



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 2, 2023 – 11:20 PM EDT

PDB ID : 1HSJ
Title : SARR MBP FUSION STRUCTURE
Authors : Zhang, G.
Deposited on : 2000-12-26
Resolution : 2.30 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtrriage (Phenix) : 1.13
EDS : 2.34
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) : 2.34

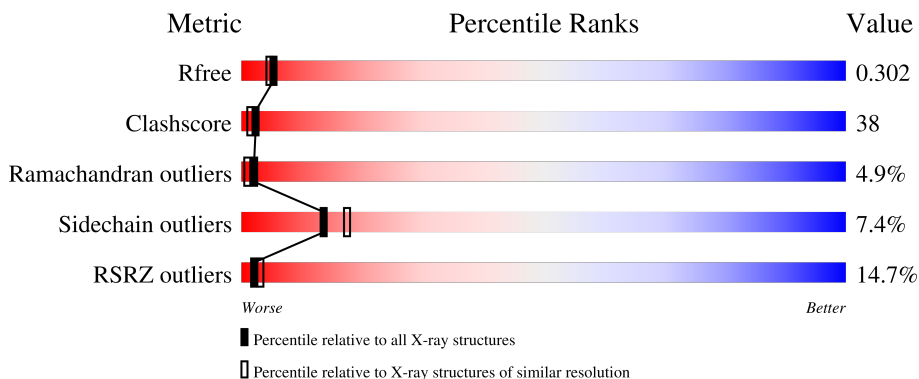
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (2.30-2.30)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. 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	487	
1	B	487	

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	GLC	A	671	-	-	X	-
2	GLC	A	672	-	-	X	-
2	GLC	B	674	-	-	X	-

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 7730 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 FUSION PROTEIN CONSISTING OF STAPHYLOCOCCUS ACCESSORY REGULATOR PROTEIN R AND MALTOSE BINDING PROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	487	3841	2471	628	734	8	0	0	0
1	B	487	3841	2471	628	734	8	0	0	0

There are 22 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	362	ALA	-	linker	UNP P0AEY0
A	363	ALA	-	linker	UNP P0AEY0
A	364	ALA	-	linker	UNP P0AEY0
A	365	GLN	-	linker	UNP P0AEY0
A	366	THR	-	linker	UNP P0AEY0
A	367	ASN	-	linker	UNP P0AEY0
A	368	ALA	-	linker	UNP P0AEY0
A	369	ALA	-	linker	UNP P0AEY0
A	370	ALA	-	linker	UNP P0AEY0
A	371	GLU	-	linker	UNP P0AEY0
A	372	PHE	-	linker	UNP P0AEY0
B	362	ALA	-	linker	UNP P0AEY0
B	363	ALA	-	linker	UNP P0AEY0
B	364	ALA	-	linker	UNP P0AEY0
B	365	GLN	-	linker	UNP P0AEY0
B	366	THR	-	linker	UNP P0AEY0
B	367	ASN	-	linker	UNP P0AEY0
B	368	ALA	-	linker	UNP P0AEY0
B	369	ALA	-	linker	UNP P0AEY0
B	370	ALA	-	linker	UNP P0AEY0
B	371	GLU	-	linker	UNP P0AEY0
B	372	PHE	-	linker	UNP P0AEY0

- Molecule 2 is alpha-D-glucopyranose (three-letter code: GLC) (formula: C₆H₁₂O₆).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total C O 12 6 6	0	0
2	A	1	Total C O 12 6 6	0	0
2	B	1	Total C O 12 6 6	0	0
2	B	1	Total C O 12 6 6	0	0

