



# Full wwPDB X-ray Structure Validation Report ⓘ

May 24, 2020 – 12:11 pm BST

PDB ID : 2X2J  
Title : Crystal structure of the Gracilariopsis lemaneiformis alpha- 1,4-glucan lyase with deoxynojirimycin  
Authors : Rozeboom, H.J.; Yu, S.; Madrid, S.; Kalk, K.H.; Dijkstra, B.W.  
Deposited on : 2010-01-13  
Resolution : 2.35 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](mailto: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 ⓘ symbol.

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The following versions of software and data (see [references ⓘ](#)) 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 : 2.11  
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) : 2.11

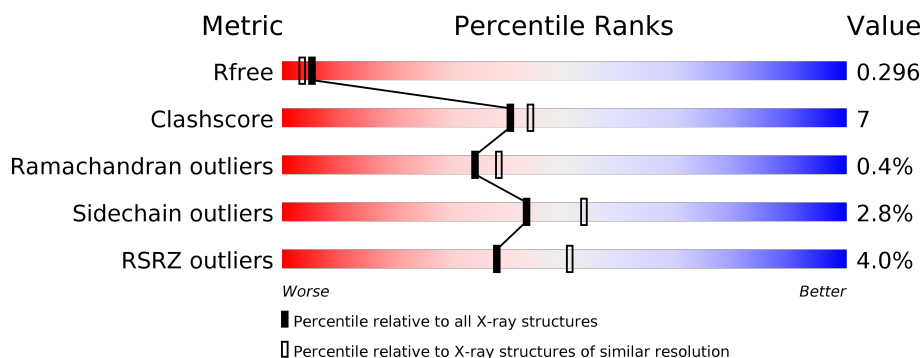
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.35 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	1164 (2.36-2.36)
Clashscore	141614	1232 (2.36-2.36)
Ramachandran outliers	138981	1211 (2.36-2.36)
Sidechain outliers	138945	1212 (2.36-2.36)
RSRZ outliers	127900	1150 (2.36-2.36)

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  $\geq 3$ , 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  $\leq 5\%$ . 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	1027	<div> <div>3%</div> <div>81%</div> <div>18%</div> <div>.</div> </div>
1	B	1027	<div> <div>5%</div> <div>81%</div> <div>18%</div> <div>.</div> </div>
1	C	1027	<div> <div>2%</div> <div>80%</div> <div>19%</div> <div>.</div> </div>
1	D	1027	<div> <div>5%</div> <div>85%</div> <div>14%</div> <div>.</div> </div>

## 2 Entry composition [i](#)

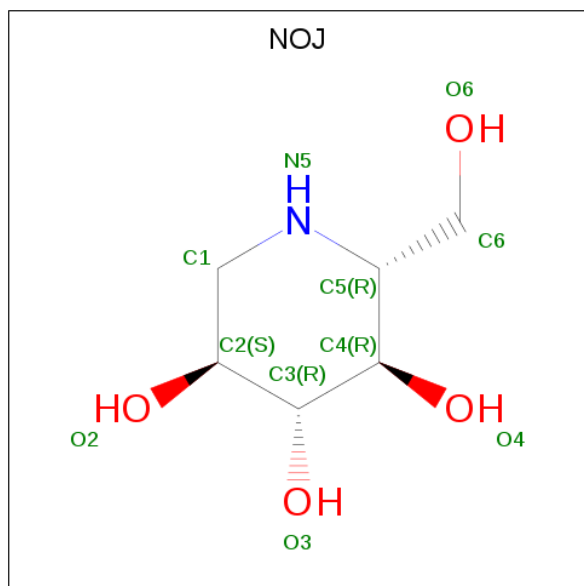
There are 5 unique types of molecules in this entry. The entry contains 34339 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 ALPHA-1,4-GLUCAN LYASE ISOZYME 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	1025	Total	C	N	O	S	0	0	0
			8162	5135	1385	1595	47			
1	B	1025	Total	C	N	O	S	0	0	0
			8162	5135	1385	1595	47			
1	C	1025	Total	C	N	O	S	0	0	0
			8162	5135	1385	1595	47			
1	D	1025	Total	C	N	O	S	0	0	0
			8162	5135	1385	1595	47			

- Molecule 2 is 1-DEOXYNOJIRIMYCIN (three-letter code: NOJ) (formula:  $C_6H_{13}NO_4$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			11	6	1	4		
2	B	1	Total	C	N	O	0	0
			11	6	1	4		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	C	1	Total	C	N	O	0	0
			11	6	1	4		
2	D	1	Total	C	N	O	0	0
			11	6	1	4		

- 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	A	1	Total	C	O	0	0
			6	3	3		
3	A	1	Total	C	O	0	0
			6	3	3		
3	A	1	Total	C	O	0	0
			6	3	3		
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	C	1	Total	C	O	0	0
			6	3	3		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
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 CHLORIDE ION (three-letter code: CL) (formula: Cl).

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

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	444	Total	O	0	0
			444	444		
5	B	362	Total	O	0	0
			362	362		
5	C	461	Total	O	0	0
			461	461		
5	D	310	Total	O	0	0
			310	310		

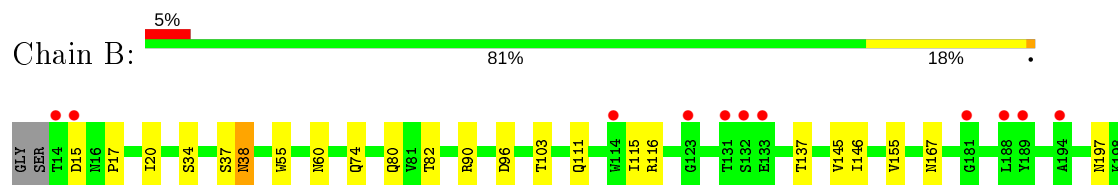
### 3 Residue-property plots [i](#)

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: ALPHA-1,4-GLUCAN LYASE ISOZYME 1

