A	459	-	5,5,5	0.59	0	5,5,5	1.44	0
2	GOL	B	457	-	5,5,5	0.91	0	5,5,5	2.14	2 (40%)
2	GOL	A	460	-	5,5,5	0.41	0	5,5,5	0.43	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	GOL	B	456	-	-	2/4/4/4	-
2	GOL	B	458	-	-	4/4/4/4	-
2	GOL	B	459	-	-	2/4/4/4	-
2	GOL	A	457	-	-	2/4/4/4	-
2	GOL	A	458	-	-	2/4/4/4	-
2	GOL	A	461	-	-	2/4/4/4	-
2	GOL	A	456	-	-	3/4/4/4	-
2	GOL	A	459	-	-	0/4/4/4	-
2	GOL	B	457	-	-	2/4/4/4	-
2	GOL	A	460	-	-	4/4/4/4	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	456	GOL	O2-C2	-6.29	1.24	1.43

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	457	GOL	O1-C1-C2	-3.01	95.75	110.20
2	B	457	GOL	C3-C2-C1	-2.77	100.92	111.70
2	A	456	GOL	O2-C2-C3	2.31	119.30	109.12
2	B	458	GOL	O1-C1-C2	-2.30	99.17	110.20
2	A	456	GOL	O2-C2-C1	-2.28	99.07	109.12

There are no chirality outliers.

All (23) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	458	GOL	O1-C1-C2-C3
2	A	461	GOL	C1-C2-C3-O3
2	B	456	GOL	O1-C1-C2-C3
2	B	457	GOL	C1-C2-C3-O3
2	B	458	GOL	O1-C1-C2-C3
2	B	459	GOL	C1-C2-C3-O3
2	A	460	GOL	O2-C2-C3-O3
2	A	461	GOL	O2-C2-C3-O3
2	B	458	GOL	O1-C1-C2-O2
2	A	456	GOL	O1-C1-C2-C3
2	A	456	GOL	C1-C2-C3-O3
2	A	460	GOL	O1-C1-C2-C3
2	A	460	GOL	C1-C2-C3-O3
2	A	458	GOL	O1-C1-C2-O2
2	A	460	GOL	O1-C1-C2-O2
2	B	456	GOL	O1-C1-C2-O2
2	B	459	GOL	O2-C2-C3-O3
2	A	457	GOL	O2-C2-C3-O3
2	B	457	GOL	O2-C2-C3-O3
2	B	458	GOL	C1-C2-C3-O3
2	B	458	GOL	O2-C2-C3-O3
2	A	456	GOL	O1-C1-C2-O2
2	A	457	GOL	C1-C2-C3-O3

There are no ring outliers.

6 monomers are involved in 14 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	456	GOL	1	0
2	B	458	GOL	1	0
2	A	457	GOL	7	0
2	A	458	GOL	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	456	GOL	9	0
2	B	457	GOL	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 (i)

6.1 Protein, DNA and RNA chains (i)

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q< 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å^2)	Q<0.9
1	A	409/410 (99%)	-0.01	21 (5%)	28	22	12, 25, 56, 77	0
1	B	409/410 (99%)	0.17	28 (6%)	17	12	13, 28, 68, 81	0
All	All	818/820 (99%)	0.08	49 (5%)	21	16	12, 26, 59, 81	0

All (49) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	383	ALA	7.5
1	B	55	VAL	7.4
1	B	384	ASP	7.2
1	B	389	ASN	5.5
1	B	387	ASP	5.3
1	B	388	MET	4.7
1	A	383	ALA	4.7
1	A	386	SER	4.6
1	B	62	ALA	4.3
1	B	386	SER	4.2
1	B	51	SER	4.1
1	B	187	MET	4.0
1	B	382	GLY	4.0
1	A	387	ASP	3.9
1	A	382	GLY	3.9
1	B	391	ASP	3.8
1	A	237	CYS	3.8
1	A	187	MET	3.8
1	A	451	ASN	3.7
1	B	385	LEU	3.6
1	B	390	SER	3.6
1	A	55	VAL	3.5
1	B	53	VAL	3.4
1	A	52	ASN	3.2

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Mol	Chain	Res	Type	RSRZ
1	B	61	ALA	3.0
1	B	52	ASN	3.0
1	A	391	ASP	2.9
1	A	185	ASP	2.8
1	A	389	ASN	2.8
1	B	63	ASP	2.8
1	A	450	TRP	2.7
1	B	64	PRO	2.7
1	B	185	ASP	2.6
1	A	64	PRO	2.6
1	A	59	LYS	2.6
1	B	122	GLN	2.6
1	B	58	THR	2.5
1	B	59	LYS	2.5
1	B	249	VAL	2.5
1	B	65	SER	2.5
1	A	384	ASP	2.4
1	A	51	SER	2.4
1	B	56	GLU	2.2
1	A	56	GLU	2.2
1	B	451	ASN	2.2
1	A	381	LEU	2.1
1	A	385	LEU	2.0
1	A	334	ASP	2.0
1	B	334	ASP	2.0

6.2 Non-standard residues in protein, DNA, RNA chains (i)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
1	LLP	A	281	24/25	0.97	0.21	16,25,27,32	0
1	LLP	B	281	24/25	0.97	0.21	20,23,29,30	0

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

6.4 Ligands (i)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	GOL	A	460	6/6	0.56	0.25	61,66,69,69	0
2	GOL	A	457	6/6	0.83	0.21	54,59,60,60	0
2	GOL	A	461	6/6	0.85	0.21	54,55,58,59	0
2	GOL	A	459	6/6	0.86	0.32	46,49,53,55	0
2	GOL	B	456	6/6	0.86	0.21	54,56,57,57	0
2	GOL	B	459	6/6	0.86	0.24	55,58,63,66	0
2	GOL	A	456	6/6	0.89	0.30	27,34,40,43	0
2	GOL	B	458	6/6	0.91	0.18	34,40,44,45	0
2	GOL	A	458	6/6	0.93	0.18	33,38,41,45	0
2	GOL	B	457	6/6	0.93	0.28	33,41,49,55	0

6.5 Other polymers (i)

There are no such residues in this entry.