



# Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 10:41 PM GMT

PDB ID : 1UR8  
Title : Interactions of a family 18 chitinase with the designed inhibitor HM508, and its degradation product, chitobiono-delta-lactone  
Authors : Vaaje-Kolstad, G.; Vasella, A.; Peter, M.G.; Netter, C.; Houston, D.R.; West-ereng, B.; Synstad, B.; Eijsink, V.G.H.; Van Aalten, D.M.F.  
Deposited on : 2003-10-27  
Resolution : 1.90 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  
<http://wwpdb.org/validation/2016/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 : 1.7 (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

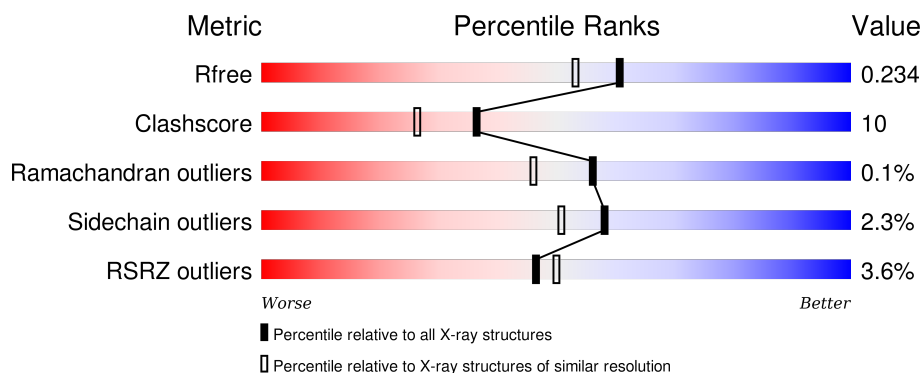
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 1.90 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	4755 (1.90-1.90)
Clashscore	102246	5398 (1.90-1.90)
Ramachandran outliers	100387	5338 (1.90-1.90)
Sidechain outliers	100360	5339 (1.90-1.90)
RSRZ outliers	91569	4766 (1.90-1.90)

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. 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	499	<div> <div>4%</div> <div>85%</div> <div>14%</div> </div>
1	B	499	<div> <div>3%</div> <div>84%</div> <div>14%</div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	GOL	A	1499	-	-	-	X
2	GOL	A	1500	-	-	X	X
2	GOL	A	1501	-	-	X	-
2	GOL	B	1501	-	-	X	X
2	GOL	B	1502	-	-	X	X
2	GOL	B	1503	-	-	-	X
2	GOL	B	1504	-	-	-	X
2	GOL	B	1505	-	-	-	X

## 2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 8649 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 CHITINASE B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	497	Total	C	N	O	S	0	0	1
			3842	2460	648	720	14			
1	B	497	Total	C	N	O	S	0	6	0
			3904	2499	659	732	14			

- Molecule 2 is GLYCEROL (three-letter code: GOL) (formula: C<sub>3</sub>H<sub>8</sub>O<sub>3</sub>).



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

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

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



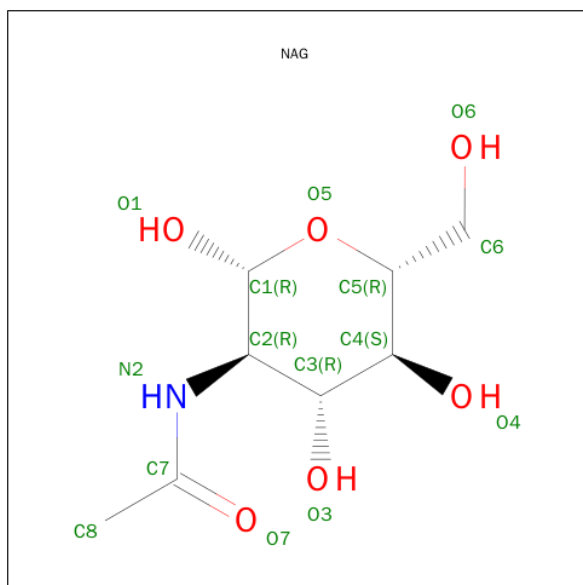
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	O	S	0	0
			5	4	1		
3	A	1	Total	O	S	0	0
			5	4	1		
3	A	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		