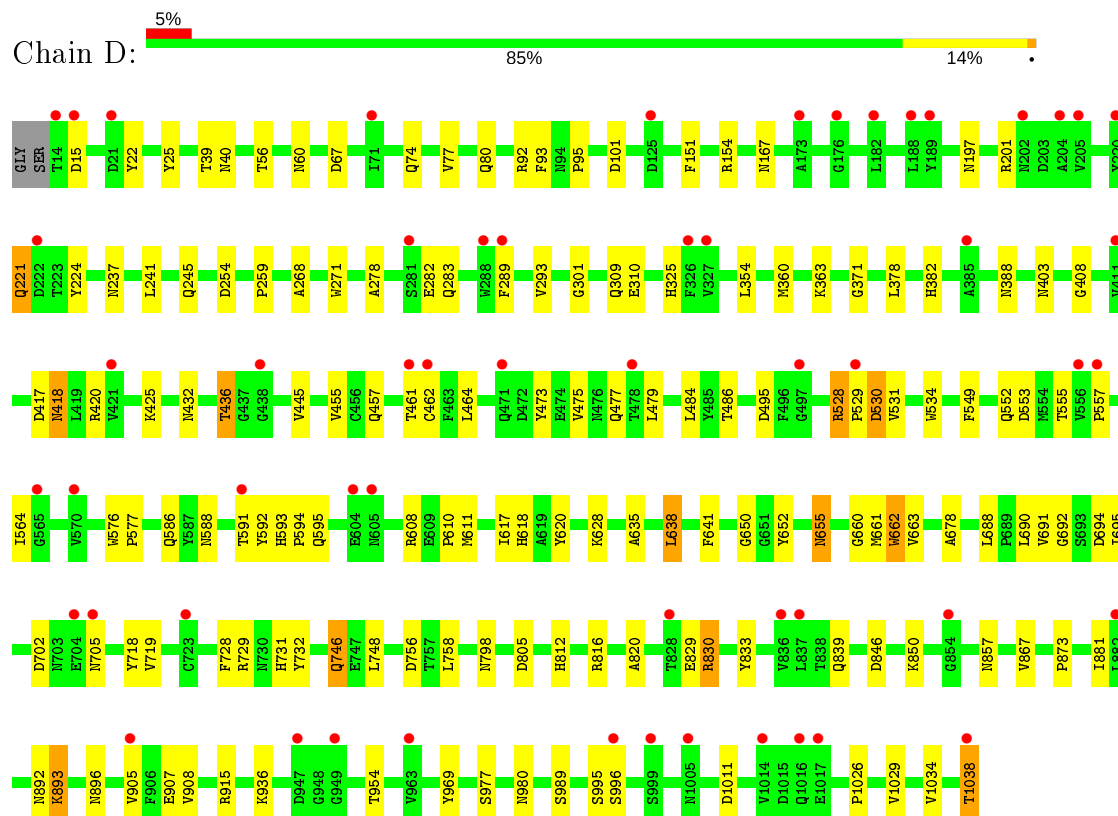


#### • Molecule 1: ALPHA-1,4-GLUCAN LYASE ISOZYME 1





• Molecule 1: ALPHA-1,4-GLUCAN LYASE ISOZYME 1





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	134.31Å 91.71Å 192.90Å 90.00° 99.33° 90.00°	Depositor
Resolution (Å)	33.19 – 2.35 31.23 – 2.35	Depositor EDS
% Data completeness (in resolution range)	91.0 (33.19-2.35) 91.0 (31.23-2.35)	Depositor EDS
$R_{merge}$	0.21	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.13 (at 2.34Å)	Xtriage
Refinement program	REFMAC 5.5.0102	Depositor
R, $R_{free}$	0.234 , 0.291 0.236 , 0.296	Depositor DCC
$R_{free}$ test set	8712 reflections (4.97%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	25.4	Xtriage
Anisotropy	0.461	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 33.9	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.52$ , $\langle L^2 \rangle = 0.36$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	34339	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	46.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 54.51 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 3.6127e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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, CSO, NOJ, 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	0.54	0/8374	0.66	0/11389
1	B	0.51	0/8374	0.63	0/11389
1	C	0.61	0/8374	0.69	0/11389
1	D	0.46	0/8374	0.59	0/11389
All	All	0.53	0/33496	0.64	0/45556

There are no bond length outliers.

There are no bond angle outliers.

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	8162	0	7606	109	0
1	B	8162	0	7606	123	0
1	C	8162	0	7606	122	0
1	D	8162	0	7606	102	0
2	A	11	0	13	1	0
2	B	11	0	13	0	0
2	C	11	0	13	1	0
2	D	11	0	13	0	0
3	A	30	0	40	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	6	0	8	0	0
3	C	24	0	32	5	0
3	D	6	0	8	0	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
4	C	1	0	0	0	0
4	D	1	0	0	0	0
5	A	444	0	0	18	0
5	B	362	0	0	16	0
5	C	461	0	0	24	0
5	D	310	0	0	28	0
All	All	34339	0	30564	455	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 7.

