



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 14, 2017 – 09:32 am GMT

PDB ID : 2YPQ
Title : 3-deoxy-D-arabino-heptulosonate 7-phosphate synthase with tryptophan and tyrosine bound
Authors : Blackmore, N.J.; Reichau, S.; Jiao, W.; Hutton, R.D.; Baker, E.N.; Jameson, G.B.; Parker, E.J.
Deposited on : 2012-10-31
Resolution : 2.76 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity	:	4.02b-467
Mogul	:	1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix)	:	1.9-1692
EDS	:	trunk28620
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	recalc28949

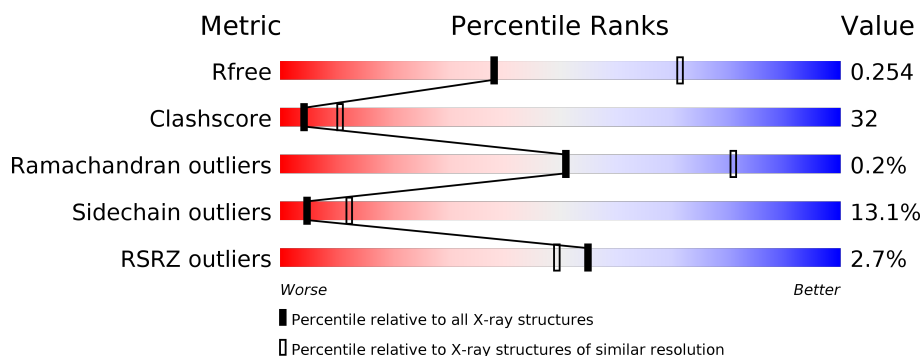
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION



The reported resolution of this entry is 2.76 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	100719	3666 (2.80-2.72)
Clashscore	112137	4174 (2.80-2.72)
Ramachandran outliers	110173	4103 (2.80-2.72)
Sidechain outliers	110143	4106 (2.80-2.72)
RSRZ outliers	101464	3697 (2.80-2.72)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	462	 3% 49% 40% 10%
1	B	462	 2% 46% 46% 7%

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
6	SO4	B	1468	-	-	X	-
8	GOL	A	1469	-	-	-	X
8	GOL	B	1469	-	-	-	X
8	GOL	B	1470	-	-	-	X
8	GOL	B	1471	-	-	-	X

2 Entry composition [i](#)

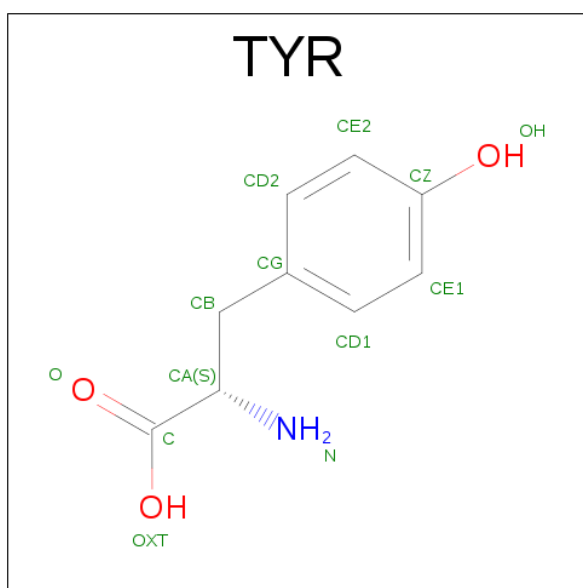
There are 9 unique types of molecules in this entry. The entry contains 7227 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 PHOSPHO-2-DEHYDRO-3-DEOXYHEPTONATE ALDOLASE AROG.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	460	Total	C	N	O	S	0	0	0
			3514	2198	642	656	18			
1	B	457	Total	C	N	O	S	0	0	0
			3515	2194	640	663	18			

- Molecule 2 is TYROSINE (three-letter code: TYR) (formula: $C_9H_{11}NO_3$).

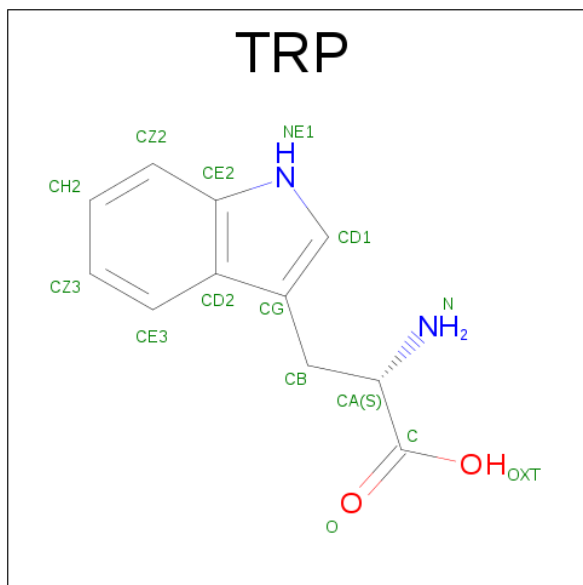


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			13	9	1	3		
2	B	1	Total	C	N	O	0	0
			13	9	1	3		
2	B	1	Total	C	N	O	0	0
			13	9	1	3		

- Molecule 3 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	1	Total	Mn	0	0
			1	1		
3	A	1	Total	Mn	0	0
			1	1		

- Molecule 4 is TRYPTOPHAN (three-letter code: TRP) (formula: $C_{11}H_{12}N_2O_2$).



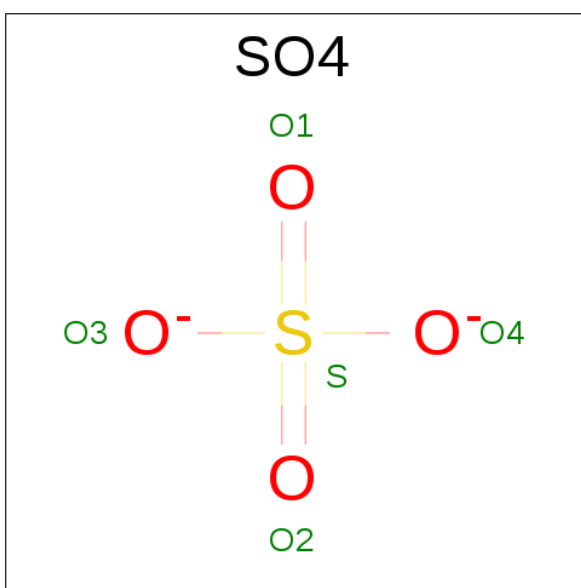
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			15	11	2	2		
4	B	1	Total	C	N	O	0	0
			15	11	2	2		

- Molecule 5 is PHOSPHATE ION (three-letter code: PO4) (formula: O_4P).



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

- Molecule 6 is SULFATE ION (three-letter code: SO4) (formula: O₄S).

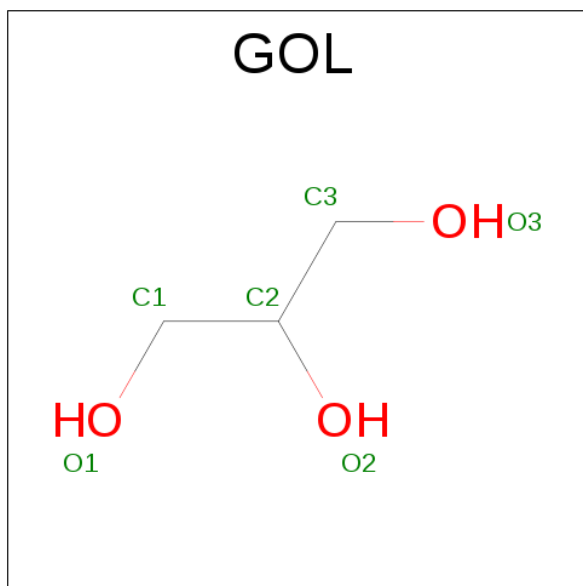


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	O	S	0	0
			5	4	1		
6	B	1	Total	O	S	0	0
			5	4	1		

- Molecule 7 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	2	Total Cl 2 2	0	0