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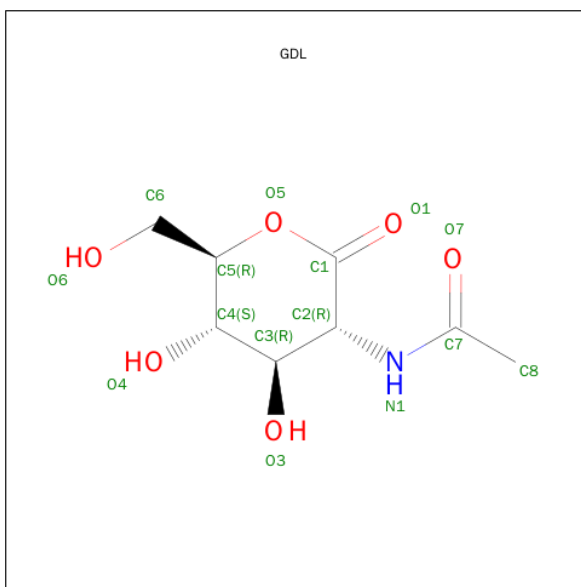
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	B	1	Total	O	S	0	0
			5	4	1		

- Molecule 4 is SUGAR (N-ACETYL-D-GLUCOSAMINE) (three-letter code: NAG) (formula:  $C_8H_{15}NO_6$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			14	8	1	5		
4	B	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 5 is 2-ACETAMIDO-2-DEOXY-D-GLUCONO-1,5-LACTONE (three-letter code: GDL) (formula:  $C_8H_{13}NO_6$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	N	O	0	0
			15	8	1	6		
5	B	1	Total	C	N	O	0	0
			15	8	1	6		

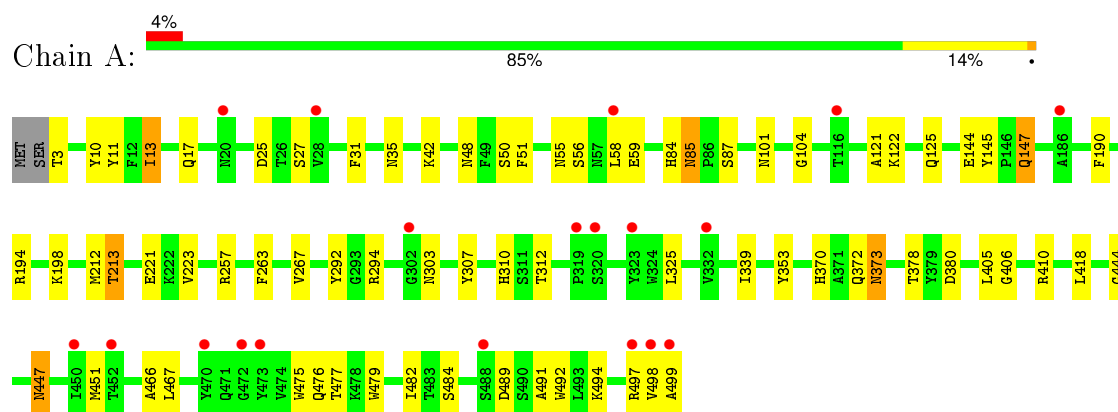
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	350	Total	O	0	0
			350	350		
6	B	406	Total	O	0	0
			406	406		