All (455) 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:D:690:LEU:HB3	5:D:3199:HOH:O	1.29	1.28
1:A:941:LYS:HB3	5:A:3401:HOH:O	1.51	1.10
1:D:418:ASN:HB3	5:D:3119:HOH:O	1.62	0.98
1:A:995:SER:HB2	1:A:1011:ASP:HB3	1.43	0.97
1:B:15:ASP:HA	5:B:3221:HOH:O	1.65	0.96
1:B:529:PRO:O	1:B:530:ASP:HB2	1.73	0.87
1:A:959:CYS:HB3	5:A:3412:HOH:O	1.76	0.85
1:C:242:ASN:ND2	1:C:667:SER:HB2	1.92	0.85
1:A:1036:THR:HG23	5:A:3440:HOH:O	1.74	0.85
1:A:15:ASP:OD1	1:A:608:ARG:HD3	1.78	0.84
1:B:282:GLU:HG2	5:B:3104:HOH:O	1.76	0.83
1:C:382:HIS:HB3	5:C:3207:HOH:O	1.79	0.81
1:B:489:ASP:HB2	1:B:608:ARG:HH22	1.46	0.80
1:D:15:ASP:OD1	1:D:608:ARG:HD3	1.80	0.80
1:C:995:SER:HB2	1:C:1011:ASP:HB3	1.63	0.79
1:B:15:ASP:OD1	1:B:608:ARG:HD3	1.82	0.78
1:B:278:ALA:HA	1:B:283:GLN:HG3	1.65	0.78
1:D:805:ASP:CG	1:D:830:ARG:HH22	1.88	0.77
1:A:93:PHE:CE2	1:A:95:PRO:HG3	2.20	0.76
1:A:38:ASN:HD21	1:A:180:ARG:HH11	1.34	0.74
1:D:660:GLY:HA3	5:D:3199:HOH:O	1.88	0.74
1:D:529:PRO:O	1:D:530:ASP:HB2	1.87	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:705:ASN:HA	5:D:3223:HOH:O	1.89	0.71
1:A:588:ASN:HB3	1:A:593:HIS:CE1	2.26	0.70
1:B:995:SER:HB2	1:B:1011:ASP:HB3	1.72	0.70
1:B:360:MET:HE1	5:B:3274:HOH:O	1.90	0.70
1:C:325:HIS:HE1	5:C:3140:HOH:O	1.74	0.69
1:D:241:LEU:HB3	1:D:245:GLN:HE21	1.58	0.69
1:C:325:HIS:HD2	5:C:3037:HOH:O	1.76	0.68
1:D:254:ASP:HB2	5:D:3061:HOH:O	1.93	0.67
1:A:990:GLN:HB2	5:A:3423:HOH:O	1.94	0.67
1:D:325:HIS:HD2	5:D:3015:HOH:O	1.78	0.67
1:D:154:ARG:HD3	5:D:3032:HOH:O	1.94	0.67
1:A:393:GLU:HG2	1:A:397:GLU:OE2	1.94	0.66
1:A:964:PHE:O	1:A:1027:ASN:HB2	1.95	0.66
1:A:286:TYR:HB3	1:A:328:TYR:CD1	2.30	0.66
1:B:805:ASP:CG	1:B:830:ARG:HH22	1.99	0.65
1:C:307:SER:HB2	5:C:3014:HOH:O	1.96	0.65
1:D:56:THR:HG23	1:D:80:GLN:HB2	1.79	0.65
1:C:222:ASP:HB2	5:C:3105:HOH:O	1.97	0.64
1:C:588:ASN:HB3	1:C:593:HIS:CE1	2.32	0.64
1:D:325:HIS:HE1	5:D:3072:HOH:O	1.80	0.64
1:B:486:THR:HG21	1:B:592:TYR:CE1	2.32	0.64
1:D:528:ARG:HD3	5:D:3145:HOH:O	1.97	0.64
1:D:846:ASP:HB3	1:D:850:LYS:HE2	1.79	0.64
1:C:905:VAL:HG22	1:C:969:TYR:HB2	1.81	0.63
1:D:586:GLN:HG2	5:D:3179:HOH:O	1.99	0.63
1:B:460:ILE:HD11	1:B:542:LEU:HD11	1.81	0.63
1:B:561:PRO:HD3	1:B:590:LYS:HG2	1.80	0.63
1:C:662:TRP:HA	1:C:692:GLY:O	2.00	0.62
1:C:360:MET:CE	5:C:3353:HOH:O	2.48	0.62
1:C:907:GLU:HG3	1:C:971:ARG:HD3	1.82	0.61
1:A:533:GLU:HA	1:A:629:GLU:HG2	1.82	0.61
1:C:591:THR:HG21	1:C:615:ARG:NH1	2.16	0.60
1:C:371:GLY:C	1:C:731:HIS:HD2	2.05	0.60
1:D:457:GLN:HA	1:D:549:PHE:O	2.01	0.60
1:B:905:VAL:HG22	1:B:969:TYR:HB2	1.83	0.60
1:B:371:GLY:C	1:B:731:HIS:HD2	2.04	0.60
1:D:694:ASP:OD1	1:D:729:ARG:NH2	2.32	0.59
1:A:93:PHE:HE2	1:A:95:PRO:HG3	1.65	0.59
1:B:588:ASN:HB3	1:B:593:HIS:CE1	2.37	0.59
1:B:103:THR:HG21	1:B:604:GLU:HG2	1.85	0.59
1:D:954:THR:HG23	1:D:1034:VAL:HG22	1.85	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:773:TYR:O	5:B:3274:HOH:O	2.17	0.59
1:D:425:LYS:HE2	5:D:3117:HOH:O	2.03	0.59
1:D:594:PRO:HG3	5:D:3190:HOH:O	2.02	0.58
1:B:886:TYR:HB3	5:B:3314:HOH:O	2.02	0.58
1:A:335:GLU:OE2	1:A:784:LYS:HG2	2.03	0.58
1:C:304:THR:HG22	1:C:305:TRP:CD2	2.38	0.58
1:A:907:GLU:HG3	1:A:971:ARG:HD3	1.84	0.58
1:B:626:THR:O	1:B:630:GLY:HA3	2.04	0.58
1:C:242:ASN:HD22	1:C:667:SER:HB2	1.67	0.58
1:A:727:TRP:HZ2	1:A:729:ARG:HD3	1.69	0.58
1:B:631:ILE:HG12	1:B:644:SER:HB3	1.85	0.57
1:A:282:GLU:HB3	5:A:3134:HOH:O	2.04	0.57
1:D:484:LEU:HB3	1:D:531:VAL:HG22	1.86	0.57
1:A:905:VAL:HG22	1:A:969:TYR:HB2	1.86	0.57
1:A:989:SER:HB3	5:A:3421:HOH:O	2.03	0.57
1:D:620:TYR:HA	1:D:655:ASN:HD21	1.69	0.57
1:D:881:ILE:HG12	1:D:908:VAL:HG22	1.87	0.57
1:D:662:TRP:HA	1:D:692:GLY:O	2.05	0.57
1:D:893:LYS:HE3	5:D:3280:HOH:O	2.03	0.57
1:D:462:CYS:O	1:D:464:LEU:HD22	2.05	0.56
1:D:479:LEU:HD12	1:D:484:LEU:HB2	1.87	0.56
1:D:641:PHE:CZ	1:D:896:ASN:HB2	2.41	0.56
1:D:688:LEU:HD12	1:D:691:VAL:HB	1.86	0.56
1:C:257:LEU:HD11	1:C:263:ILE:HD11	1.87	0.56
1:A:713:ASP:OD1	1:A:869:GLN:HG3	2.05	0.56
1:D:678:ALA:HB2	5:D:3050:HOH:O	2.06	0.56
1:C:562:HIS:HB3	1:C:588:ASN:ND2	2.21	0.56
1:C:242:ASN:HD21	1:C:667:SER:HB2	1.71	0.56
1:D:378:LEU:HD13	1:D:445:VAL:HG23	1.87	0.55
1:B:640:LYS:HE2	5:B:3321:HOH:O	2.05	0.55
1:C:805:ASP:CG	1:C:830:ARG:HH22	2.10	0.55
1:C:238:TYR:CD2	1:C:248:LEU:HD11	2.42	0.54
1:A:242:ASN:ND2	1:A:667:SER:HB2	2.22	0.54
1:B:685:MET:N	5:B:3248:HOH:O	2.40	0.54
1:B:479:LEU:HD13	1:B:534:TRP:CH2	2.42	0.54
1:D:382:HIS:CD2	1:D:432:ASN:HB2	2.42	0.54
1:D:388:ASN:N	5:D:3107:HOH:O	2.33	0.54
1:D:408:GLY:HA3	1:D:455:VAL:O	2.07	0.54
1:B:360:MET:CE	5:B:3274:HOH:O	2.54	0.54
1:D:529:PRO:O	1:D:530:ASP:CB	2.55	0.54
1:A:661:MET:O	1:A:691:VAL:HA	2.08	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:539:TYR:CZ	1:A:626:THR:HG23	2.42	0.54
1:C:68:ASN:OD1	1:C:70:SER:OG	2.26	0.54
1:D:588:ASN:HB3	1:D:593:HIS:CE1	2.43	0.54
1:B:271:TRP:HE3	1:B:289:PHE:HB2	1.73	0.54
1:B:237:ASN:HA	1:B:265:MET:O	2.09	0.53
1:C:804:ASN:HB2	5:C:3369:HOH:O	2.07	0.53
1:B:242:ASN:O	1:B:243:TYR:HB2	2.07	0.53
1:C:479:LEU:HD13	1:C:534:TRP:CH2	2.43	0.53
1:B:60:ASN:HB3	1:B:74:GLN:NE2	2.24	0.53