- Molecule 8 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



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

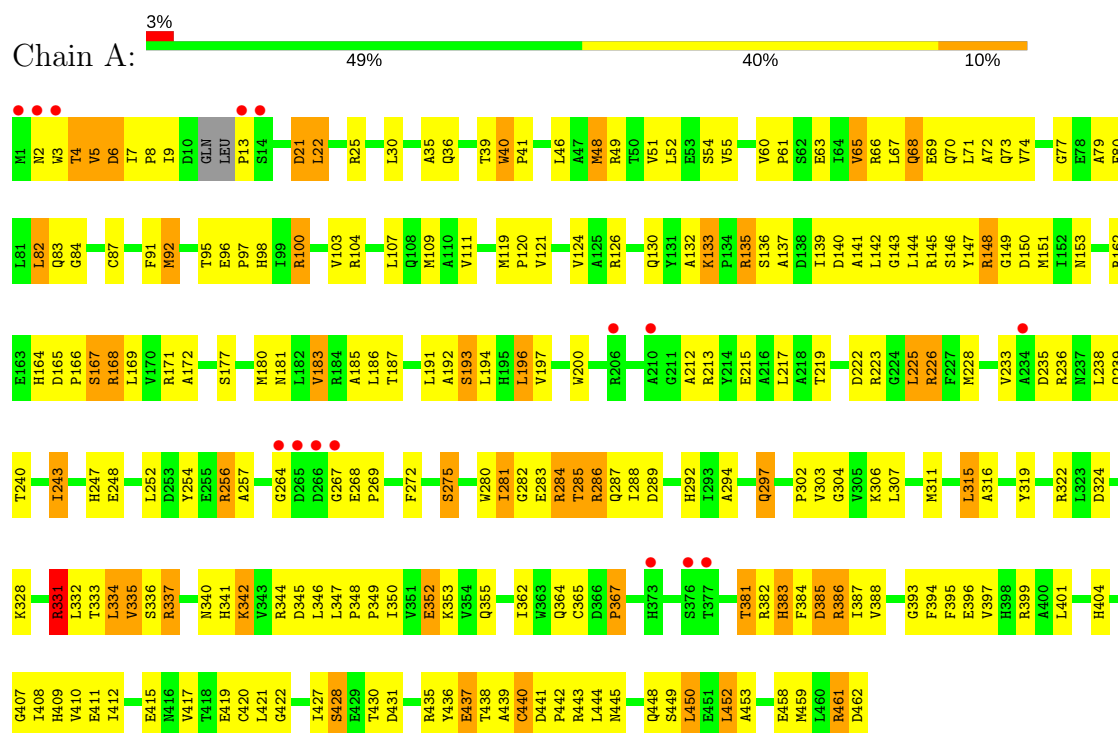
- Molecule 9 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
9	A	35	Total O 35 35	0	0
9	B	46	Total O 46 46	0	0

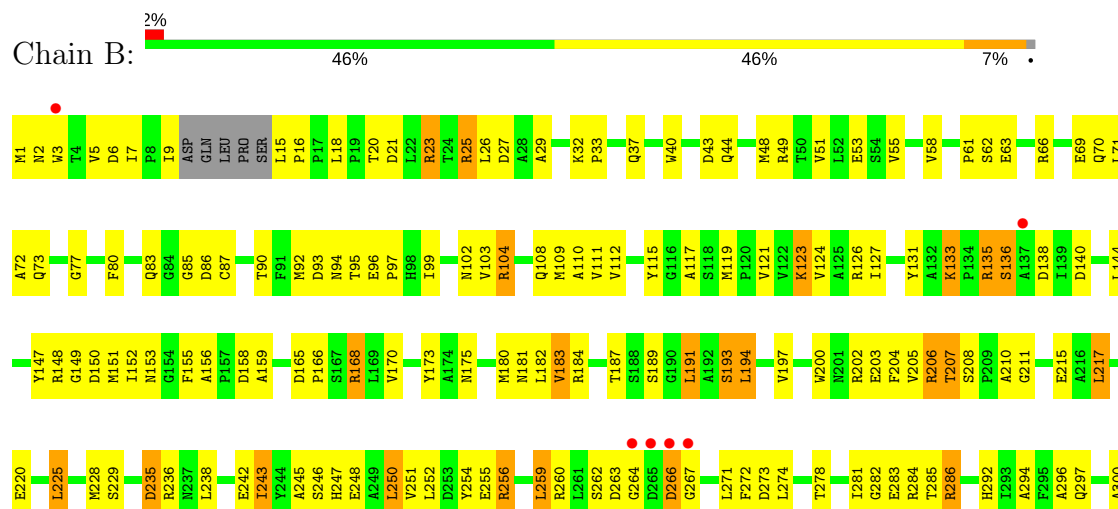
3 Residue-property plots

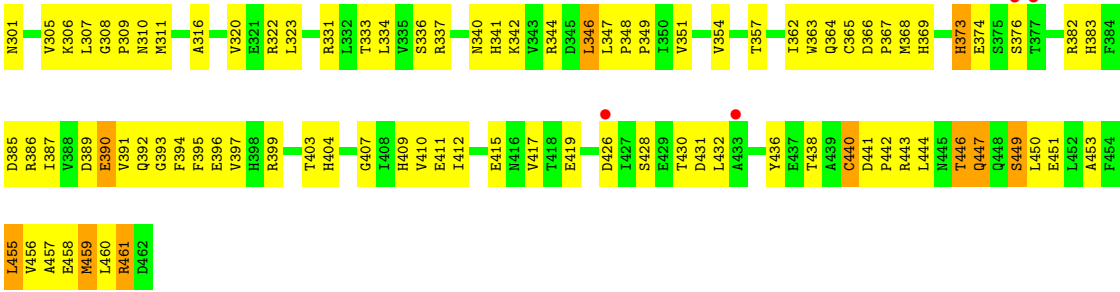
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are 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: PHOSPHO-2-DEHYDRO-3-DEOXYHEPTONATE ALDOLASE AROG



• Molecule 1: PHOSPHO-2-DEHYDRO-3-DEOXYHEPTONATE ALDOLASE AROG





4 Data and refinement statistics

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, α , β , γ	202.78Å 202.78Å 66.75Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	175.67 – 2.76 38.32 – 2.76	Depositor EDS
% Data completeness (in resolution range)	98.1 (175.67-2.76) 98.2 (38.32-2.76)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	27.88 (at 2.77Å)	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
R, R_{free}	0.177 , 0.249 0.199 , 0.254	Depositor DCC
R_{free} test set	1924 reflections (4.83%)	DCC
Wilson B-factor (Å ²)	48.0	Xtriage
Anisotropy	0.035	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 50.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.000 for -h,-k,l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	7227	wwPDB-VP
Average B, all atoms (Å ²)	41.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.03% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, PO4, MN, SO4, 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	0.74	1/3587 (0.0%)	1.29	18/4881 (0.4%)
1	B	0.74	0/3587	1.31	24/4879 (0.5%)
All	All	0.74	1/7174 (0.0%)	1.30	42/9760 (0.4%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	3	TRP	CD2-CE2	5.31	1.47	1.41

All (42) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	71	LEU	CB-CG-CD2	5.96	121.13	111.00
1	B	20	THR	CA-CB-CG2	-5.91	104.13	112.40
1	A	223	ARG	NE-CZ-NH2	-5.89	117.35	120.30
1	B	217	LEU	CB-CG-CD1	-5.82	101.11	111.00
1	A	345	ASP	CB-CG-OD1	5.79	123.52	118.30
1	A	226	ARG	NE-CZ-NH1	-5.77	117.42	120.30
1	B	131	TYR	CB-CG-CD1	5.70	124.42	121.00
1	B	202	ARG	NE-CZ-NH1	-5.68	117.46	120.30
1	A	82	LEU	CB-CG-CD2	5.65	120.61	111.00
1	B	206	ARG	NE-CZ-NH2	-5.63	117.48	120.30
1	B	455	LEU	CB-CG-CD2	-5.62	101.44	111.00
1	B	170	VAL	CB-CA-C	-5.59	100.77	111.40
1	B	183	VAL	CG1-CB-CG2	5.59	119.84	110.90
1	A	331	ARG	NE-CZ-NH1	5.57	123.08	120.30
1	B	346	LEU	CB-CG-CD2	-5.55	101.56	111.00
1	A	144	LEU	CB-CG-CD2	5.55	120.44	111.00
1	A	196	LEU	CB-CG-CD2	-5.52	101.61	111.00
1	A	67	LEU	CB-CG-CD2	-5.50	101.64	111.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	322	ARG	NE-CZ-NH2	5.50	123.05	120.30
1	B	191	LEU	CB-CG-CD1	-5.45	101.73	111.00
1	A	335	VAL	CG1-CB-CG2	5.39	119.52	110.90
1	B	27	ASP	CB-CG-OD1	-5.36	113.48	118.30
1	A	272	PHE	CB-CA-C	-5.35	99.69	110.40
1	B	206	ARG	NE-CZ-NH1	5.35	122.97	120.30
1	B	447	GLN	CA-CB-CG	-5.32	101.70	113.40
1	A	100	ARG	NE-CZ-NH1	5.31	122.95	120.30
1	B	86	ASP	CB-CG-OD1	-5.30	113.53	118.30
1	B	205	VAL	CB-CA-C	-5.30	101.33	111.40
1	A	324	ASP	CB-CG-OD2	5.29	123.06	118.30
1	A	180	MET	CG-SD-CE	5.28	108.65	100.20
1	B	58	VAL	CA-CB-CG1	-5.28	102.98	110.90
1	A	121	VAL	CG1-CB-CG2	5.27	119.33	110.90
1	B	443	ARG	NE-CZ-NH1	5.27	122.94	120.30
1	A	452	LEU	CB-CG-CD2	5.26	119.94	111.00
1	B	51	VAL	CG1-CB-CG2	-5.26	102.48	110.90
1	A	162	ARG	NE-CZ-NH2	-5.25	117.68	120.30
1	B	225	LEU	CB-CG-CD2	-5.23	102.11	111.00
1	B	58	VAL	CB-CA-C	-5.19	101.54	111.40
1	B	112	VAL	CG1-CB-CG2	-5.18	102.61	110.90
1	B	109	MET	CA-CB-CG	5.15	122.06	113.30
1	A	183	VAL	CA-CB-CG1	-5.13	103.21	110.90
1	B	259	LEU	CB-CG-CD2	-5.06	102.39	111.00