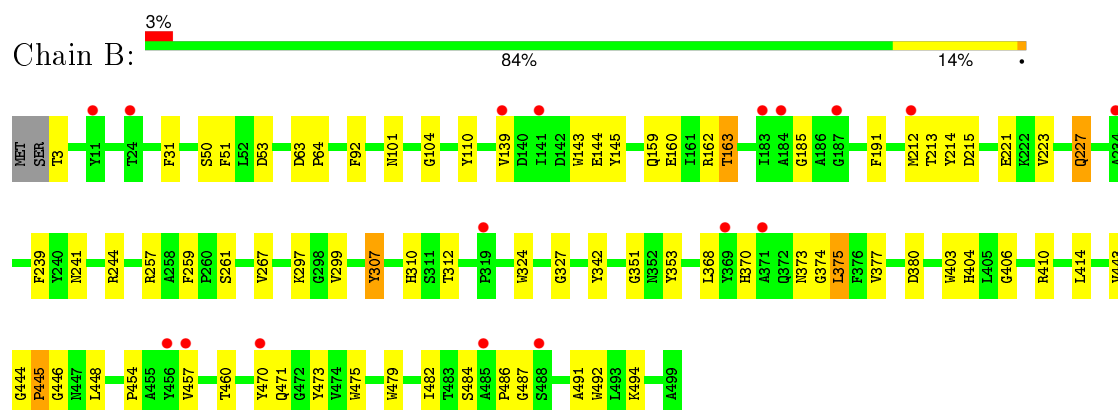
### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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: CHITINASE B



#### • Molecule 1: CHITINASE B





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	55.40Å 103.48Å 186.02Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.70 – 1.90 29.70 – 1.90	Depositor EDS
% Data completeness (in resolution range)	99.1 (29.70-1.90) 99.2 (29.70-1.90)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.68 (at 1.91Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, $R_{free}$	0.211 , 0.248 0.204 , 0.234	Depositor DCC
$R_{free}$ test set	1230 reflections (1.48%)	DCC
Wilson B-factor (Å <sup>2</sup> )	22.9	Xtriage
Anisotropy	0.593	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 55.3	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.34$	Xtriage
Outliers	0 of 84276 reflections	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	8649	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	30.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.33% of the height of the origin peak. No significant pseudotranslation is detected.*

<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, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, GDL, NAG, SO4

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 5$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z  > 5$	RMSZ	$\# Z  > 5$
1	A	0.62	0/3952	0.72	0/5398
1	B	0.64	0/4039	0.72	1/5506 (0.0%)
All	All	0.63	0/7991	0.72	1/10904 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	B	0	1
All	All	0	2

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
1	B	53	ASP	CB-CG-OD2	5.18	122.96	118.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	292	TYR	Sidechain
1	B	110	TYR	Sidechain

## 5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3842	0	3621	72	0
1	B	3904	0	3705	72	0
2	A	18	0	24	13	0
2	B	36	0	48	13	0
3	A	15	0	0	1	0
3	B	20	0	0	0	0
4	A	14	0	13	0	0
4	B	14	0	13	0	0
5	A	15	0	12	2	0
5	B	15	0	12	2	0
6	A	350	0	0	2	0
6	B	406	0	0	4	0
All	All	8649	0	7448	146	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 10.