1:C:848:ASP:HB2	5:C:3348:HOH:O	2.08	0.53
1:A:553:ASP:OD1	1:A:554:MET:N	2.41	0.53
1:C:553:ASP:OD2	2:C:1050:NOJ:H2	2.09	0.53
1:C:266:TYR:HB3	1:C:649:ARG:O	2.09	0.53
1:A:727:TRP:CZ2	1:A:729:ARG:HD3	2.43	0.53
1:A:1009:ASN:HB3	1:A:1026:PRO:HG3	1.91	0.53
1:A:529:PRO:O	1:A:530:ASP:HB2	2.09	0.53
1:B:533:GLU:HA	1:B:533:GLU:OE1	2.09	0.53
1:B:765:ARG:HH11	1:B:765:ARG:HG3	1.73	0.53
1:C:403:ASN:O	1:C:759:ARG:HD2	2.09	0.53
1:B:812:HIS:CD2	1:B:917:ASP:HB2	2.44	0.52
1:C:901:GLU:HG2	5:C:3415:HOH:O	2.10	0.52
1:A:645:TYR:CE2	1:A:690:LEU:HD13	2.44	0.52
1:A:145:VAL:HG22	1:A:155:VAL:HG22	1.90	0.52
1:A:642:ARG:NH2	5:A:3282:HOH:O	2.35	0.52
1:A:371:GLY:C	1:A:731:HIS:HD2	2.13	0.52
1:B:930:ASN:HB3	1:B:936:LYS:HD3	1.92	0.52
1:D:371:GLY:C	1:D:731:HIS:HD2	2.11	0.52
1:A:1038:THR:HB	5:A:3441:HOH:O	2.10	0.52
1:A:53:THR:HG21	5:A:3025:HOH:O	2.08	0.52
1:B:289:PHE:CZ	1:B:291:ASP:OD1	2.63	0.52
1:B:714:LEU:O	1:B:718:TYR:HB2	2.09	0.52
1:C:383:MET:HE1	5:C:3189:HOH:O	2.10	0.52
1:A:526:TRP:HB3	1:A:621:THR:HG21	1.92	0.52
1:A:661:MET:HG2	1:A:688:LEU:HD11	1.92	0.52
1:C:464:LEU:HD23	1:C:479:LEU:HD22	1.92	0.52
1:D:473:TYR:CZ	1:D:475:VAL:HB	2.45	0.52
1:C:969:TYR:HA	1:C:1023:LEU:O	2.10	0.51
1:C:325:HIS:CD2	5:C:3037:HOH:O	2.57	0.51
1:C:28:VAL:HG11	3:C:2039:GOL:O2	2.10	0.51
1:D:905:VAL:HG22	1:D:969:TYR:HB2	1.92	0.51
1:B:443:ARG:NH1	1:B:451:ASP:OD2	2.44	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:378:LEU:HD13	1:C:445:VAL:HG23	1.93	0.51
1:B:489:ASP:HB2	1:B:608:ARG:NH2	2.21	0.51
1:D:628:LYS:HD2	5:D:3053:HOH:O	2.10	0.51
1:D:278:ALA:HA	1:D:283:GLN:HG3	1.92	0.51
1:C:17:PRO:HG3	1:C:606:HIS:O	2.10	0.51
1:B:378:LEU:HD13	1:B:445:VAL:HG23	1.92	0.51
1:A:988:GLY:HA2	5:A:3420:HOH:O	2.11	0.51
1:B:17:PRO:HG3	1:B:606:HIS:O	2.10	0.51
1:B:680:ASN:ND2	1:B:725:LEU:HB3	2.26	0.51
1:C:669:THR:OG1	1:C:672:TYR:HD2	1.94	0.51
1:C:689:PRO:HB2	1:C:786:ILE:HG13	1.92	0.51
1:D:486:THR:HG21	1:D:592:TYR:CE1	2.46	0.51
1:C:360:MET:HE1	5:C:3353:HOH:O	2.09	0.51
1:C:815:TYR:CZ	3:C:2042:GOL:H31	2.47	0.50
1:C:533:GLU:HA	1:C:629:GLU:HG2	1.92	0.50
1:B:561:PRO:HB2	1:B:572:PRO:HD2	1.92	0.50
1:C:856:MET:HE3	1:C:875:PHE:CD1	2.47	0.50
1:D:241:LEU:HB3	1:D:245:GLN:NE2	2.26	0.50
1:B:611:MET:HE2	5:B:3216:HOH:O	2.11	0.50
1:D:425:LYS:NZ	5:D:3102:HOH:O	2.44	0.50
1:C:575:ASN:HD22	1:D:989:SER:HB2	1.76	0.50
1:B:382:HIS:CD2	1:B:432:ASN:HB2	2.47	0.50
1:A:545:ILE:HG23	5:A:3247:HOH:O	2.12	0.50
1:B:399:TYR:HE1	1:B:748:LEU:HB2	1.77	0.50
1:D:748:LEU:HB3	1:D:758:LEU:HD13	1.94	0.50
1:B:557:PRO:HG3	1:B:618:HIS:CE1	2.47	0.50
1:A:614:GLN:O	1:A:617:ILE:HG22	2.12	0.50
1:A:620:TYR:HA	1:A:655:ASN:ND2	2.26	0.50
1:B:324:GLN:HG2	1:B:326:PHE:CZ	2.47	0.50
1:B:540:LYS:HD3	1:B:637:THR:HG21	1.92	0.50
1:C:272:LEU:HG	1:C:315:MET:HE2	1.93	0.50
1:D:1026:PRO:O	1:D:1029:VAL:HG22	2.12	0.50
1:D:867:VAL:HG11	1:D:873:PRO:HD3	1.93	0.50
1:A:981:ILE:HG12	1:A:1037:ILE:HG12	1.93	0.49
1:B:954:THR:HG23	1:B:1034:VAL:HG22	1.93	0.49
1:C:1009:ASN:HB3	1:C:1026:PRO:HG3	1.94	0.49
1:D:661:MET:HB2	1:D:691:VAL:HG23	1.93	0.49
1:D:719:VAL:HG13	1:D:728:PHE:HZ	1.76	0.49
1:A:663:VAL:HG23	5:A:3297:HOH:O	2.12	0.49
1:A:87:ASN:HB3	1:A:143:LEU:HD12	1.93	0.49
1:A:620:TYR:HA	1:A:655:ASN:HD21	1.78	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:457:GLN:HA	1:C:549:PHE:O	2.12	0.49
1:C:477:GLN:O	1:C:481:GLU:HB2	2.13	0.49
1:C:663:VAL:HG11	1:C:679:ASN:OD1	2.12	0.49
1:A:421:VAL:O	1:A:422:PHE:HB2	2.13	0.49
1:B:881:ILE:HB	1:B:918:GLY:HA3	1.94	0.49
1:D:403:ASN:OD1	1:D:892:ASN:HB2	2.12	0.49
1:A:167:ASN:HA	1:A:197:ASN:HA	1.93	0.48
1:A:969:TYR:HA	1:A:1023:LEU:O	2.13	0.48
1:D:167:ASN:HA	1:D:197:ASN:HA	1.96	0.48
1:A:553:ASP:OD2	2:A:1050:NOJ:H2	2.13	0.48
1:C:811:GLY:HA3	1:C:816:ARG:HG3	1.96	0.48
1:A:663:VAL:CG2	5:A:3297:HOH:O	2.61	0.48
1:D:732:TYR:HB3	1:D:746:GLN:NE2	2.29	0.48
1:A:272:LEU:HD11	1:A:298:MET:HB3	1.96	0.48
1:B:486:THR:HG21	1:B:592:TYR:HE1	1.75	0.48
1:C:672:TYR:HA	1:C:675:MET:HE3	1.95	0.48
1:D:995:SER:HB2	1:D:1011:ASP:HB3	1.94	0.48
1:B:145:VAL:HG22	1:B:155:VAL:HG13	1.95	0.48
1:D:22:TYR:CZ	1:D:610:PRO:HD2	2.49	0.48
1:D:980:ASN:O	1:D:1038:THR:HG23	2.13	0.48
1:C:496:PHE:CE1	1:C:593:HIS:HB2	2.49	0.47
1:C:698:PHE:HA	1:C:732:TYR:HA	1.96	0.47
1:B:554:MET:HB3	1:B:558:ALA:HB3	1.96	0.47
1:A:879:GLY:HA2	1:A:916:ALA:HA	1.96	0.47
1:B:297:TYR:C	1:B:298:MET:HG3	2.34	0.47
1:C:834:LEU:O	1:C:859:GLY:N	2.39	0.47
1:B:693:SER:O	1:B:694:ASP:C	2.53	0.47
1:B:936:LYS:HA	1:B:961:GLU:HB3	1.96	0.47
1:C:347:LYS:HB2	1:C:352:GLN:HG3	1.95	0.47
1:C:829:GLU:HG2	5:C:3378:HOH:O	2.15	0.47
1:D:820:ALA:HB3	1:D:873:PRO:HB2	1.97	0.47
1:B:242:ASN:ND2	1:B:667:SER:HB2	2.30	0.47
1:B:641:PHE:CZ	1:B:896:ASN:HB2	2.48	0.47
1:B:931:ALA:O	1:B:935:GLY:HA2	2.15	0.47
1:C:529:PRO:O	1:C:530:ASP:HB2	2.14	0.47
1:A:680:ASN:HB2	5:A:3292:HOH:O	2.14	0.47
1:B:221:GLN:HA	1:B:221:GLN:NE2	2.29	0.47
1:C:808:LEU:HA	1:C:817:ILE:O	2.14	0.47
1:D:576:TRP:CG	1:D:577:PRO:HA	2.50	0.47
1:D:93:PHE:CE2	1:D:95:PRO:HG3	2.50	0.47
1:D:39:THR:O	1:D:40:ASN:HB2	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:399:TYR:HE1	1:A:748:LEU:HB2	1.79	0.47