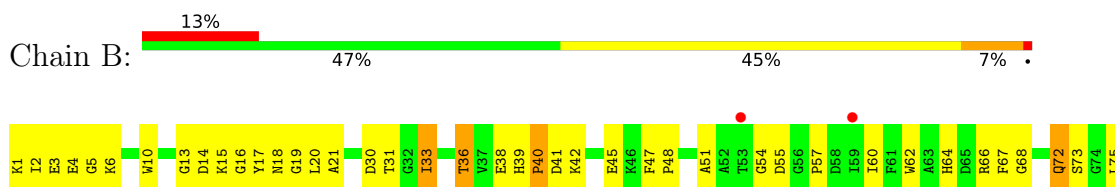
3 Residue-property plots

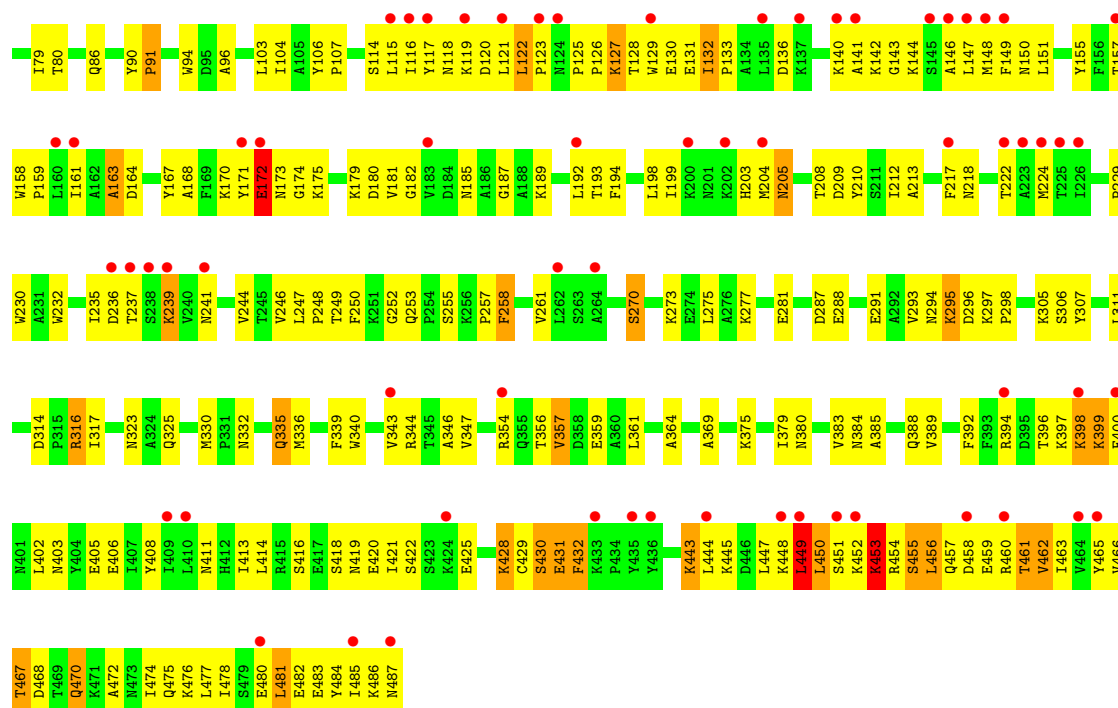
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density.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

- Molecule 1: FUSION PROTEIN CONSISTING OF STAPHYLOCOCCUS ACCESSORY REGULATOR PROTEIN R AND MALTOSE BINDING PROTEIN



- Molecule 1: FUSION PROTEIN CONSISTING OF STAPHYLOCOCCUS ACCESSORY REGULATOR PROTEIN R AND MALTOSE BINDING PROTEIN





4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	64.74Å 70.64Å 75.47Å 65.72° 67.18° 69.58°	Depositor
Resolution (Å)	19.95 – 2.30 19.94 – 2.21	Depositor EDS
% Data completeness (in resolution range)	80.6 (19.95-2.30) 85.1 (19.94-2.21)	Depositor EDS
R_{merge}	0.03	Depositor
R_{sym}	0.03	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.26 (at 2.21Å)	Xtrriage
Refinement program	CNS 0.9	Depositor
R, R_{free}	0.263 , 0.304 0.266 , 0.302	Depositor DCC
R_{free} test set	2202 reflections (4.76%)	wwPDB-VP
Wilson B-factor (Å ²)	49.0	Xtrriage
Anisotropy	0.292	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 67.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	7730	wwPDB-VP
Average B, all atoms (Å ²)	71.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.23% 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: GLC

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.46	0/3924	0.66	1/5310 (0.0%)
1	B	0.46	0/3924	0.66	1/5310 (0.0%)
All	All	0.46	0/7848	0.66	2/10620 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	453	LYS	N-CA-C	-6.02	94.75	111.00
1	A	453	LYS	N-CA-C	-5.95	94.94	111.00

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	3841	0	3851	301	0
1	B	3841	0	3851	303	0
2	A	24	0	24	8	0
2	B	24	0	24	6	0
All	All	7730	0	7750	594	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 38.