All (146) 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:410:ARG:HE	2:A:1501:GOL:H32	1.05	1.11
1:A:56:SER:H	2:A:1500:GOL:H31	1.03	1.11
1:A:410:ARG:NE	2:A:1501:GOL:H32	1.75	1.01
1:A:444:GLY:H	1:A:447:ASN:HD21	1.10	1.00
1:A:55:ASN:HB2	2:A:1500:GOL:H32	1.44	0.99
1:A:56:SER:H	2:A:1500:GOL:C3	1.79	0.96
1:A:35:ASN:HD21	1:A:410:ARG:HH11	1.07	0.94
1:B:445:PRO:HA	1:B:448:LEU:HD21	1.47	0.94
1:A:56:SER:N	2:A:1500:GOL:H31	1.82	0.94
1:A:410:ARG:HH21	2:A:1501:GOL:H12	1.32	0.92
1:A:55:ASN:HB2	2:A:1500:GOL:C3	2.07	0.83
1:A:444:GLY:H	1:A:447:ASN:ND2	1.76	0.82
1:A:35:ASN:ND2	1:A:410:ARG:HH11	1.82	0.77
1:B:221:GLU:O	1:B:310:HIS:HE1	1.69	0.76
1:B:160:GLU:O	1:B:163[A]:THR:HG23	1.86	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:410:ARG:HE	2:A:1501:GOL:C3	1.93	0.75
1:A:479:TRP:HE1	2:B:1504:GOL:H12	1.54	0.71
1:B:327:GLY:H	2:B:1501:GOL:H31	1.55	0.70
1:B:310:HIS:HD2	1:B:312:THR:H	1.39	0.70
1:A:310:HIS:HD2	1:A:312:THR:H	1.40	0.69
1:B:370:HIS:CD2	1:B:373:ASN:H	2.11	0.69
1:A:55:ASN:CB	2:A:1500:GOL:H32	2.21	0.68
1:B:159[B]:GLN:NE2	6:B:2173:HOH:O	2.24	0.67
1:A:444:GLY:N	1:A:447:ASN:HD21	1.89	0.67
1:A:263:PHE:HB2	2:A:1499:GOL:H12	1.78	0.66
1:B:444:GLY:C	1:B:446:GLY:H	1.99	0.65
1:A:11:TYR:CZ	1:A:13:ILE:HD11	2.32	0.65
1:A:35:ASN:HD21	1:A:410:ARG:NH1	1.89	0.64
1:B:470:TYR:CD2	1:B:471:GLN:HG3	2.32	0.64
1:A:221:GLU:O	1:A:310:HIS:HE1	1.80	0.63
1:A:194:ARG:HE	2:B:1502:GOL:H2	1.63	0.63
1:A:294:ARG:NH1	1:A:339:ILE:HD11	2.15	0.62
1:B:327:GLY:N	2:B:1501:GOL:H31	2.15	0.61
1:B:445:PRO:CA	1:B:448:LEU:HD21	2.26	0.60
1:B:370:HIS:HD2	1:B:373:ASN:H	1.48	0.60
1:B:444:GLY:O	1:B:446:GLY:N	2.35	0.59
1:A:310:HIS:CD2	1:A:312:THR:H	2.20	0.59
1:A:11:TYR:CE2	1:A:13:ILE:HD11	2.37	0.59
1:B:244:ARG:HD3	1:B:259:PHE:HB2	1.85	0.59
1:B:454:PRO:HA	2:B:1505:GOL:H12	1.84	0.59
1:A:373:ASN:N	1:A:373:ASN:HD22	1.99	0.58
1:A:447:ASN:HD22	1:A:447:ASN:H	1.52	0.57
1:B:368:LEU:HB2	1:B:377:VAL:HB	1.88	0.56
5:A:2502:GDL:C1	5:A:2502:GDL:O7	2.54	0.56
1:A:145:TYR:OH	1:A:212:MET:HE3	2.06	0.56
1:B:444:GLY:C	1:B:446:GLY:N	2.59	0.56
1:B:479:TRP:HZ2	2:B:1502:GOL:H31	1.71	0.56
1:A:212:MET:SD	5:A:2502:GDL:O1	2.64	0.56
1:B:257:ARG:CD	1:B:443:VAL:O	2.53	0.56