1:B:137:THR:HB	5:B:3048:HOH:O	2.15	0.47
1:D:201:ARG:HH12	1:D:310:GLU:HG2	1.80	0.47
1:A:87:ASN:O	1:A:328:TYR:HD2	1.98	0.47
1:B:273:ILE:HG23	1:B:337:VAL:HG11	1.96	0.47
1:B:680:ASN:HD22	1:B:725:LEU:HD13	1.80	0.47
1:B:289:PHE:HZ	1:B:291:ASP:OD1	1.98	0.47
1:B:555:THR:OG1	1:B:650:GLY:HA3	2.15	0.47
1:C:661:MET:HG2	1:C:688:LEU:HD11	1.97	0.47
1:B:830:ARG:NH1	1:B:831:GLU:O	2.48	0.46
1:B:20:ILE:CD1	1:B:96:ASP:HB3	2.45	0.46
1:A:510:HIS:ND1	1:A:520:ASP:OD1	2.47	0.46
1:C:402:ASN:O	1:C:759:ARG:NH1	2.43	0.46
1:D:101:ASP:HA	5:D:3021:HOH:O	2.15	0.46
1:A:747:GLU:HB3	1:A:749:TYR:CE1	2.51	0.46
1:A:842:LYS:HB2	1:A:856:MET:HE1	1.97	0.46
1:A:128:MET:HG2	1:A:138:PHE:CB	2.45	0.46
1:B:228:ARG:HB3	1:B:231:ILE:HD11	1.98	0.46
1:B:37:SER:O	1:B:38:ASN:HB2	2.16	0.46
1:D:301:GLY:HA2	1:D:309:GLN:O	2.16	0.46
1:D:479:LEU:HB2	1:D:534:TRP:CZ2	2.50	0.46
1:A:716:VAL:O	1:A:720:GLN:HG3	2.15	0.46
1:D:378:LEU:HB3	5:D:3127:HOH:O	2.15	0.46
1:D:268:ALA:HB3	1:D:652:TYR:HD1	1.81	0.46
1:D:881:ILE:HA	1:D:907:GLU:O	2.16	0.46
1:A:270:PRO:HB2	1:A:290:MET:O	2.15	0.46
1:A:689:PRO:O	1:A:726:PRO:HG2	2.16	0.46
1:B:240:ASN:HA	1:B:245:GLN:HG2	1.97	0.46
1:B:798:ASN:HD22	1:B:861:ARG:NH2	2.14	0.46
1:C:271:TRP:HA	1:C:288:TRP:O	2.16	0.46
1:A:136:LEU:HD23	1:A:147:ILE:HD12	1.97	0.46
1:A:293:VAL:O	1:A:614:GLN:HA	2.15	0.46
1:B:249:ARG:NH2	1:B:578:ASN:HB3	2.31	0.46
1:C:167:ASN:HA	1:C:197:ASN:HA	1.98	0.46
1:D:695:ILE:HG13	1:D:728:PHE:CE1	2.51	0.46
1:C:495:ASP:O	1:C:564:ILE:HD12	2.16	0.46
1:B:221:GLN:HA	1:B:221:GLN:HE21	1.80	0.45
1:B:526:TRP:HE1	1:B:618:HIS:CE1	2.34	0.45
1:B:680:ASN:ND2	1:B:725:LEU:HD13	2.31	0.45
1:B:723:CYS:O	1:B:765:ARG:HG3	2.16	0.45
1:A:674:GLN:HG3	1:A:823:VAL:HB	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1012:PHE:HA	1:B:1022:TRP:O	2.17	0.45
1:B:881:ILE:HG12	1:B:908:VAL:HG13	1.98	0.45
1:C:150:ASN:O	1:C:179:CYS:HB2	2.16	0.45
1:C:378:LEU:HD11	1:C:448:TRP:CE3	2.52	0.45
1:D:662:TRP:CD1	1:D:729:ARG:NH2	2.85	0.45
1:A:128:MET:HG2	1:A:138:PHE:HB3	1.98	0.45
1:B:199:ASN:OD1	1:B:199:ASN:C	2.54	0.45
1:B:485:TYR:CE2	1:B:506:ALA:HB2	2.51	0.45
1:B:849:THR:HG23	5:B:3299:HOH:O	2.16	0.45
1:C:528:ARG:HB2	1:C:531:VAL:HG23	1.97	0.45
1:C:648:SER:O	1:C:661:MET:HA	2.16	0.45
1:C:856:MET:CE	1:C:875:PHE:CD1	3.00	0.45
1:A:591:THR:OG1	1:A:592:TYR:N	2.50	0.45
1:A:760:LYS:NZ	5:A:3325:HOH:O	2.49	0.45
1:C:332:GLY:HA3	5:C:3155:HOH:O	2.17	0.45
1:C:635:ALA:HA	1:C:638:LEU:HD12	1.97	0.45
1:C:655:ASN:HB3	5:C:3293:HOH:O	2.16	0.45
1:C:846:ASP:HB3	1:C:850:LYS:HE2	1.99	0.45
1:D:661:MET:O	1:D:691:VAL:HA	2.17	0.45
1:A:526:TRP:HA	1:A:531:VAL:HG11	1.98	0.45
1:A:837:LEU:O	1:A:838:THR:HB	2.16	0.45
1:C:490:SER:HA	1:C:597:LEU:HG	1.98	0.45
1:D:77:VAL:HA	1:D:93:PHE:HB3	1.98	0.45
1:B:510:HIS:ND1	1:B:520:ASP:OD1	2.49	0.45
1:C:345:GLN:O	1:C:657:HIS:CE1	2.70	0.45
1:C:557:PRO:HG3	1:C:618:HIS:CE1	2.51	0.45
1:D:555:THR:OG1	1:D:650:GLY:HA3	2.17	0.45
1:A:981:ILE:HD11	1:A:1021:LEU:HD21	1.99	0.45
1:C:403:ASN:O	1:C:759:ARG:CD	2.65	0.45
1:A:36:LEU:HD12	1:A:308:GLY:HA2	1.98	0.45
1:A:378:LEU:HD11	1:A:448:TRP:CE3	2.52	0.45
1:B:226:LEU:HB3	1:B:803:GLN:HG3	1.99	0.45
1:B:511:LEU:HD11	1:B:513:TYR:CZ	2.52	0.45
1:A:691:VAL:HG22	1:A:692:GLY:N	2.31	0.45
1:C:201:ARG:HD3	1:C:310:GLU:O	2.17	0.45
1:C:503:PRO:HG2	1:C:506:ALA:HB2	1.99	0.45
1:A:458:THR:O	1:A:551:TRP:HB3	2.17	0.44
1:C:185:VAL:HG12	1:C:186:ASP:O	2.16	0.44
1:C:598:VAL:O	1:C:608:ARG:HB3	2.17	0.44
1:A:38:ASN:ND2	1:A:180:ARG:HH11	2.10	0.44
1:A:524:PRO:HG2	1:A:526:TRP:CZ2	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:641:PHE:CZ	1:A:896:ASN:HB2	2.52	0.44
1:D:839:GLN:OE1	1:D:857:ASN:HA	2.17	0.44
1:D:816:ARG:HG3	5:D:3284:HOH:O	2.17	0.44
1:B:686:SER:O	1:B:687:CYS:HB2	2.18	0.44
1:B:20:ILE:HD11	1:B:96:ASP:HB3	1.99	0.44
1:C:22:TYR:HD1	1:C:319:TYR:CE1	2.35	0.44
1:D:271:TRP:HE3	1:D:289:PHE:HB2	1.82	0.44
1:D:325:HIS:CE1	5:D:3072:HOH:O	2.64	0.44
1:A:325:HIS:HD2	5:A:3040:HOH:O	2.00	0.44
1:B:325:HIS:HD2	5:B:3018:HOH:O	2.00	0.44
1:C:165:MET:HE2	1:C:326:PHE:CE1	2.53	0.44
1:B:777:TYR:CE2	1:B:919:MET:CE	3.01	0.44
1:C:243:TYR:HB2	1:C:259:PRO:HB3	2.00	0.44
1:C:528:ARG:HB2	1:C:531:VAL:CG2	2.47	0.44
1:D:420:ARG:HB3	1:D:473:TYR:CE1	2.53	0.44
1:B:463:PHE:CD1	1:B:511:LEU:HB2	2.52	0.44
1:D:436:THR:HB	5:D:3129:HOH:O	2.18	0.44
1:D:936:LYS:HG2	5:D:3298:HOH:O	2.17	0.44
1:C:318:GLN:HE22	3:C:2039:GOL:H11	1.83	0.43
1:D:557:PRO:HG3	1:D:618:HIS:CE1	2.53	0.43
1:B:685:MET:HB3	5:B:3248:HOH:O	2.17	0.43
1:C:23:LYS:HG3	1:C:190:GLY:HA2	1.99	0.43
1:C:915:ARG:HG3	1:C:916:ALA:N	2.33	0.43
1:D:417:ASP:O	1:D:418:ASN:C	2.55	0.43
1:B:457:GLN:HA	1:B:549:PHE:O	2.18	0.43
1:A:661:MET:CG	1:A:688:LEU:HD11	2.49	0.43
1:C:208:GLU:OE2	5:C:3099:HOH:O	2.21	0.43
1:C:421:VAL:O	1:C:422:PHE:HB2	2.19	0.43
1:D:461:THR:HG22	1:D:553:ASP:O	2.18	0.43
1:B:55:TRP:CE3	1:B:116:ARG:HG3	2.53	0.43
1:B:271:TRP:CE3	1:B:289:PHE:HB2	2.52	0.43
1:C:241:LEU:O	1:C:242:ASN:HB2	2.18	0.43
1:A:273:ILE:HG23	1:A:337:VAL:HG11	2.01	0.43
1:B:765:ARG:NH1	1:B:765:ARG:HG3	2.33	0.43