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3514	0	3466	234	0
1	B	3515	0	3464	229	0
2	A	13	0	8	0	0
2	B	26	0	16	1	0
3	A	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	1	0	0	0	0
4	A	15	0	9	2	0
4	B	15	0	9	1	0
5	A	5	0	0	0	0
5	B	5	0	0	0	0
6	A	5	0	0	1	0
6	B	5	0	0	2	0
7	A	2	0	0	1	0
8	A	6	0	8	1	0
8	B	18	0	24	3	0
9	A	35	0	0	2	0
9	B	46	0	0	6	0
All	All	7227	0	7004	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 32.

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:B:133:LYS:HE3	1:B:440:CYS:SG	1.67	1.33
1:B:21:ASP:O	1:B:25:ARG:HG3	1.39	1.22
1:B:150:ASP:O	1:B:168:ARG:HG2	1.37	1.20
1:A:48:MET:CE	1:A:167:SER:HA	1.79	1.12
1:B:391:VAL:CG1	1:B:459:MET:HE1	1.82	1.09
1:B:391:VAL:HG12	1:B:459:MET:CE	1.84	1.07
1:A:332:LEU:HD21	1:A:334:LEU:HD21	1.36	1.07
1:A:30:LEU:HD12	1:A:256:ARG:NH2	1.67	1.06
1:A:148:ARG:HB3	1:A:148:ARG:NH1	1.69	1.04
1:A:48:MET:HE3	1:A:167:SER:HA	1.38	1.02
1:A:168:ARG:HH11	1:A:168:ARG:HG2	1.22	1.00
1:B:307:LEU:HD11	1:B:334:LEU:HD22	1.41	0.99
1:B:391:VAL:HG12	1:B:459:MET:HE1	1.42	0.98
1:B:228:MET:CE	1:B:238:LEU:HD11	1.94	0.97
1:A:133:LYS:NZ	1:A:440:CYS:SG	2.38	0.97
1:B:393:GLY:O	1:B:397:VAL:HG23	1.65	0.96
1:B:228:MET:HE3	1:B:238:LEU:HD11	1.45	0.96
1:B:26:LEU:O	1:B:29:ALA:HB3	1.65	0.96
1:B:133:LYS:CE	1:B:440:CYS:SG	2.54	0.96
1:B:365:CYS:O	1:B:367:PRO:HD3	1.65	0.96
1:B:340:ASN:HB2	1:B:389:ASP:OD2	1.68	0.93