1:A:144:GLU:HA	1:A:145:TYR:CG	2.41	0.56
1:B:257:ARG:HD3	1:B:443:VAL:HB	1.86	0.56
2:B:1505:GOL:H32	6:B:2392:HOH:O	2.06	0.55
1:B:351:GLY:HA3	1:B:353:TYR:CE2	2.42	0.55
1:B:257:ARG:HD3	1:B:443:VAL:O	2.07	0.55
1:A:294:ARG:HG2	1:A:339:ILE:CD1	2.37	0.54
1:B:310:HIS:CD2	1:B:312:THR:H	2.23	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:145:TYR:OH	1:A:212:MET:CE	2.56	0.53
1:B:448:LEU:H	1:B:448:LEU:HD22	1.72	0.53
1:A:213:THR:HB	1:A:267:VAL:HG22	1.90	0.53
1:B:221:GLU:O	1:B:310:HIS:CE1	2.55	0.52
1:B:473:TYR:CD2	1:B:494:LYS:HD3	2.45	0.52
1:A:497:ARG:O	1:A:498:VAL:HB	2.10	0.52
1:A:372:GLN:HG2	1:A:373:ASN:HD22	1.74	0.52
1:A:372:GLN:HG2	1:A:373:ASN:ND2	2.25	0.52
1:A:17:GLN:HG3	3:A:1504:SO4:O3	2.11	0.51
1:A:482:ILE:HD12	1:A:491:ALA:CB	2.41	0.51
5:B:2502:GDL:C1	5:B:2502:GDL:O7	2.58	0.51
1:B:370:HIS:HB3	1:B:375:LEU:HB2	1.92	0.51
1:A:294:ARG:HG2	1:A:339:ILE:HD11	1.92	0.51
1:A:59:GLU:CG	1:A:122:LYS:HE2	2.42	0.50
1:A:370:HIS:CE1	1:A:372:GLN:HB3	2.47	0.49
1:A:484:SER:CB	1:A:489:ASP:HB2	2.42	0.49
1:B:297:LYS:HD3	1:B:324:TRP:CE2	2.46	0.49
1:A:25:ASP:OD1	1:A:27:SER:HB3	2.12	0.49
1:B:144:GLU:HA	1:B:145:TYR:CG	2.48	0.49
1:A:410:ARG:NH2	2:A:1501:GOL:H12	2.15	0.48
1:B:191:PHE:CE1	2:B:1504:GOL:H2	2.48	0.48
1:A:25:ASP:C	1:A:27:SER:H	2.16	0.48
1:B:475:TRP:CH2	1:B:487:GLY:HA2	2.49	0.48
1:B:215:ASP:H	1:B:227:GLN:NE2	2.12	0.48
1:B:327:GLY:CA	2:B:1501:GOL:H31	2.44	0.48
1:B:162:ARG:CZ	2:B:1503:GOL:H32	2.44	0.48
1:A:198:LYS:HE2	6:A:2134:HOH:O	2.13	0.48
1:B:353:TYR:O	1:B:370:HIS:HE1	1.97	0.47
1:A:257:ARG:NH2	1:A:494:LYS:O	2.44	0.47
1:B:223:VAL:HG12	1:B:307:TYR:HA	1.97	0.47
1:A:223:VAL:HG12	1:A:307:TYR:HA	1.96	0.47
1:B:244:ARG:HD3	1:B:259:PHE:O	2.15	0.46
1:A:370:HIS:HE1	1:A:372:GLN:HB3	1.81	0.46
1:A:85:ASN:ND2	1:A:87:SER:H	2.14	0.46
1:B:92:PHE:CE1	1:B:139:VAL:HG22	2.50	0.46
1:B:50:SER:HA	1:B:51:PHE:HA	1.75	0.46
1:A:451:MET:O	1:A:499:ALA:N	2.49	0.46
1:B:479:TRP:CZ2	2:B:1502:GOL:H31	2.50	0.46
1:B:445:PRO:HA	1:B:448:LEU:CD2	2.34	0.46
1:A:50:SER:HB3	1:A:51:PHE:CD1	2.51	0.46
1:B:327:GLY:H	2:B:1501:GOL:C3	2.27	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:212:MET:SD	5:B:2502:GDL:O1	2.74	0.45
1:A:467:LEU:HA	1:A:475:TRP:O	2.15	0.45