1:B:807:PHE:CE2	1:B:819:CYS:HB2	2.54	0.43
1:C:631:ILE:CG2	1:C:644:SER:HB3	2.48	0.43
1:D:25:TYR:CE1	1:D:595:GLN:HA	2.54	0.43
1:B:589:TRP:O	1:B:591:THR:HG22	2.18	0.43
1:B:808:LEU:HA	1:B:817:ILE:O	2.18	0.43
1:A:556:VAL:CG1	1:A:591:THR:HB	2.49	0.43
1:B:240:ASN:HA	1:B:245:GLN:CG	2.49	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:555:THR:HG22	1:C:622:LEU:HD23	2.00	0.43
1:B:648:SER:O	1:B:661:MET:HA	2.19	0.43
1:B:798:ASN:HB2	1:B:833:TYR:CZ	2.54	0.43
1:C:900:ASP:OD1	3:C:2040:GOL:O1	2.37	0.43
1:A:235:ASN:ND2	1:A:298:MET:CE	2.81	0.42
1:C:499:THR:HG21	1:C:520:ASP:OD2	2.19	0.42
1:C:560:MET:HA	5:C:3252:HOH:O	2.19	0.42
1:A:56:THR:CG2	1:A:78:GLN:HG2	2.49	0.42
1:B:457:GLN:HG3	1:B:551:TRP:HB2	2.02	0.42
1:C:924:ASP:O	1:C:927:VAL:HG23	2.18	0.42
1:D:729:ARG:HB2	5:D:3231:HOH:O	2.18	0.42
1:B:274:VAL:O	1:B:285:SER:HA	2.19	0.42
1:D:201:ARG:NH1	1:D:301:GLY:O	2.52	0.42
1:D:812:HIS:HE1	5:D:3257:HOH:O	2.02	0.42
1:A:794:ASN:H	3:A:2039:GOL:H12	1.84	0.42
1:C:76:PRO:HD2	5:C:3043:HOH:O	2.19	0.42
1:C:776:MET:SD	1:C:786:ILE:HD11	2.59	0.42
1:A:247:ASP:OD1	1:A:247:ASP:N	2.53	0.42
1:B:241:LEU:HB3	1:B:245:GLN:NE2	2.34	0.42
1:C:916:ALA:HB3	1:C:944:ALA:HB3	2.02	0.42
1:D:39:THR:HG22	1:D:67:ASP:HB3	2.01	0.42
1:A:695:ILE:HG13	1:A:728:PHE:CE1	2.54	0.42
1:C:707:ARG:HA	1:C:743:LYS:HA	2.01	0.42
1:B:1026:PRO:O	1:B:1029:VAL:HG22	2.19	0.42
1:B:620:TYR:HA	1:B:655:ASN:HD21	1.84	0.42
1:A:631:ILE:HG23	1:A:644:SER:HB3	2.02	0.42
1:C:385:ALA:HA	5:C:3184:HOH:O	2.18	0.42
1:C:473:TYR:CZ	1:C:475:VAL:HB	2.55	0.42
1:C:805:ASP:O	1:C:820:ALA:HA	2.20	0.42
1:A:36:LEU:HD21	1:A:196:VAL:HG11	2.02	0.42
1:A:88:SER:HA	1:A:326:PHE:O	2.20	0.42
1:B:278:ALA:HA	1:B:283:GLN:CG	2.41	0.42
1:B:82:THR:HB	1:B:344:LEU:CD2	2.49	0.42
1:D:293:VAL:HG11	1:D:617:ILE:HB	2.01	0.42
1:D:702:ASP:HB3	1:D:705:ASN:O	2.20	0.42
1:C:293:VAL:HG11	1:C:617:ILE:HD12	2.01	0.42
1:A:668:THR:HG23	1:A:696:GLY:O	2.20	0.41
1:B:335:GLU:OE1	1:B:815:TYR:OH	2.28	0.41
1:A:288:TRP:HE1	1:A:324:GLN:CD	2.20	0.41
1:A:790:ALA:HB1	1:A:799:VAL:HB	2.00	0.41
1:B:146:ILE:HG22	5:B:3049:HOH:O	2.19	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:200:PHE:HB2	1:C:208:GLU:HG3	2.03	0.41
1:C:740:ASP:HB2	5:C:3330:HOH:O	2.20	0.41
1:A:39:THR:O	1:A:40:ASN:HB2	2.20	0.41
1:B:247:ASP:N	1:B:247:ASP:OD1	2.53	0.41
1:B:265:MET:HB3	1:B:266:TYR:H	1.65	0.41
1:B:669:THR:HA	5:B:3244:HOH:O	2.20	0.41
1:C:226:LEU:O	1:C:228:ARG:NH1	2.53	0.41
1:C:236:TYR:HD1	1:C:295:GLN:HB2	1.86	0.41
1:D:237:ASN:HB3	5:D:3065:HOH:O	2.20	0.41
1:A:20:ILE:H	1:A:20:ILE:HG12	1.55	0.41
1:A:23:LYS:HG3	1:A:190:GLY:HA2	2.02	0.41
1:A:288:TRP:NE1	1:A:324:GLN:OE1	2.34	0.41
1:A:942:VAL:HA	1:A:954:THR:O	2.20	0.41
1:B:807:PHE:CZ	1:B:819:CYS:HB2	2.56	0.41
1:D:371:GLY:O	1:D:731:HIS:HA	2.21	0.41
1:A:304:THR:HG22	1:A:305:TRP:CD2	2.55	0.41
1:C:17:PRO:HB2	5:C:3002:HOH:O	2.20	0.41
1:D:635:ALA:HA	1:D:638:LEU:HD12	2.01	0.41
1:A:955:PHE:O	1:A:1032:ASP:HA	2.20	0.41
1:A:805:ASP:CG	1:A:830:ARG:HH22	2.24	0.41
1:B:680:ASN:HD21	1:B:725:LEU:HB3	1.85	0.41
1:C:674:GLN:HG3	1:C:823:VAL:HB	2.03	0.41
1:C:990:GLN:HE21	1:C:990:GLN:HB3	1.62	0.41
1:B:1030:LEU:N	1:B:1031:PRO:CD	2.84	0.41
1:B:270:PRO:HA	1:B:298:MET:SD	2.61	0.41
1:B:460:ILE:HD11	1:B:542:LEU:CD1	2.47	0.41
1:B:770:GLU:HG2	1:B:885:ARG:HG2	2.02	0.41
1:C:202:ASN:HA	5:C:3093:HOH:O	2.21	0.41
1:C:420:ARG:HG2	1:C:473:TYR:CG	2.56	0.41
1:C:447:GLU:O	1:C:450:HIS:HB2	2.21	0.41
1:D:420:ARG:NH1	5:D:3119:HOH:O	2.52	0.41
1:A:25:TYR:HB3	1:A:594:PRO:HB2	2.03	0.41
1:B:657:HIS:HD2	5:B:3137:HOH:O	2.03	0.41
1:C:36:LEU:HD12	1:C:308:GLY:HA2	2.02	0.41
1:C:796:ASP:CG	1:C:799:VAL:HG13	2.41	0.41
1:D:354:LEU:HD21	1:D:360:MET:HG3	2.03	0.41
1:A:227:GLU:HB2	5:A:3113:HOH:O	2.20	0.41
1:A:570:VAL:HA	5:A:3253:HOH:O	2.20	0.41
1:B:111:GLN:O	1:B:115:ILE:HG13	2.21	0.41
1:B:836:VAL:HG22	1:B:837:LEU:N	2.36	0.41
1:C:815:TYR:CE2	3:C:2042:GOL:H31	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:325:HIS:CD2	5:D:3015:HOH:O	2.62	0.41
1:A:925:GLY:CA	3:A:2041:GOL:H11	2.51	0.40
1:A:415:MET:SD	1:A:424:THR:HG22	2.61	0.40
1:B:638:LEU:HD23	1:B:638:LEU:HA	1.89	0.40
1:D:403:ASN:CG	1:D:403:ASN:O	2.60	0.40
1:D:588:ASN:HB2	1:D:591:THR:O	2.21	0.40
1:D:60:ASN:HB3	1:D:74:GLN:NE2	2.36	0.40
1:C:350:GLU:O	1:C:351:ASN:HB2	2.21	0.40
1:A:459:ASN:O	1:A:460:ILE:HD13	2.21	0.40
1:A:479:LEU:HD12	1:A:484:LEU:HB2	2.02	0.40
1:A:775:ALA:HB1	1:A:786:ILE:HG23	2.04	0.40
1:B:465:ARG:HG3	1:B:519:CYS:SG	2.61	0.40
1:C:184:PHE:HA	1:C:193:ILE:HA	2.04	0.40
1:A:125:ASP:HA	1:A:126:PRO:HD2	1.93	0.40
1:B:167:ASN:HA	1:B:197:ASN:HA	2.03	0.40
1:B:80:GLN:O	1:B:90:ARG:N	2.53	0.40
1:C:207:GLN:HG2	5:C:3094:HOH:O	2.21	0.40
1:C:482:ARG:O	1:C:484:LEU:HG	2.22	0.40
1:C:597:LEU:HD23	1:C:597:LEU:HA	1.75	0.40
1:D:495:ASP:O	1:D:564:ILE:HG23	2.21	0.40
1:C:971:ARG:HD2	5:C:3407:HOH:O	2.20	0.40
1:D:224:TYR:HE2	1:D:259:PRO:O	2.04	0.40
1:D:798:ASN:HB2	1:D:833:TYR:CZ	2.57	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	1022/1027 (100%)	969 (95%)	50 (5%)	3 (0%)	41	47
1	B	1022/1027 (100%)	957 (94%)	60 (6%)	5 (0%)	29	32