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:133:LYS:HE3	1:B:440:CYS:HG	1.10	0.92
1:B:250:LEU:O	1:B:250:LEU:HD12	1.70	0.92
1:A:77:GLY:HA2	1:A:404:HIS:CD2	2.04	0.92
1:B:194:LEU:HD12	1:B:238:LEU:HD22	1.52	0.90
1:B:382:ARG:HD2	1:B:442:PRO:HG2	1.51	0.90
1:B:99:ILE:O	1:B:103:VAL:HG23	1.71	0.90
1:B:151:MET:HE1	1:B:254:TYR:CD2	2.07	0.89
1:A:226:ARG:NH2	7:A:1468:CL:CL	2.43	0.89
1:B:252:LEU:O	1:B:256:ARG:HB3	1.72	0.89
1:B:48:MET:HG3	1:B:166:PRO:O	1.72	0.89
1:B:150:ASP:O	1:B:168:ARG:CG	2.22	0.88
1:A:194:LEU:HD23	1:A:225:LEU:HD21	1.56	0.87
1:B:135:ARG:HG3	6:B:1468:SO4:O2	1.77	0.84
1:B:85:GLY:HA3	1:B:126:ARG:HB2	1.58	0.83
1:A:382:ARG:HD2	1:A:442:PRO:HG2	1.59	0.82
1:A:148:ARG:HB3	1:A:148:ARG:HH11	1.44	0.81
1:A:303:VAL:HG22	1:A:331:ARG:HH11	1.44	0.81
1:A:303:VAL:HG22	1:A:331:ARG:NH1	1.95	0.81
1:A:30:LEU:CD1	1:A:256:ARG:NH2	2.44	0.80
1:B:242:GLU:OE1	8:B:1470:GOL:H31	1.80	0.80
1:B:21:ASP:O	1:B:25:ARG:CG	2.25	0.80
1:B:7:ILE:O	1:B:9:ILE:HD12	1.82	0.80
1:A:306:LYS:O	1:A:307:LEU:HD23	1.83	0.79
1:A:48:MET:HG3	1:A:166:PRO:O	1.82	0.79
1:A:168:ARG:HG2	1:A:168:ARG:NH1	1.97	0.78
1:A:252:LEU:O	1:A:256:ARG:HB3	1.82	0.78
1:B:395:PHE:O	1:B:399:ARG:HG2	1.83	0.78
1:B:391:VAL:HG12	1:B:459:MET:HE3	1.63	0.78
1:A:80:PHE:CE1	1:A:407:GLY:HA2	2.18	0.78
1:A:5:VAL:HG12	1:B:7:ILE:HD11	1.66	0.78
1:A:169:LEU:HD22	1:A:254:TYR:HB2	1.67	0.77
1:B:187:THR:HG21	1:B:243:ILE:HG13	1.65	0.76
1:A:419:GLU:O	1:A:442:PRO:HB2	1.85	0.76
1:B:365:CYS:O	1:B:367:PRO:CD	2.34	0.75
1:A:181:ASN:HB2	1:B:181:ASN:HB2	1.66	0.75
1:A:286:ARG:NH1	1:A:311:MET:HE1	2.02	0.75
1:A:315:LEU:HD12	1:A:315:LEU:O	1.88	0.73
1:B:301:ASN:O	1:B:331:ARG:NH1	2.21	0.73
1:B:151:MET:CE	1:B:254:TYR:CG	2.73	0.72
1:B:367:PRO:HB2	1:B:387:ILE:HG23	1.72	0.72
1:B:391:VAL:HG11	1:B:459:MET:HE1	1.69	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:381:THR:HG21	1:A:421:LEU:HD11	1.70	0.72
1:B:136:SER:HB2	6:B:1468:SO4:O1	1.88	0.72
1:A:169:LEU:CD2	1:A:254:TYR:HB2	2.20	0.71
1:A:49:ARG:NE	1:A:256:ARG:HD3	2.04	0.71
1:B:263:ASP:HB2	9:B:2029:HOH:O	1.89	0.71
1:A:48:MET:HE2	1:A:167:SER:HA	1.68	0.71
1:B:373:HIS:CD2	1:B:373:HIS:C	2.64	0.71
1:B:228:MET:HE1	1:B:238:LEU:HD11	1.73	0.70
1:A:417:VAL:HG12	1:A:437:GLU:HG3	1.73	0.70
1:A:165:ASP:O	1:A:168:ARG:HB2	1.91	0.70
1:A:284:ARG:CG	1:A:284:ARG:HH11	2.05	0.70
1:A:435:ARG:NH2	1:A:437:GLU:OE1	2.23	0.70
1:B:266:ASP:OD1	1:B:266:ASP:C	2.30	0.70
1:A:342:LYS:O	1:A:346:LEU:HB2	1.91	0.70
1:A:9:ILE:HG13	1:B:2:ASN:HA	1.74	0.70
1:B:281:ILE:HD11	1:B:296:ALA:HB2	1.73	0.70
1:A:126:ARG:HD2	1:A:409:HIS:HE1	1.57	0.70
1:A:264:GLY:HA2	1:A:267:GLY:O	1.91	0.69
1:A:21:ASP:OD2	1:A:22:LEU:HD13	1.93	0.69
1:A:30:LEU:HD12	1:A:256:ARG:CZ	2.22	0.69
1:A:91:PHE:CE2	1:A:171:ARG:HG2	2.29	0.68
1:B:151:MET:HE2	1:B:254:TYR:CD1	2.27	0.68
1:B:151:MET:CE	1:B:254:TYR:CD2	2.76	0.68
1:A:148:ARG:CB	1:A:148:ARG:HH11	2.06	0.68
1:B:395:PHE:CD2	1:B:459:MET:HE3	2.30	0.67
1:B:151:MET:HE2	1:B:254:TYR:CG	2.29	0.67
1:B:311:MET:HE2	1:B:311:MET:HA	1.76	0.67
1:A:283:GLU:CD	1:A:286:ARG:HH21	1.98	0.67
1:A:382:ARG:NH1	1:A:411:GLU:OE1	2.24	0.67
1:A:60:VAL:HB	1:A:61:PRO:CD	2.25	0.67
1:B:251:VAL:HG12	1:B:254:TYR:H	1.59	0.67
1:A:60:VAL:HB	1:A:61:PRO:HD2	1.75	0.67
1:A:35:ALA:HB3	1:A:285:THR:HG22	1.77	0.67
1:A:96:GLU:OE2	1:A:100:ARG:NH2	2.27	0.67
1:A:183:VAL:O	1:A:187:THR:HG23	1.96	0.66
1:A:193:SER:O	1:A:197:VAL:HG23	1.95	0.66
1:B:228:MET:CE	1:B:238:LEU:CD1	2.71	0.66
1:B:228:MET:HE1	1:B:238:LEU:CD1	2.25	0.66
1:B:194:LEU:CD1	1:B:238:LEU:HD22	2.24	0.66
1:B:428:SER:H	1:B:431:ASP:HB2	1.60	0.66
1:A:30:LEU:CD1	1:A:256:ARG:CZ	2.73	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:333:THR:HG23	1:A:362:ILE:HB	1.78	0.66
1:B:250:LEU:HD12	1:B:250:LEU:C	2.12	0.66
1:A:22:LEU:HD12	1:A:25:ARG:HE	1.59	0.66
1:A:65:VAL:O	1:A:69:GLU:HG3	1.94	0.66
1:B:136:SER:OG	1:B:284:ARG:NH1	2.28	0.66
1:B:70:GLN:OE1	8:B:1470:GOL:H2	1.96	0.66
1:B:432:LEU:O	1:B:436:TYR:HB2	1.96	0.66
1:A:365:CYS:HB2	1:A:394:PHE:CG	2.30	0.66
1:A:419:GLU:OE2	1:A:438:THR:N	2.29	0.66
1:B:99:ILE:HG21	1:B:182:LEU:HD23	1.78	0.65
1:A:281:ILE:HD13	1:A:292:HIS:HB3	1.79	0.65
1:B:104:ARG:HG2	1:B:104:ARG:HH11	1.62	0.64
1:B:264:GLY:O	1:B:267:GLY:N	2.30	0.64
1:A:148:ARG:CB	1:A:148:ARG:NH1	2.54	0.64
1:A:22:LEU:CD1	1:A:25:ARG:HE	2.09	0.64
1:A:364:GLN:NE2	1:A:409:HIS:HB2	2.12	0.64
1:A:393:GLY:O	1:A:397:VAL:HG23	1.97	0.64
1:B:391:VAL:CG1	1:B:459:MET:CE	2.54	0.64
1:A:60:VAL:HG22	1:A:63:GLU:HG3	1.80	0.63
1:B:2:ASN:OD1	1:B:2:ASN:C	2.36	0.63
1:B:165:ASP:O	1:B:168:ARG:HB2	1.98	0.63
1:A:84:GLY:HA2	1:A:410:VAL:O	1.99	0.62
1:A:36:GLN:O	1:A:148:ARG:NH2	2.32	0.62
1:A:381:THR:HG21	1:A:421:LEU:CD1	2.30	0.62
1:B:77:GLY:HA2	1:B:404:HIS:CD2	2.35	0.62
1:A:381:THR:HG23	1:A:382:ARG:N	2.14	0.62
1:A:168:ARG:CG	1:A:168:ARG:NH1	2.62	0.62
1:B:104:ARG:NH1	1:B:104:ARG:HG2	2.13	0.62
1:B:87:CYS:SG	1:B:441:ASP:HB2	2.40	0.62
1:B:347:LEU:O	1:B:351:VAL:HG23	1.99	0.62
1:A:40:TRP:HB2	1:A:41:PRO:HD2	1.81	0.62
1:A:228:MET:HE1	1:A:238:LEU:HD11	1.82	0.61
1:A:83:GLN:HA	1:A:124:VAL:O	2.01	0.61
1:A:5:VAL:CG2	1:A:5:VAL:O	2.47	0.61
1:B:260:ARG:HG3	1:B:274:LEU:HD12	1.83	0.61
1:A:194:LEU:CD2	1:A:225:LEU:HD21	2.29	0.60
1:B:256:ARG:HG3	2:B:1466:TYR:O	2.01	0.60
1:A:168:ARG:HH11	1:A:168:ARG:CG	2.02	0.60
1:A:419:GLU:OE1	1:A:438:THR:HB	2.02	0.60
1:B:191:LEU:CD1	1:B:200:TRP:HH2	2.15	0.60
1:A:165:ASP:OD1	1:A:165:ASP:C	2.40	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:18:LEU:HD21	1:B:271:LEU:HD21	1.84	0.60
1:B:395:PHE:HD2	1:B:459:MET:HE3	1.65	0.59
1:A:385:ASP:N	1:A:385:ASP:OD1	2.34	0.59
1:A:445:ASN:C	1:A:445:ASN:OD1	2.39	0.59
1:B:248:GLU:HG2	1:B:250:LEU:HB2	1.85	0.59
1:B:419:GLU:OE2	1:B:438:THR:N	2.34	0.59
1:B:348:PRO:HG3	1:B:397:VAL:HG13	1.84	0.59
1:A:347:LEU:HB3	1:A:348:PRO:HD3	1.85	0.58
1:B:264:GLY:O	1:B:267:GLY:HA2	2.04	0.58
1:B:399:ARG:NH2	1:B:459:MET:O	2.36	0.58
1:B:94:ASN:ND2	1:B:175:ASN:HB3	2.19	0.58
1:A:222:ASP:OD2	1:A:226:ARG:NH1	2.37	0.58
1:A:5:VAL:CG1	1:B:7:ILE:HD11	2.34	0.58
1:B:115:TYR:CE2	1:B:220:GLU:HG2	2.39	0.58
1:A:264:GLY:O	1:A:267:GLY:O	2.22	0.58
1:B:203:GLU:OE1	1:B:206:ARG:NH1	2.37	0.57
1:B:373:HIS:HD2	1:B:374:GLU:N	2.01	0.57
1:B:264:GLY:O	1:B:267:GLY:CA	2.52	0.57
1:A:133:LYS:CE	1:A:440:CYS:SG	2.93	0.57
1:B:194:LEU:HD22	1:B:225:LEU:CD1	2.35	0.57
1:B:49:ARG:O	1:B:53:GLU:HG3	2.04	0.57