1:A:104:GLY:HA2	6:A:2089:HOH:O	2.15	0.45
1:A:85:ASN:C	1:A:85:ASN:HD22	2.18	0.45
1:A:223:VAL:CG1	1:A:307:TYR:HA	2.46	0.45
1:B:299:VAL:HG22	1:B:374:GLY:C	2.37	0.45
1:A:101:ASN:HA	1:A:144:GLU:O	2.16	0.45
1:B:448:LEU:N	1:B:448:LEU:HD22	2.32	0.45
1:A:410:ARG:HH21	2:A:1501:GOL:C1	2.16	0.44
1:A:42:LYS:HE2	1:A:84:HIS:O	2.18	0.44
1:A:447:ASN:HD22	1:A:447:ASN:N	2.08	0.44
1:B:470:TYR:CE2	1:B:471:GLN:HG3	2.52	0.44
1:B:473:TYR:CE2	1:B:494:LYS:HD3	2.51	0.44
1:B:257:ARG:NH2	1:B:494:LYS:O	2.43	0.44
1:A:121:ALA:O	1:A:125:GLN:HG3	2.18	0.44
1:B:213:THR:HB	1:B:267:VAL:HG22	2.00	0.44
1:B:31:PHE:CG	1:B:406:GLY:HA2	2.52	0.44
1:A:56:SER:C	1:A:58:LEU:H	2.21	0.43
1:B:104:GLY:HA2	6:B:2112:HOH:O	2.18	0.43
1:A:190:PHE:O	2:B:1502:GOL:H32	2.18	0.43
1:B:342:TYR:CG	1:B:414:LEU:HD11	2.53	0.43
1:B:457:VAL:HB	1:B:460:THR:OG1	2.17	0.43
1:A:147:GLN:HE21	1:B:484:SER:HB3	1.82	0.43
1:B:299:VAL:HG22	1:B:374:GLY:O	2.17	0.43
1:A:477:THR:HG23	1:A:492:TRP:CZ3	2.53	0.43
1:A:25:ASP:C	1:A:27:SER:N	2.72	0.43
1:A:31:PHE:CG	1:A:406:GLY:HA2	2.53	0.43
1:B:101:ASN:HA	1:B:144:GLU:O	2.19	0.43
1:B:143:TRP:O	1:B:145:TYR:HA	2.19	0.43
1:A:466:ALA:O	1:A:476:GLN:HA	2.19	0.43
1:B:215:ASP:H	1:B:227:GLN:HE21	1.67	0.42
1:A:10:TYR:HA	1:A:48:ASN:HB2	2.02	0.42
1:B:241:ASN:O	1:B:244:ARG:HG3	2.19	0.42
1:B:3:THR:HG23	6:B:2001:HOH:O	2.19	0.42
1:B:214:TYR:O	1:B:215:ASP:HB2	2.19	0.42
1:B:185:GLY:O	1:B:212:MET:HE2	2.19	0.42
1:B:160:GLU:HA	1:B:163[A]:THR:CG2	2.50	0.42
1:B:482:ILE:HD12	1:B:491:ALA:HB1	2.01	0.42
1:B:63:ASP:OD1	1:B:64:PRO:HD2	2.20	0.41
1:B:244:ARG:NH2	1:B:261:SER:HB3	2.36	0.41
1:A:59:GLU:HG3	1:A:122:LYS:HE2	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:486:PRO:HA	1:B:492:TRP:CD1	2.56	0.41
1:A:418:LEU:HA	1:A:418:LEU:HD23	1.90	0.41
1:B:307:TYR:CD1	1:B:307:TYR:N	2.88	0.41
1:A:353:TYR:O	1:A:370:HIS:NE2	2.55	0.40
1:B:403:TRP:CD2	1:B:404:HIS:HB3	2.56	0.40
1:B:221:GLU:OE1	1:B:239:PHE:HE2	2.05	0.40
1:B:297:LYS:O	1:B:310:HIS:HB2	2.21	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	495/499 (99%)	482 (97%)	13 (3%)	0	100	100
1	B	501/499 (100%)	487 (97%)	13 (3%)	1 (0%)	52	42
All	All	996/998 (100%)	969 (97%)	26 (3%)	1 (0%)	56	46