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	1022/1027 (100%)	957 (94%)	60 (6%)	5 (0%)	29	32
1	D	1022/1027 (100%)	966 (94%)	51 (5%)	5 (0%)	29	32
All	All	4088/4108 (100%)	3849 (94%)	221 (5%)	18 (0%)	34	38

All (18) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	746	GLN
1	C	663	VAL
1	C	746	GLN
1	D	530	ASP
1	D	746	GLN
1	A	854	GLY
1	D	221	GLN
1	D	418	ASN
1	B	38	ASN
1	B	358	SER
1	B	530	ASP
1	C	348	GLU
1	C	986	GLY
1	A	558	ALA
1	C	988	GLY
1	D	663	VAL
1	B	653	ILE
1	B	689	PRO

### 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	877/878 (100%)	853 (97%)	24 (3%)	44	55
1	B	877/878 (100%)	856 (98%)	21 (2%)	49	59
1	C	877/878 (100%)	846 (96%)	31 (4%)	36	44
1	D	877/878 (100%)	855 (98%)	22 (2%)	47	58

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	3508/3512 (100%)	3410 (97%)	98 (3%)	43 53

All (98) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	14	THR
1	A	20	ILE
1	A	24	THR
1	A	53	THR
1	A	92	ARG
1	A	100	ARG
1	A	110	GLN
1	A	165	MET
1	A	222	ASP
1	A	322	PHE
1	A	457	GLN
1	A	472	ASP
1	A	477	GLN
1	A	549	PHE
1	A	552	GLN
1	A	628	LYS
1	A	662	TRP
1	A	667	SER
1	A	690	LEU
1	A	718	TYR
1	A	816	ARG
1	A	830	ARG
1	A	936	LYS
1	A	1038	THR
1	B	34	SER
1	B	342	SER
1	B	343	LEU
1	B	376	SER
1	B	477	GLN
1	B	552	GLN
1	B	655	ASN
1	B	690	LEU
1	B	704	GLU
1	B	718	TYR
1	B	773	TYR
1	B	808	LEU
1	B	809	LEU

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Mol	Chain	Res	Type
1	B	829	GLU
1	B	830	ARG
1	B	893	LYS
1	B	915	ARG
1	B	934	ASN
1	B	936	LYS
1	B	977	SER
1	B	989	SER
1	C	15	ASP
1	C	24	THR
1	C	34	SER
1	C	70	SER
1	C	92	ARG
1	C	132	SER
1	C	151	PHE
1	C	238	TYR
1	C	254	ASP
1	C	285	SER
1	C	298	MET
1	C	306	ASN
1	C	364	TYR
1	C	464	LEU
1	C	474	GLU
1	C	477	GLN
1	C	498	MET
1	C	552	GLN
1	C	614	GLN
1	C	638	LEU
1	C	662	TRP
1	C	690	LEU
1	C	693	SER
1	C	718	TYR
1	C	829	GLU
1	C	830	ARG
1	C	915	ARG
1	C	936	LYS
1	C	990	GLN
1	C	1036	THR
1	C	1038	THR
1	D	92	ARG
1	D	151	PHE
1	D	221	GLN

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Mol	Chain	Res	Type
1	D	282	GLU
1	D	363	LYS
1	D	436	THR
1	D	477	GLN
1	D	528	ARG
1	D	552	GLN
1	D	611	MET
1	D	638	LEU
1	D	655	ASN
1	D	662	TRP
1	D	718	TYR
1	D	756	ASP
1	D	829	GLU
1	D	830	ARG
1	D	893	LYS
1	D	915	ARG
1	D	977	SER
1	D	996	SER
1	D	1038	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (59) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	38	ASN
1	A	177	ASN
1	A	221	GLN
1	A	242	ASN
1	A	309	GLN
1	A	325	HIS
1	A	471	GLN
1	A	552	GLN
1	A	586	GLN
1	A	605	ASN
1	A	655	ASN
1	A	657	HIS
1	A	671	ASN
1	A	731	HIS
1	A	798	ASN
1	A	812	HIS
1	B	74	GLN
1	B	177	ASN
1	B	221	GLN

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Mol	Chain	Res	Type
1	B	235	ASN
1	B	242	ASN
1	B	552	GLN
1	B	605	ASN
1	B	657	HIS
1	B	671	ASN
1	B	731	HIS
1	B	794	ASN
1	B	798	ASN
1	B	930	ASN
1	C	177	ASN
1	C	217	ASN
1	C	242	ASN
1	C	325	HIS
1	C	477	GLN
1	C	552	GLN
1	C	586	GLN
1	C	605	ASN
1	C	657	HIS
1	C	671	ASN
1	C	731	HIS
1	C	798	ASN
1	C	812	HIS
1	C	930	ASN
1	C	934	ASN
1	C	990	GLN
1	D	74	GLN
1	D	177	ASN
1	D	217	ASN
1	D	221	GLN
1	D	242	ASN
1	D	245	GLN
1	D	605	ASN
1	D	655	ASN
1	D	657	HIS
1	D	671	ASN
1	D	679	ASN
1	D	731	HIS
1	D	798	ASN
1	D	930	ASN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

4 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	CSO	B	336	1	3,6,7	0.60	0	0,6,8	0.00	-
1	CSO	C	336	1	3,6,7	0.67	0	0,6,8	0.00	-
1	CSO	A	336	1	3,6,7	0.66	0	0,6,8	0.00	-
1	CSO	D	336	1	3,6,7	0.58	0	0,6,8	0.00	-

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	CSO	B	336	1	-	0/1/5/7	-
1	CSO	C	336	1	-	0/1/5/7	-
1	CSO	A	336	1	-	0/1/5/7	-
1	CSO	D	336	1	-	0/1/5/7	-

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.

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

Of 19 ligands modelled in this entry, 4 are monoatomic - leaving 15 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	C	2041	-	5,5,5	0.30	0	5,5,5	0.31	0
3	GOL	A	2039	-	5,5,5	0.36	0	5,5,5	0.53	0
3	GOL	C	2039	-	5,5,5	0.41	0	5,5,5	0.48	0
3	GOL	A	2040	-	5,5,5	0.30	0	5,5,5	0.29	0
3	GOL	C	2040	-	5,5,5	0.38	0	5,5,5	0.61	0
2	NOJ	A	1050	-	11,11,11	0.77	0	13,15,15	1.27	1 (7%)
3	GOL	A	2043	-	5,5,5	0.31	0	5,5,5	0.30	0
2	NOJ	B	1050	-	11,11,11	0.50	0	13,15,15	1.55	1 (7%)
3	GOL	D	2039	-	5,5,5	0.46	0	5,5,5	0.50	0
2	NOJ	D	1050	-	11,11,11	0.76	0	13,15,15	1.43	1 (7%)
3	GOL	B	2039	-	5,5,5	0.31	0	5,5,5	0.90	0
3	GOL	A	2041	-	5,5,5	0.51	0	5,5,5	0.52	0
3	GOL	C	2042	-	5,5,5	0.53	0	5,5,5	0.37	0
3	GOL	A	2042	-	5,5,5	0.48	0	5,5,5	0.23	0
2	NOJ	C	1050	-	11,11,11	0.68	0	13,15,15	1.41	1 (7%)

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	C	2041	-	-	0/4/4/4	-
3	GOL	A	2039	-	-	3/4/4/4	-
3	GOL	C	2039	-	-	2/4/4/4	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	GOL	A	2040	-	-	0/4/4/4	-
3	GOL	C	2040	-	-	0/4/4/4	-
2	NOJ	A	1050	-	-	0/2/19/19	0/1/1/1
3	GOL	A	2043	-	-	2/4/4/4	-
2	NOJ	B	1050	-	-	0/2/19/19	0/1/1/1
3	GOL	D	2039	-	-	4/4/4/4	-
2	NOJ	D	1050	-	-	1/2/19/19	0/1/1/1
3	GOL	B	2039	-	-	4/4/4/4	-
3	GOL	A	2041	-	-	4/4/4/4	-
3	GOL	C	2042	-	-	2/4/4/4	-
3	GOL	A	2042	-	-	4/4/4/4	-
2	NOJ	C	1050	-	-	0/2/19/19	0/1/1/1

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1050	NOJ	C1-N5-C5	5.20	120.86	109.61
2	C	1050	NOJ	C1-N5-C5	4.57	119.49	109.61
2	D	1050	NOJ	C1-N5-C5	4.45	119.24	109.61
2	A	1050	NOJ	C1-N5-C5	4.06	118.39	109.61

There are no chirality outliers.

All (26) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	2039	GOL	C1-C2-C3-O3
3	A	2039	GOL	O2-C2-C3-O3
3	A	2043	GOL	C1-C2-C3-O3
3	D	2039	GOL	O1-C1-C2-C3
3	D	2039	GOL	C1-C2-C3-O3
3	D	2039	GOL	O2-C2-C3-O3
3	B	2039	GOL	O1-C1-C2-C3
3	A	2041	GOL	O1-C1-C2-C3
3	A	2041	GOL	C1-C2-C3-O3
3	C	2042	GOL	O1-C1-C2-C3
3	A	2042	GOL	O1-C1-C2-O2
3	A	2042	GOL	O1-C1-C2-C3
3	A	2042	GOL	C1-C2-C3-O3
3	A	2041	GOL	O2-C2-C3-O3

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Mol	Chain	Res	Type	Atoms
3	C	2039	GOL	C1-C2-C3-O3
3	C	2039	GOL	O2-C2-C3-O3
3	B	2039	GOL	O1-C1-C2-O2
3	A	2041	GOL	O1-C1-C2-O2
3	C	2042	GOL	O1-C1-C2-O2
3	A	2042	GOL	O2-C2-C3-O3
3	D	2039	GOL	O1-C1-C2-O2
2	D	1050	NOJ	N5-C5-C6-O6
3	A	2043	GOL	O2-C2-C3-O3
3	B	2039	GOL	O2-C2-C3-O3
3	A	2039	GOL	O1-C1-C2-C3
3	B	2039	GOL	C1-C2-C3-O3

There are no ring outliers.