1:B:389:ASP:O	1:B:392:GLN:HB3	2.04	0.57
1:B:204:PHE:CG	1:B:450:LEU:HD23	2.39	0.57
1:A:348:PRO:N	1:A:349:PRO:CD	2.68	0.57
1:A:68:GLN:O	1:A:68:GLN:NE2	2.30	0.57
1:B:450:LEU:O	1:B:453:ALA:HB3	2.05	0.57
1:A:133:LYS:O	1:A:148:ARG:NH1	2.33	0.57
1:B:283:GLU:OE2	1:B:308:GLY:HA3	2.05	0.57
1:B:210:ALA:O	1:B:211:GLY:C	2.44	0.56
1:A:87:CYS:SG	1:A:441:ASP:HB2	2.44	0.56
1:A:60:VAL:CG2	1:A:63:GLU:HG3	2.34	0.56
1:B:37:GLN:HA	1:B:37:GLN:NE2	2.20	0.56
1:A:140:ASP:C	1:A:140:ASP:OD1	2.40	0.56
1:A:233:VAL:HG23	1:A:233:VAL:O	2.03	0.56
1:A:98:HIS:ND1	1:A:415:GLU:OE2	2.32	0.56
1:B:457:ALA:O	1:B:461:ARG:HG2	2.06	0.56
1:A:30:LEU:HD12	1:A:256:ARG:HH21	1.61	0.56
1:B:7:ILE:O	1:B:9:ILE:CD1	2.53	0.56
1:A:68:GLN:OE1	1:A:331:ARG:HA	2.05	0.56
1:B:217:LEU:O	1:B:217:LEU:HD12	2.06	0.56
1:A:286:ARG:NH1	1:A:311:MET:CE	2.68	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:428:SER:O	1:A:431:ASP:N	2.37	0.56
1:B:307:LEU:HD11	1:B:334:LEU:CD2	2.26	0.56
1:A:39:THR:H	1:A:164:HIS:HD2	1.53	0.56
1:A:228:MET:HE2	1:A:238:LEU:HD21	1.87	0.56
1:B:283:GLU:OE1	1:B:286:ARG:NH1	2.38	0.56
1:A:452:LEU:O	1:A:452:LEU:HG	2.06	0.55
1:A:49:ARG:CZ	1:A:256:ARG:HD3	2.37	0.55
1:A:197:VAL:HA	1:A:200:TRP:CE3	2.42	0.55
1:B:151:MET:HG2	1:B:151:MET:O	2.05	0.55
1:B:147:TYR:HE1	1:B:153:ASN:O	1.89	0.55
1:B:294:ALA:HA	1:B:297:GLN:HG3	1.89	0.55
1:B:183:VAL:O	1:B:187:THR:HG23	2.07	0.55
1:B:80:PHE:O	1:B:121:VAL:HA	2.07	0.55
1:B:96:GLU:HB3	1:B:97:PRO:HD3	1.89	0.55
1:B:383:HIS:HD2	1:B:385:ASP:H	1.54	0.55
1:A:68:GLN:C	1:A:68:GLN:HE21	2.11	0.55
1:A:233:VAL:CG2	1:A:233:VAL:O	2.54	0.54
1:A:145:ARG:NH2	6:A:1467:SO4:O4	2.28	0.54
1:A:445:ASN:OD1	1:A:448:GLN:N	2.37	0.54
1:A:415:GLU:HB2	1:A:417:VAL:HG13	1.90	0.54
1:A:51:VAL:O	1:A:55:VAL:HG13	2.07	0.54
1:A:141:ALA:C	1:A:143:GLY:H	2.10	0.54
1:A:147:TYR:OH	1:A:150:ASP:OD1	2.23	0.54
1:A:264:GLY:CA	1:A:267:GLY:O	2.55	0.54
1:A:461:ARG:O	1:A:462:ASP:OD1	2.25	0.54
1:B:115:TYR:OH	1:B:220:GLU:HG3	2.08	0.54
1:B:191:LEU:HD11	1:B:200:TRP:HH2	1.73	0.54
1:B:180:MET:SD	1:B:245:ALA:HB2	2.48	0.54
1:B:447:GLN:HB3	9:B:2045:HOH:O	2.08	0.54
1:A:282:GLY:O	1:A:286:ARG:HB3	2.09	0.53
1:A:63:GLU:HG2	1:B:189:SER:OG	2.08	0.53
1:A:186:LEU:HD13	1:A:191:LEU:HD22	1.90	0.53
1:B:373:HIS:CD2	1:B:374:GLU:N	2.76	0.53
4:A:1464:TRP:CE3	4:A:1464:TRP:OXT	2.61	0.53
1:B:90:THR:OG1	1:B:93:ASP:HB2	2.07	0.53
1:A:5:VAL:HG22	1:A:5:VAL:O	2.07	0.53
1:A:306:LYS:C	1:A:307:LEU:HD23	2.29	0.53
1:A:22:LEU:HD12	1:A:25:ARG:NE	2.23	0.53
1:A:364:GLN:HE21	1:A:408:ILE:C	2.12	0.53
1:B:55:VAL:HG21	1:B:173:TYR:CE1	2.43	0.53
1:A:191:LEU:HD12	1:A:200:TRP:HH2	1.72	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:288:ILE:HG13	1:A:322:ARG:NH1	2.23	0.53
1:A:80:PHE:CZ	1:A:407:GLY:HA2	2.43	0.53
1:A:439:ALA:O	1:A:440:CYS:HB2	2.08	0.52
1:B:32:LYS:HB3	1:B:33:PRO:HD2	1.92	0.52
1:A:417:VAL:HB	1:A:419:GLU:HG3	1.90	0.52
1:B:457:ALA:O	1:B:460:LEU:HB2	2.09	0.52
1:A:284:ARG:NH1	1:A:284:ARG:HG3	2.23	0.52
1:A:303:VAL:CG2	1:A:331:ARG:NH1	2.71	0.52
1:A:91:PHE:CZ	1:A:172:ALA:HA	2.44	0.52
1:B:331:ARG:O	1:B:331:ARG:HD2	2.10	0.52
1:A:148:ARG:HB3	1:A:148:ARG:CZ	2.37	0.51
1:A:194:LEU:HD23	1:A:225:LEU:CD2	2.34	0.51
1:B:260:ARG:HH11	1:B:260:ARG:HG2	1.75	0.51
1:B:333:THR:HG21	1:B:364:GLN:OE1	2.11	0.51
1:B:366:ASP:OD2	1:B:369:HIS:ND1	2.42	0.51
1:B:366:ASP:C	1:B:366:ASP:OD1	2.49	0.51
1:A:48:MET:HE3	1:A:167:SER:CA	2.27	0.51
1:A:74:VAL:HG22	1:A:79:ALA:C	2.31	0.51
1:B:341:HIS:CD2	1:B:342:LYS:HG3	2.45	0.51
1:B:344:ARG:CD	9:B:2037:HOH:O	2.58	0.51
1:A:287:GLN:CD	1:A:287:GLN:H	2.12	0.51
1:A:332:LEU:CD2	1:A:334:LEU:HD21	2.25	0.51
1:B:286:ARG:NH2	1:B:311:MET:HE1	2.26	0.51
1:B:412:ILE:CG2	1:B:449:SER:HB3	2.41	0.51
1:B:71:LEU:HB3	1:B:362:ILE:HD11	1.93	0.51
1:A:256:ARG:NH1	9:A:2024:HOH:O	2.43	0.51
1:A:328:LYS:O	1:A:331:ARG:HB3	2.11	0.51
1:A:365:CYS:O	1:A:367:PRO:HD3	2.11	0.51
1:B:83:GLN:HA	1:B:124:VAL:O	2.11	0.51
1:B:367:PRO:HD2	1:B:409:HIS:O	2.10	0.51
1:A:281:ILE:CD1	1:A:292:HIS:HB3	2.41	0.51
1:B:458:GLU:HA	1:B:461:ARG:HG3	1.92	0.50
1:B:450:LEU:O	1:B:451:GLU:C	2.47	0.50
1:A:96:GLU:N	1:A:97:PRO:CD	2.74	0.50
1:B:348:PRO:HB2	1:B:349:PRO:HD3	1.92	0.50
1:A:384:PHE:O	1:A:388:VAL:HG23	2.12	0.50
1:A:61:PRO:O	1:A:65:VAL:CG1	2.60	0.50
4:B:1464:TRP:N	4:B:1464:TRP:CD1	2.78	0.50
1:B:354:VAL:O	1:B:357:THR:OG1	2.22	0.50
1:A:294:ALA:O	1:A:297:GLN:HB2	2.12	0.50
1:A:419:GLU:O	1:A:442:PRO:CB	2.58	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:457:ALA:HA	1:B:460:LEU:HD12	1.93	0.50
1:A:284:ARG:NH1	1:A:284:ARG:CG	2.68	0.50
1:B:15:LEU:N	1:B:16:PRO:CD	2.75	0.50
1:A:450:LEU:O	1:A:453:ALA:N	2.40	0.49
1:A:68:GLN:HA	1:A:68:GLN:NE2	2.26	0.49
1:B:99:ILE:CG2	1:B:182:LEU:HD23	2.42	0.49
1:A:52:LEU:HB2	1:A:257:ALA:HB1	1.92	0.49
1:B:140:ASP:CB	1:B:144:LEU:O	2.60	0.49
1:B:417:VAL:CG2	1:B:419:GLU:HG3	2.42	0.49
1:A:68:GLN:CA	1:A:68:GLN:NE2	2.74	0.49
1:B:80:PHE:CE1	1:B:407:GLY:HA2	2.48	0.49
1:A:119:MET:HB2	1:A:120:PRO:HD2	1.94	0.49
1:B:285:THR:HB	1:B:292:HIS:ND1	2.27	0.49
1:B:348:PRO:N	1:B:349:PRO:HD2	2.27	0.49
1:B:49:ARG:O	1:B:53:GLU:CG	2.60	0.49
1:B:281:ILE:HD11	1:B:296:ALA:CB	2.43	0.49
1:A:139:ILE:HG22	1:A:140:ASP:O	2.13	0.49
1:A:150:ASP:HB3	1:A:168:ARG:HH12	1.78	0.49
1:A:103:VAL:O	1:A:104:ARG:C	2.49	0.48
1:B:282:GLY:O	1:B:286:ARG:HG2	2.14	0.48
1:B:395:PHE:CD2	1:B:459:MET:CE	2.95	0.48
1:A:386:ARG:NH1	9:A:2033:HOH:O	2.46	0.48
1:B:412:ILE:HG21	1:B:449:SER:HB3	1.95	0.48
1:B:456:VAL:O	1:B:459:MET:HB2	2.13	0.48
1:B:37:GLN:CA	1:B:37:GLN:NE2	2.76	0.48
1:B:194:LEU:HD22	1:B:225:LEU:HD13	1.94	0.48
1:B:247:HIS:HD2	1:B:248:GLU:O	1.95	0.48
1:A:340:ASN:N	1:A:340:ASN:OD1	2.47	0.48
1:A:286:ARG:O	1:A:287:GLN:C	2.50	0.48
1:A:445:ASN:OD1	1:A:448:GLN:HG3	2.14	0.48
1:B:147:TYR:CZ	1:B:149:GLY:HA2	2.49	0.48
1:B:316:ALA:O	1:B:320:VAL:HG23	2.14	0.48
1:B:450:LEU:O	1:B:453:ALA:N	2.45	0.48
1:B:286:ARG:NH2	1:B:311:MET:CE	2.77	0.48
1:B:323:LEU:HA	1:B:323:LEU:HD23	1.54	0.48
1:A:315:LEU:HD12	1:A:315:LEU:C	2.30	0.47
1:A:383:HIS:O	1:A:387:ILE:HG13	2.13	0.47
1:A:66:ARG:O	1:A:70:GLN:HG3	2.13	0.47
1:B:273:ASP:C	1:B:273:ASP:OD1	2.51	0.47
1:A:151:MET:O	1:A:168:ARG:HB3	2.14	0.47
1:B:251:VAL:O	1:B:255:GLU:HG2	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:13:PRO:HG2	1:B:92:MET:HG3	1.95	0.47
1:B:148:ARG:CB	1:B:152:ILE:HD12	2.45	0.47
1:A:69:GLU:O	1:A:72:ALA:HB3	2.15	0.47