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	445	PRO

### 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	385/405 (95%)	373 (97%)	12 (3%)	47	37
1	B	397/405 (98%)	390 (98%)	7 (2%)	66	61
All	All	782/810 (96%)	763 (98%)	19 (2%)	58	49

All (19) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3	THR
1	A	13	ILE
1	A	85	ASN
1	A	147	GLN
1	A	213	THR
1	A	303	ASN
1	A	325	LEU
1	A	373	ASN
1	A	378	THR
1	A	380	ASP
1	A	405	LEU
1	A	447	ASN
1	B	163[A]	THR
1	B	163[B]	THR
1	B	227	GLN
1	B	307	TYR
1	B	375	LEU
1	B	380	ASP
1	B	410	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (20) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	17	GLN
1	A	20	ASN
1	A	35	ASN
1	A	57	ASN
1	A	85	ASN
1	A	109	ASN
1	A	112	ASN
1	A	125	GLN
1	A	310	HIS
1	A	347	GLN
1	A	372	GLN

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Mol	Chain	Res	Type
1	A	373	ASN
1	A	447	ASN
1	B	125	GLN
1	B	227	GLN
1	B	247	ASN
1	B	310	HIS
1	B	347	GLN
1	B	370	HIS
1	B	395	GLN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

20 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
2	GOL	A	1499	-	5,5,5	0.33	0	5,5,5	0.32	0
2	GOL	A	1500	-	5,5,5	0.34	0	5,5,5	0.28	0
2	GOL	A	1501	-	5,5,5	0.29	0	5,5,5	0.07	0
3	SO4	A	1503	-	4,4,4	0.25	0	6,6,6	0.17	0
3	SO4	A	1504	-	4,4,4	0.23	0	6,6,6	0.07	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
3	SO4	A	1505	-	4,4,4	0.30	0	6,6,6	0.25	0
4	NAG	A	2501	5	14,14,15	0.69	0	15,19,21	1.01	0
5	GDL	A	2502	4	13,15,15	1.87	1 (7%)	14,21,21	1.30	2 (14%)
2	GOL	B	1500	-	5,5,5	0.36	0	5,5,5	0.08	0
2	GOL	B	1501	-	5,5,5	0.28	0	5,5,5	0.11	0
2	GOL	B	1502	-	5,5,5	0.40	0	5,5,5	0.14	0
2	GOL	B	1503	-	5,5,5	0.39	0	5,5,5	0.13	0
2	GOL	B	1504	-	5,5,5	0.29	0	5,5,5	0.16	0
2	GOL	B	1505	-	5,5,5	0.23	0	5,5,5	0.22	0
3	SO4	B	1507	-	4,4,4	0.23	0	6,6,6	0.11	0
3	SO4	B	1508	-	4,4,4	0.30	0	6,6,6	0.13	0
3	SO4	B	1509	-	4,4,4	0.27	0	6,6,6	0.09	0
3	SO4	B	1510	-	4,4,4	0.38	0	6,6,6	0.07	0
4	NAG	B	2501	5	14,14,15	0.58	0	15,19,21	0.74	0
5	GDL	B	2502	4	13,15,15	1.85	1 (7%)	14,21,21	1.30	2 (14%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	GOL	A	1499	-	-	0/4/4/4	0/0/0/0
2	GOL	A	1500	-	-	0/4/4/4	0/0/0/0
2	GOL	A	1501	-	-	0/4/4/4	0/0/0/0
3	SO4	A	1503	-	-	0/0/0/0	0/0/0/0
3	SO4	A	1504	-	-	0/0/0/0	0/0/0/0
3	SO4	A	1505	-	-	0/0/0/0	0/0/0/0
4	NAG	A	2501	5	-	0/6/23/26	0/1/1/1
5	GDL	A	2502	4	-	0/6/26/26	0/1/1/1
2	GOL	B	1500	-	-	0/4/4/4	0/0/0/0
2	GOL	B	1501	-	-	0/4/4/4	0/0/0/0
2	GOL	B	1502	-	-	0/4/4/4	0/0/0/0
2	GOL	B	1503	-	-	0/4/4/4	0/0/0/0
2	GOL	B	1504	-	-	0/4/4/4	0/0/0/0
2	GOL	B	1505	-	-	0/4/4/4	0/0/0/0
3	SO4	B	1507	-	-	0/0/0/0	0/0/0/0
3	SO4	B	1508	-	-	0/0/0/0	0/0/0/0
3	SO4	B	1509	-	-	0/0/0/0	0/0/0/0
3	SO4	B	1510	-	-	0/0/0/0	0/0/0/0
4	NAG	B	2501	5	-	0/6/23/26	0/1/1/1
5	GDL	B	2502	4	-	0/6/26/26	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	B	2502	GDL	O1-C1	6.03	1.36	1.21
5	A	2502	GDL	O1-C1	6.09	1.36	1.21

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	2502	GDL	C3-C4-C5	-2.53	105.78	110.20
5	B	2502	GDL	C3-C4-C5	-2.38	106.05	110.20
5	B	2502	GDL	C8-C7-N1	2.03	119.98	116.11
5	A	2502	GDL	C8-C7-N1	2.25	120.41	116.11