7 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	2039	GOL	1	0
3	C	2039	GOL	2	0
3	C	2040	GOL	1	0
2	A	1050	NOJ	1	0
3	A	2041	GOL	1	0
3	C	2042	GOL	2	0
2	C	1050	NOJ	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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	1024/1027 (99%)	0.29	34 (3%)	46	59	35, 42, 53, 79	0
1	B	1024/1027 (99%)	0.41	56 (5%)	25	36	36, 47, 63, 79	0
1	C	1024/1027 (99%)	0.17	19 (1%)	66	76	31, 39, 51, 73	0
1	D	1024/1027 (99%)	0.52	56 (5%)	25	36	39, 53, 72, 91	0
All	All	4096/4108 (99%)	0.35	165 (4%)	38	51	31, 44, 64, 91	0

All (165) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	987	ALA	8.0
1	C	987	ALA	5.3
1	C	988	GLY	5.0
1	B	837	LEU	4.5
1	D	189	TYR	4.4
1	D	837	LEU	4.1
1	D	704	GLU	4.1
1	B	220	TYR	3.8
1	D	14	THR	3.7
1	B	189	TYR	3.7
1	D	949	GLY	3.6
1	D	605	ASN	3.6
1	D	202	ASN	3.5
1	D	471	GLN	3.4
1	A	988	GLY	3.3
1	D	565	GLY	3.3
1	B	882	LEU	3.3
1	B	14	THR	3.2
1	D	438	GLY	3.2
1	D	188	LEU	3.1
1	C	280	THR	3.1

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Mol	Chain	Res	Type	RSRZ
1	B	470	GLY	3.1
1	A	188	LEU	3.1
1	B	914	ASN	3.1
1	A	471	GLN	3.0
1	B	947	ASP	3.0
1	A	949	GLY	3.0
1	D	854	GLY	3.0
1	B	411	VAL	3.0
1	C	579	ALA	2.9
1	D	1005	ASN	2.9
1	B	704	GLU	2.9
1	D	905	VAL	2.9
1	B	605	ASN	2.8
1	D	71	ILE	2.8
1	B	221	GLN	2.8
1	A	529	PRO	2.8
1	D	529	PRO	2.8
1	B	913	ASN	2.8
1	D	421	VAL	2.8
1	D	1038	THR	2.8
1	D	220	TYR	2.8
1	A	740	ASP	2.7
1	B	482	ARG	2.8
1	D	204	ALA	2.7
1	D	591	THR	2.7
1	B	222	ASP	2.7
1	B	912	GLY	2.7
1	C	570	VAL	2.7
1	D	385	ALA	2.7
1	A	189	TYR	2.7
1	D	947	ASP	2.7
1	A	516	GLY	2.7
1	C	580	ASP	2.7
1	D	289	PHE	2.7
1	B	905	VAL	2.6
1	A	470	GLY	2.6
1	C	883	PRO	2.6
1	A	40	ASN	2.6
1	B	15	ASP	2.6
1	A	1016	GLN	2.6
1	A	517	VAL	2.6
1	C	386	GLY	2.6

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Mol	Chain	Res	Type	RSRZ
1	D	173	ALA	2.6
1	D	462	CYS	2.5
1	B	1014	VAL	2.5
1	D	1014	VAL	2.5
1	D	205	VAL	2.5
1	B	431	ALA	2.5
1	A	19	GLY	2.5
1	B	181	GLY	2.5
1	D	836	VAL	2.4
1	B	114	TRP	2.4
1	D	288	TRP	2.4
1	A	328	TYR	2.4
1	C	434	VAL	2.4
1	B	828	THR	2.4
1	A	385	ALA	2.4
1	D	556	VAL	2.4
1	B	996	SER	2.4
1	C	385	ALA	2.4
1	B	906	PHE	2.4
1	D	570	VAL	2.4
1	D	828	THR	2.4
1	D	705	ASN	2.4
1	C	947	ASP	2.4
1	B	529	PRO	2.4
1	B	836	VAL	2.4
1	C	252	HIS	2.3
1	B	194	ALA	2.3
1	D	1016	GLN	2.3
1	B	928	THR	2.3
1	D	999	SER	2.3
1	C	503	PRO	2.3
1	B	351	ASN	2.3
1	B	436	THR	2.3
1	D	411	VAL	2.3
1	A	481	GLU	2.3
1	C	725	LEU	2.3
1	B	977	SER	2.3
1	D	497	GLY	2.3
1	A	252	HIS	2.3
1	A	254	ASP	2.3
1	C	281	SER	2.3
1	B	891	GLU	2.2

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Mol	Chain	Res	Type	RSRZ
1	D	15	ASP	2.2
1	B	768	TRP	2.2
1	B	976	GLN	2.2
1	A	79	VAL	2.2
1	A	996	SER	2.2
1	D	281	SER	2.2
1	B	987	ALA	2.2
1	B	133	GLU	2.2
1	B	1016	GLN	2.2
1	B	994	VAL	2.2
1	B	132	SER	2.2
1	D	222	ASP	2.2
1	D	326	PHE	2.2
1	B	317	ALA	2.2
1	B	705	ASN	2.2
1	D	604	GLU	2.2
1	A	281	SER	2.2
1	A	1035	ILE	2.2
1	B	851	PRO	2.2
1	C	504	SER	2.2
1	B	131	THR	2.1
1	B	884	THR	2.1
1	B	998	THR	2.1
1	B	305	TRP	2.1
1	B	1013	TRP	2.1
1	D	557	PRO	2.1
1	A	1014	VAL	2.1
1	D	963	VAL	2.1
1	B	530	ASP	2.1
1	C	740	ASP	2.1
1	D	21	ASP	2.1
1	D	461	THR	2.1
1	B	254	ASP	2.1
1	B	472	ASP	2.1
1	A	934	ASN	2.1
1	A	120	LEU	2.1
1	D	723	CYS	2.1
1	B	864	ASN	2.1
1	B	289	PHE	2.1
1	D	176	GLY	2.1
1	B	188	LEU	2.1
1	D	882	LEU	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	515	GLY	2.1
1	D	125	ASP	2.0
1	D	182	LEU	2.0
1	C	306	ASN	2.0
1	A	461	THR	2.0
1	D	478	THR	2.0
1	A	989	SER	2.0
1	B	123	GLY	2.0
1	D	996	SER	2.0
1	A	947	ASP	2.0
1	A	605	ASN	2.0
1	A	1008	GLU	2.0
1	A	998	THR	2.0
1	C	205	VAL	2.0
1	D	327	VAL	2.0
1	B	857	ASN	2.0
1	A	460	ILE	2.0
1	D	1017	GLU	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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	CSO	B	336	7/8	0.92	0.12	45,45,47,47	0
1	CSO	D	336	7/8	0.92	0.15	49,49,51,52	0
1	CSO	A	336	7/8	0.93	0.14	40,40,41,41	0
1	CSO	C	336	7/8	0.96	0.11	36,36,37,38	0

## 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. The B-factors column lists the minimum,

median, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
3	GOL	D	2039	6/6	0.76	0.25	54,57,57,58	0
3	GOL	A	2043	6/6	0.78	0.26	58,59,59,59	0
3	GOL	A	2041	6/6	0.83	0.20	47,49,50,50	0
3	GOL	B	2039	6/6	0.85	0.28	42,48,49,49	0
3	GOL	A	2040	6/6	0.86	0.18	46,47,48,48	0
3	GOL	C	2039	6/6	0.88	0.17	36,37,37,38	0
3	GOL	A	2042	6/6	0.88	0.41	42,44,44,45	0
3	GOL	C	2041	6/6	0.89	0.15	47,47,48,48	0
3	GOL	A	2039	6/6	0.90	0.20	37,38,39,39	0
2	NOJ	B	1050	11/11	0.93	0.38	56,57,57,58	0
3	GOL	C	2040	6/6	0.94	0.14	41,41,42,44	0
2	NOJ	C	1050	11/11	0.94	0.27	55,57,57,58	0
3	GOL	C	2042	6/6	0.95	0.18	38,39,40,40	0
2	NOJ	A	1050	11/11	0.95	0.32	54,56,57,57	0
2	NOJ	D	1050	11/11	0.95	0.29	55,56,58,58	0
4	CL	A	2044	1/1	0.98	0.09	34,34,34,34	0
4	CL	B	2040	1/1	0.98	0.19	41,41,41,41	0
4	CL	C	2043	1/1	0.99	0.07	37,37,37,37	0
4	CL	D	2040	1/1	0.99	0.11	35,35,35,35	0

## 6.5 Other polymers

There are no such residues in this entry.