1:B:391:VAL:O	1:B:394:PHE:HB3	2.15	0.47
1:A:288:ILE:CG2	1:A:289:ASP:N	2.77	0.46
1:A:77:GLY:HA2	1:A:404:HIS:CG	2.48	0.46
1:A:235:ASP:O	1:A:238:LEU:HB2	2.15	0.46
1:A:40:TRP:HD1	1:A:40:TRP:O	1.98	0.46
1:A:243:ILE:O	8:A:1469:GOL:O2	2.33	0.46
1:A:82:LEU:HD12	1:A:83:GLN:N	2.30	0.46
1:A:92:MET:HE3	1:A:92:MET:HB3	1.92	0.46
1:B:306:LYS:NZ	1:B:366:ASP:OD2	2.43	0.46
1:B:419:GLU:OE1	1:B:438:THR:HB	2.15	0.46
1:B:2:ASN:O	1:B:2:ASN:OD1	2.34	0.46
1:A:61:PRO:O	1:A:65:VAL:HG13	2.16	0.46
1:B:66:ARG:CZ	1:B:70:GLN:HE21	2.28	0.46
1:A:284:ARG:HG3	1:A:284:ARG:HH11	1.77	0.46
1:B:151:MET:O	1:B:168:ARG:HB3	2.16	0.46
1:B:344:ARG:HD2	9:B:2037:HOH:O	2.16	0.46
1:B:309:PRO:HA	1:B:346:LEU:HD13	1.97	0.46
1:A:132:ALA:HA	1:A:149:GLY:HA3	1.98	0.46
1:A:335:VAL:HA	1:A:364:GLN:O	2.16	0.46
1:A:387:ILE:O	1:A:388:VAL:C	2.53	0.46
1:B:180:MET:O	1:B:181:ASN:C	2.52	0.46
1:B:117:ALA:HA	1:B:460:LEU:HD22	1.97	0.46
1:A:365:CYS:HB2	1:A:394:PHE:CD1	2.51	0.45
1:A:382:ARG:NH1	1:A:441:ASP:HB3	2.30	0.45
1:B:266:ASP:OD1	1:B:267:GLY:N	2.49	0.45
1:B:1:MET:HB3	1:B:2:ASN:H	1.54	0.45
1:A:341:HIS:ND1	1:A:341:HIS:N	2.63	0.45
1:A:285:THR:HA	1:A:287:GLN:HE22	1.80	0.45
1:A:91:PHE:CD2	1:A:171:ARG:HG2	2.51	0.45
1:B:80:PHE:CZ	1:B:407:GLY:HA2	2.51	0.45
1:B:410:VAL:HG23	1:B:412:ILE:HG23	1.98	0.45
1:A:264:GLY:C	1:A:267:GLY:O	2.55	0.45
1:B:194:LEU:HD22	1:B:225:LEU:HD11	1.97	0.45
1:A:239:GLN:C	1:A:240:THR:HG23	2.37	0.45
1:A:348:PRO:HB2	1:A:349:PRO:HD3	1.99	0.45
1:A:396:GLU:HA	1:A:399:ARG:HD2	1.98	0.45
1:A:256:ARG:HG2	1:A:257:ALA:N	2.30	0.45
1:A:7:ILE:HG21	1:B:3:TRP:CZ2	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:286:ARG:HG3	1:A:319:TYR:OH	2.17	0.45
1:B:104:ARG:O	1:B:108:GLN:HG3	2.17	0.45
1:B:94:ASN:HD22	1:B:175:ASN:HB3	1.82	0.45
1:B:191:LEU:HA	1:B:191:LEU:HD12	1.74	0.45
1:A:135:ARG:HG2	1:A:148:ARG:HD2	1.99	0.45
1:A:5:VAL:HG12	1:B:7:ILE:CD1	2.44	0.45
1:A:5:VAL:HG23	1:A:7:ILE:CD1	2.47	0.45
1:A:186:LEU:HA	1:A:186:LEU:HD23	1.56	0.44
1:B:155:PHE:O	1:B:156:ALA:C	2.54	0.44
1:B:436:TYR:CE1	1:B:438:THR:HG22	2.52	0.44
1:A:419:GLU:CD	1:A:438:THR:HB	2.38	0.44
1:B:102:ASN:ND2	9:B:2009:HOH:O	2.49	0.44
1:B:207:THR:O	1:B:208:SER:C	2.52	0.44
1:B:348:PRO:N	1:B:349:PRO:CD	2.80	0.44
1:A:130:GLN:OE1	1:A:247:HIS:HA	2.17	0.44
1:A:2:ASN:O	1:A:4:THR:HG23	2.17	0.44
1:A:135:ARG:CG	1:A:146:SER:HB3	2.47	0.44
1:B:382:ARG:NH1	1:B:411:GLU:OE1	2.39	0.44
1:A:119:MET:HB2	1:A:120:PRO:CD	2.48	0.44
1:B:55:VAL:HB	1:B:173:TYR:CZ	2.52	0.44
1:A:150:ASP:O	1:A:168:ARG:NH1	2.51	0.43
1:A:422:GLY:H	1:A:427:ILE:HB	1.83	0.43
1:B:191:LEU:HD12	1:B:200:TRP:HH2	1.81	0.43
1:B:203:GLU:O	1:B:207:THR:HG23	2.18	0.43
1:B:23:ARG:HA	1:B:23:ARG:HD3	1.73	0.43
1:B:259:LEU:HD23	1:B:273:ASP:HA	1.98	0.43
1:A:365:CYS:HB2	1:A:394:PHE:CD2	2.52	0.43
1:B:386:ARG:NH1	9:B:2042:HOH:O	2.50	0.43
1:B:104:ARG:CG	1:B:104:ARG:HH11	2.26	0.43
1:A:185:ALA:HB2	1:B:184:ARG:CZ	2.48	0.43
1:B:354:VAL:HG11	1:B:363:TRP:CZ2	2.53	0.43
1:A:193:SER:HG	1:A:196:LEU:H	1.66	0.43
1:A:52:LEU:CB	1:A:257:ALA:HB1	2.48	0.43
1:A:461:ARG:HH11	1:A:461:ARG:HG2	1.83	0.43
1:B:110:ALA:CB	1:B:123:LYS:HD3	2.48	0.43
1:B:368:MET:H	1:B:368:MET:HG2	1.54	0.43
1:B:390:GLU:O	1:B:390:GLU:HG3	2.18	0.43
1:B:242:GLU:HG2	8:B:1469:GOL:H32	2.00	0.43
1:B:367:PRO:HA	1:B:390:GLU:HG2	2.00	0.43
1:A:140:ASP:OD1	1:A:142:LEU:N	2.44	0.43
1:B:61:PRO:O	1:B:62:SER:C	2.57	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:95:THR:OG1	1:B:97:PRO:HD2	2.18	0.43
1:A:288:ILE:HG23	1:A:289:ASP:N	2.33	0.43
1:B:395:PHE:CE2	1:B:459:MET:HE2	2.52	0.43
1:B:63:GLU:O	1:B:66:ARG:HB3	2.18	0.43
1:B:193:SER:O	1:B:197:VAL:HG23	2.19	0.43
1:B:115:TYR:OH	1:B:220:GLU:CG	2.67	0.43
1:B:415:GLU:HB2	1:B:417:VAL:HG13	1.99	0.43
1:A:212:ALA:O	1:A:213:ARG:C	2.57	0.43
1:A:228:MET:CE	1:A:238:LEU:HD11	2.47	0.43
1:A:304:GLY:HA2	1:A:333:THR:O	2.19	0.43
1:A:316:ALA:O	1:A:319:TYR:HB2	2.18	0.42
1:A:109:MET:HE3	1:A:449:SER:O	2.19	0.42
1:B:412:ILE:HG22	1:B:444:LEU:HB2	2.00	0.42
1:A:247:HIS:HE1	1:A:275:SER:HB2	1.85	0.42
1:B:148:ARG:HB2	1:B:152:ILE:HD12	2.01	0.42
1:B:191:LEU:HD11	1:B:200:TRP:CH2	2.52	0.42
1:B:6:ASP:N	1:B:6:ASP:OD1	2.48	0.42
1:A:337:ARG:O	1:A:337:ARG:NH1	2.52	0.42
1:A:95:THR:HB	1:A:97:PRO:HD2	2.01	0.42
1:B:158:ASP:O	1:B:159:ALA:C	2.58	0.42
1:A:147:TYR:HE1	1:A:153:ASN:O	2.03	0.42
1:A:181:ASN:HB2	1:B:181:ASN:CB	2.44	0.42
1:A:288:ILE:HG13	1:A:322:ARG:HH12	1.84	0.42
1:B:110:ALA:HB1	1:B:123:LYS:HD3	2.01	0.42
1:B:259:LEU:HA	1:B:259:LEU:HD23	1.81	0.42
1:B:194:LEU:HD13	1:B:225:LEU:HD11	2.01	0.42
4:A:1464:TRP:OXT	4:A:1464:TRP:HE3	2.01	0.42
1:A:217:LEU:HD12	1:A:217:LEU:O	2.20	0.42
1:A:332:LEU:HD21	1:A:334:LEU:CD2	2.26	0.42
1:A:194:LEU:HD12	1:A:194:LEU:HA	1.86	0.41
1:A:213:ARG:NH1	1:A:213:ARG:HB2	2.35	0.41
1:A:419:GLU:HG2	1:A:436:TYR:HA	2.01	0.41
1:A:430:THR:O	1:A:430:THR:HG22	2.18	0.41
1:A:6:ASP:O	1:A:8:PRO:HD3	2.20	0.41
1:A:248:GLU:HB2	1:A:280:TRP:CE2	2.55	0.41
1:A:364:GLN:CD	1:A:409:HIS:HB2	2.39	0.41
1:B:194:LEU:HD13	1:B:225:LEU:CD1	2.50	0.41
1:B:458:GLU:OE1	1:B:458:GLU:HA	2.21	0.41
1:A:268:GLU:HA	1:A:269:PRO:HD3	1.95	0.41
1:A:395:PHE:O	1:A:399:ARG:HG3	2.20	0.41
1:A:7:ILE:HG21	1:B:3:TRP:CE2	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:392:GLN:O	1:B:396:GLU:HG3	2.20	0.41
1:A:346:LEU:HA	1:A:346:LEU:HD23	1.68	0.41
1:B:5:VAL:CG1	1:B:6:ASP:N	2.80	0.41
1:A:319:TYR:HD1	1:A:319:TYR:HA	1.73	0.41
1:A:461:ARG:NH1	1:A:461:ARG:HG2	2.36	0.41
1:A:412:ILE:HG22	1:A:444:LEU:HB2	2.01	0.41
1:B:264:GLY:C	1:B:267:GLY:H	2.22	0.41
1:B:272:PHE:CD2	1:B:300:ALA:HB3	2.55	0.41
1:A:348:PRO:O	1:A:352:GLU:HG2	2.21	0.41
1:A:91:PHE:CE1	1:A:172:ALA:HA	2.56	0.41
1:B:151:MET:HE1	1:B:254:TYR:CE2	2.53	0.41
1:B:69:GLU:O	1:B:72:ALA:HB3	2.21	0.41
1:A:137:ALA:O	1:A:146:SER:OG	2.38	0.41
1:A:355:GLN:NE2	1:A:355:GLN:HA	2.36	0.41
1:A:46:LEU:HA	1:A:46:LEU:HD12	1.65	0.41
1:B:246:SER:HB3	1:B:278:THR:HG23	2.03	0.41
1:B:346:LEU:HA	1:B:346:LEU:HD23	1.77	0.40
1:B:455:LEU:HA	1:B:455:LEU:HD23	1.86	0.40
1:A:458:GLU:O	1:A:459:MET:C	2.59	0.40
1:B:235:ASP:HB2	1:B:236:ARG:H	1.54	0.40
1:B:457:ALA:O	1:B:461:ARG:CG	2.69	0.40
1:A:107:LEU:HD13	1:A:192:ALA:HA	2.04	0.40
1:B:305:VAL:HG12	1:B:306:LYS:O	2.21	0.40
1:B:446:THR:CG2	1:B:447:GLN:N	2.84	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	456/462 (99%)	430 (94%)	25 (6%)	1 (0%)	51 81