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

11 monomers are involved in 31 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1499	GOL	1	0
2	A	1500	GOL	6	0
2	A	1501	GOL	6	0
3	A	1504	SO4	1	0
5	A	2502	GDL	2	0
2	B	1501	GOL	4	0
2	B	1502	GOL	4	0
2	B	1503	GOL	1	0
2	B	1504	GOL	2	0
2	B	1505	GOL	2	0
5	B	2502	GDL	2	0

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 6 Fit of model and data ⓘ

### 6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 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	497/499 (99%)	0.35	19 (3%) 44 48	14, 30, 48, 61	0
1	B	497/499 (99%)	0.18	17 (3%) 49 52	17, 27, 47, 57	0
All	All	994/998 (99%)	0.26	36 (3%) 46 50	14, 28, 47, 61	0

All (36) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	499	ALA	9.7
1	A	319	PRO	4.1
1	A	498	VAL	4.1
1	B	457	VAL	3.9
1	B	488	SER	3.4
1	A	116	THR	3.3
1	B	371	ALA	3.3
1	A	302	GLY	3.2
1	B	319	PRO	3.2
1	A	28	VAL	3.0
1	B	456	TYR	3.0
1	B	183	ILE	2.9
1	A	320	SER	2.8
1	A	472	GLY	2.7
1	A	450	ILE	2.7
1	B	141	ILE	2.6
1	A	452	THR	2.6
1	A	470	TYR	2.6
1	A	323	TYR	2.6
1	B	139	VAL	2.5
1	A	332	VAL	2.5
1	A	58	LEU	2.5
1	A	497	ARG	2.4
1	B	234	ALA	2.4

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Mol	Chain	Res	Type	RSRZ
1	B	369	TYR	2.4
1	A	473	TYR	2.3
1	A	488	SER	2.2
1	B	24	THR	2.2
1	B	212	MET	2.1
1	B	11	TYR	2.1
1	A	20	ASN	2.0
1	A	186	ALA	2.0
1	B	485	ALA	2.0
1	B	470	TYR	2.0
1	B	184	ALA	2.0
1	B	187	GLY	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, 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	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
2	GOL	B	1504	6/6	0.59	0.40	10.30	64,64,65,67	0
2	GOL	B	1501	6/6	0.83	0.23	5.62	66,67,68,68	0
2	GOL	A	1499	6/6	0.85	0.18	4.59	35,37,40,41	0
2	GOL	B	1502	6/6	0.80	0.22	3.33	53,56,57,58	0
2	GOL	A	1500	6/6	0.79	0.23	2.97	56,59,59,61	0
2	GOL	B	1505	6/6	0.86	0.16	2.65	56,57,57,58	0
2	GOL	B	1503	6/6	0.80	0.15	2.08	49,50,51,52	0
3	SO4	B	1509	5/5	0.94	0.18	1.88	89,89,90,90	0
2	GOL	B	1500	6/6	0.83	0.21	1.83	44,47,52,52	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
3	SO4	A	1503	5/5	0.95	0.13	1.10	60,62,64,64	0
5	GDL	B	2502	15/15	0.95	0.13	-0.10	19,21,23,27	0
5	GDL	A	2502	15/15	0.95	0.14	-0.14	20,24,25,29	0
3	SO4	A	1504	5/5	0.91	0.17	-0.33	93,93,94,94	0
4	NAG	B	2501	14/15	0.97	0.10	-0.72	20,24,26,26	0
4	NAG	A	2501	14/15	0.94	0.11	-1.26	25,28,32,34	0
2	GOL	A	1501	6/6	0.85	0.16	-	62,63,63,64	0
3	SO4	B	1507	5/5	0.96	0.09	-	73,73,73,74	0
3	SO4	A	1505	5/5	0.92	0.15	-	69,70,70,70	0
3	SO4	B	1508	5/5	0.97	0.24	-	60,60,60,61	0
3	SO4	B	1510	5/5	0.83	0.15	-	82,83,83,84	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.