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	453/462 (98%)	418 (92%)	34 (8%)	1 (0%)	51	81
All	All	909/924 (98%)	848 (93%)	59 (6%)	2 (0%)	51	81

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	440	CYS
1	B	440	CYS

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	366/376 (97%)	310 (85%)	56 (15%)	3	8
1	B	369/376 (98%)	328 (89%)	41 (11%)	7	19
All	All	735/752 (98%)	638 (87%)	97 (13%)	5	12

All (97) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	4	THR
1	A	5	VAL
1	A	6	ASP
1	A	21	ASP
1	A	22	LEU
1	A	40	TRP
1	A	48	MET
1	A	54	SER
1	A	65	VAL
1	A	68	GLN
1	A	73	GLN
1	A	92	MET
1	A	111	VAL
1	A	133	LYS

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Mol	Chain	Res	Type
1	A	135	ARG
1	A	136	SER
1	A	148	ARG
1	A	167	SER
1	A	168	ARG
1	A	177	SER
1	A	193	SER
1	A	215	GLU
1	A	219	THR
1	A	225	LEU
1	A	236	ARG
1	A	243	ILE
1	A	256	ARG
1	A	275	SER
1	A	281	ILE
1	A	284	ARG
1	A	285	THR
1	A	286	ARG
1	A	297	GLN
1	A	302	PRO
1	A	315	LEU
1	A	331	ARG
1	A	334	LEU
1	A	336	SER
1	A	337	ARG
1	A	342	LYS
1	A	344	ARG
1	A	350	ILE
1	A	352	GLU
1	A	353	LYS
1	A	367	PRO
1	A	381	THR
1	A	383	HIS
1	A	385	ASP
1	A	386	ARG
1	A	401	LEU
1	A	420	CYS
1	A	428	SER
1	A	437	GLU
1	A	443	ARG
1	A	450	LEU
1	A	461	ARG

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Mol	Chain	Res	Type
1	B	23	ARG
1	B	25	ARG
1	B	40	TRP
1	B	43	ASP
1	B	44	GLN
1	B	73	GLN
1	B	104	ARG
1	B	111	VAL
1	B	119	MET
1	B	123	LYS
1	B	127	ILE
1	B	133	LYS
1	B	135	ARG
1	B	136	SER
1	B	138	ASP
1	B	168	ARG
1	B	193	SER
1	B	194	LEU
1	B	207	THR
1	B	215	GLU
1	B	229	SER
1	B	235	ASP
1	B	243	ILE
1	B	250	LEU
1	B	256	ARG
1	B	262	SER
1	B	266	ASP
1	B	286	ARG
1	B	310	ASN
1	B	336	SER
1	B	337	ARG
1	B	373	HIS
1	B	376	SER
1	B	390	GLU
1	B	403	THR
1	B	426	ASP
1	B	430	THR
1	B	446	THR
1	B	449	SER
1	B	459	MET
1	B	461	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such

sidechains are listed below:

Mol	Chain	Res	Type
1	A	83	GLN
1	A	164	HIS
1	A	198	HIS
1	A	292	HIS
1	A	327	ASN
1	A	359	HIS
1	A	364	GLN
1	A	373	HIS
1	A	409	HIS
1	B	68	GLN
1	B	297	GLN
1	B	341	HIS
1	B	373	HIS
1	B	383	HIS
1	B	404	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](#)

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](#)

Of 17 ligands modelled in this entry, 4 are monoatomic - leaving 13 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
4	TRP	A	1464	-	11,16,16	1.41	1 (9%)	11,22,22	1.05	0
2	TYR	A	1465	-	9,13,13	0.59	0	12,17,17	1.08	1 (8%)
5	PO4	A	1466	-	4,4,4	1.17	0	6,6,6	0.94	0
6	SO4	A	1467	-	4,4,4	0.81	0	6,6,6	2.19	3 (50%)
8	GOL	A	1469	-	5,5,5	0.43	0	5,5,5	0.56	0
4	TRP	B	1464	-	11,16,16	1.59	2 (18%)	11,22,22	1.35	2 (18%)
2	TYR	B	1465	-	9,13,13	0.72	0	12,17,17	0.88	0
2	TYR	B	1466	-	9,13,13	0.85	0	12,17,17	0.95	1 (8%)
5	PO4	B	1467	-	4,4,4	0.78	0	6,6,6	2.13	2 (33%)
6	SO4	B	1468	-	4,4,4	0.71	0	6,6,6	0.76	0
8	GOL	B	1469	-	5,5,5	0.71	0	5,5,5	0.80	0
8	GOL	B	1470	-	5,5,5	1.16	0	5,5,5	1.36	0
8	GOL	B	1471	-	5,5,5	0.55	0	5,5,5	1.35	1 (20%)

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
4	TRP	A	1464	-	-	0/3/8/8	0/2/2/2
2	TYR	A	1465	-	-	0/4/8/8	0/1/1/1
5	PO4	A	1466	-	-	0/0/0/0	0/0/0/0
6	SO4	A	1467	-	-	0/0/0/0	0/0/0/0
8	GOL	A	1469	-	-	0/4/4/4	0/0/0/0
4	TRP	B	1464	-	-	0/3/8/8	0/2/2/2
2	TYR	B	1465	-	-	0/4/8/8	0/1/1/1
2	TYR	B	1466	-	-	0/4/8/8	0/1/1/1
5	PO4	B	1467	-	-	0/0/0/0	0/0/0/0
6	SO4	B	1468	-	-	0/0/0/0	0/0/0/0
8	GOL	B	1469	-	-	0/4/4/4	0/0/0/0
8	GOL	B	1470	-	-	0/4/4/4	0/0/0/0
8	GOL	B	1471	-	-	0/4/4/4	0/0/0/0

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	1464	TRP	CE3-CD2	-3.60	1.34	1.42
4	B	1464	TRP	CZ2-CE2	-2.80	1.36	1.41
4	B	1464	TRP	CH2-CZ2	2.13	1.41	1.36

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1465	TYR	CG-CB-CA	-3.44	107.31	114.43
6	A	1467	SO4	O4-S-O3	-3.41	93.61	108.96
5	B	1467	PO4	O2-P-O1	-3.14	97.60	110.97
4	B	1464	TRP	CH2-CZ2-CE2	-3.08	115.42	120.07
4	B	1464	TRP	CZ3-CH2-CZ2	2.04	123.36	120.45
8	B	1471	GOL	C3-C2-C1	2.14	120.04	111.52
2	B	1466	TYR	CG-CB-CA	2.30	119.18	114.43
6	A	1467	SO4	O4-S-O1	2.51	123.12	109.26
6	A	1467	SO4	O3-S-O2	2.65	123.87	109.26
5	B	1467	PO4	O4-P-O3	3.34	120.18	107.90

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

8 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	1464	TRP	2	0
6	A	1467	SO4	1	0
8	A	1469	GOL	1	0
4	B	1464	TRP	1	0
2	B	1466	TYR	1	0
6	B	1468	SO4	2	0
8	B	1469	GOL	1	0
8	B	1470	GOL	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, 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	460/462 (99%)	-0.01	15 (3%) 47 41	16, 39, 73, 121	1 (0%)
1	B	457/462 (98%)	-0.08	10 (2%) 62 57	13, 35, 70, 120	2 (0%)
All	All	917/924 (99%)	-0.05	25 (2%) 55 49	13, 37, 71, 121	3 (0%)

All (25) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	234	ALA	5.1
1	B	376	SER	4.4
1	B	433	ALA	4.0
1	A	265	ASP	4.0
1	A	267	GLY	3.8
1	B	426	ASP	3.8
1	B	265	ASP	3.3
1	B	377	THR	3.2
1	A	377	THR	3.0
1	B	267	GLY	3.0
1	A	3	TRP	2.9
1	A	266	ASP	2.9
1	A	1	MET	2.8
1	A	373	HIS	2.8
1	A	2	ASN	2.7
1	B	266	ASP	2.6
1	A	206	ARG	2.5
1	A	264	GLY	2.4
1	B	137	ALA	2.3
1	A	210	ALA	2.3
1	A	376	SER	2.3
1	B	264	GLY	2.2
1	A	14	SER	2.2
1	B	3	TRP	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	13	PRO	2.1

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

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

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
8	GOL	B	1469	6/6	0.79	0.48	6.42	50,69,93,105	0
8	GOL	B	1471	6/6	0.86	0.21	5.25	54,72,78,82	0
8	GOL	A	1469	6/6	0.95	0.28	4.21	50,65,69,71	0
8	GOL	B	1470	6/6	0.82	0.23	2.70	54,57,80,86	0
2	TYR	B	1465	13/13	0.93	0.26	1.84	35,47,73,75	0
3	MN	B	1463	1/1	0.95	0.26	1.22	29,29,29,29	1
2	TYR	B	1466	13/13	0.93	0.19	0.91	26,37,52,54	0
6	SO4	A	1467	5/5	0.95	0.17	0.61	52,58,74,92	0
2	TYR	A	1465	13/13	0.95	0.18	0.55	32,47,60,65	0
4	TRP	B	1464	15/15	0.98	0.13	-0.08	16,27,35,37	0
4	TRP	A	1464	15/15	0.98	0.12	-0.74	17,32,40,41	0
6	SO4	B	1468	5/5	0.96	0.15	-0.79	55,77,84,120	0
5	PO4	A	1466	5/5	0.97	0.14	-0.97	23,39,47,54	0
5	PO4	B	1467	5/5	0.98	0.14	-1.84	34,36,40,59	0
3	MN	A	1463	1/1	0.99	0.03	-1.93	48,48,48,48	0
7	CL	A	1468	1/1	0.93	0.12	-	80,80,80,80	0
7	CL	A	1500	1/1	0.85	0.12	-	73,73,73,73	0

6.5 Other polymers [i](#)

There are no such residues in this entry.