All (594) 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:1:LYS:HE2	1:B:354:ARG:HB3	1.25	1.16
1:A:451:SER:HB2	1:A:470:GLN:HG2	1.29	1.12
1:B:451:SER:HB2	1:B:470:GLN:HG2	1.28	1.12
1:A:414:LEU:HD12	1:A:478:ILE:HD12	1.33	1.10
1:B:414:LEU:HD12	1:B:478:ILE:HD12	1.28	1.06
1:B:456:LEU:HD13	1:B:457:GLN:H	1.14	1.06
1:A:456:LEU:CD1	1:A:457:GLN:H	1.69	1.04
1:A:456:LEU:HD13	1:A:457:GLN:H	1.21	1.01
2:B:673:GLC:O1	2:B:674:GLC:H62	1.65	0.96
1:A:33:ILE:HD13	1:A:275:LEU:HD13	1.47	0.95
1:B:335:GLN:H	1:B:335:GLN:NE2	1.65	0.95
1:A:335:GLN:NE2	1:A:335:GLN:H	1.63	0.95
1:A:456:LEU:HD12	1:A:458:ASP:H	1.29	0.95
1:B:467:THR:HG22	1:B:468:ASP:H	1.31	0.95
1:A:192:LEU:HD23	1:A:357:VAL:HG13	1.49	0.93
1:B:456:LEU:CD1	1:B:457:GLN:H	1.80	0.93
1:B:192:LEU:HD23	1:B:357:VAL:HG13	1.49	0.93
1:B:33:ILE:HD13	1:B:275:LEU:HD13	1.48	0.92
1:A:467:THR:HG22	1:A:468:ASP:H	1.32	0.92
2:A:671:GLC:O1	2:A:672:GLC:H62	1.73	0.89
1:A:373:MET:HB2	1:B:384:ASN:HD21	1.36	0.88
1:A:456:LEU:HD12	1:A:458:ASP:N	1.91	0.86
1:A:31:THR:HG22	1:A:33:ILE:HG23	1.57	0.86
1:A:411:ASN:HD21	1:B:380:ASN:HD22	1.23	0.86
1:A:414:LEU:HD11	1:A:475:GLN:HA	1.57	0.85
1:B:398:LYS:HG3	1:B:399:LYS:H	1.39	0.84
1:A:380:ASN:HD22	1:B:411:ASN:HD21	1.25	0.83
1:B:31:THR:HG22	1:B:33:ILE:HG23	1.59	0.82
1:B:80:THR:O	1:B:80:THR:HG22	1.81	0.81
1:A:316:ARG:HH11	1:A:316:ARG:CG	1.94	0.81
1:A:467:THR:CB	1:A:470:GLN:HB2	2.11	0.80
1:B:467:THR:CB	1:B:470:GLN:HB2	2.11	0.80
1:B:316:ARG:HH11	1:B:316:ARG:CG	1.95	0.80
1:A:1:LYS:HE2	1:B:354:ARG:CB	2.09	0.80
1:A:80:THR:HG22	1:A:80:THR:O	1.81	0.80
1:B:68:GLY:HA3	1:B:332:ASN:O	1.82	0.79
1:A:405:GLU:HA	1:A:432:PHE:CZ	2.18	0.79
1:A:68:GLY:HA3	1:A:332:ASN:O	1.82	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:354:ARG:HH11	1:A:354:ARG:HG3	1.48	0.79
1:B:31:THR:CG2	1:B:33:ILE:HG23	2.13	0.79
1:B:384:ASN:O	1:B:388:GLN:HG2	1.84	0.78
1:A:486:LYS:O	1:A:486:LYS:HD3	1.83	0.78
1:A:31:THR:CG2	1:A:33:ILE:HG23	2.13	0.78
1:B:335:GLN:H	1:B:335:GLN:HE21	1.31	0.78
1:B:451:SER:HB2	1:B:470:GLN:CG	2.12	0.78
1:A:10:TRP:CD1	1:A:57:PRO:HB3	2.19	0.77
1:B:405:GLU:HA	1:B:432:PHE:CZ	2.20	0.77
1:B:218:ASN:HD21	1:B:235:ILE:HG12	1.49	0.77
1:B:354:ARG:HG3	1:B:354:ARG:HH11	1.50	0.77
1:A:467:THR:HB	1:A:470:GLN:HB2	1.66	0.77
1:B:10:TRP:CD1	1:B:57:PRO:HB3	2.20	0.77
1:A:218:ASN:HD21	1:A:235:ILE:HG12	1.48	0.76
1:A:316:ARG:HH11	1:A:316:ARG:HG3	1.48	0.76
1:A:335:GLN:H	1:A:335:GLN:HE21	1.30	0.76
1:B:467:THR:HB	1:B:470:GLN:HB2	1.66	0.76
1:B:447:LEU:HD22	1:B:449:LEU:HD12	1.68	0.76
1:B:181:VAL:HG21	1:B:369:ALA:HB2	1.66	0.75
1:A:384:ASN:O	1:A:388:GLN:HG2	1.85	0.75
1:B:316:ARG:HH11	1:B:316:ARG:HG3	1.50	0.75
1:A:447:LEU:HD22	1:A:449:LEU:HD12	1.68	0.74
1:A:444:LEU:HB3	1:A:450:LEU:HB2	1.69	0.74
1:A:128:THR:OG1	1:A:131:GLU:HG2	1.88	0.74
1:B:128:THR:OG1	1:B:131:GLU:HG2	1.87	0.74
1:A:456:LEU:HD13	1:A:457:GLN:N	2.01	0.74
1:B:129:TRP:HA	1:B:132:ILE:HD12	1.70	0.74
1:B:244:VAL:HG21	1:B:316:ARG:HA	1.68	0.73
1:B:483:GLU:HA	1:B:486:LYS:HG2	1.71	0.73
1:A:244:VAL:HG21	1:A:316:ARG:HA	1.69	0.73
1:A:115:LEU:HD22	1:A:248:PRO:HD3	1.71	0.73
1:B:115:LEU:HD22	1:B:248:PRO:HD3	1.70	0.73
1:B:444:LEU:HB3	1:B:450:LEU:HB2	1.70	0.73
1:A:451:SER:HB2	1:A:470:GLN:CG	2.14	0.73
1:A:209:ASP:OD1	1:A:212:ILE:HD13	1.89	0.72
1:B:136:ASP:O	1:B:140:LYS:HB2	1.89	0.72
1:A:181:VAL:HG21	1:A:369:ALA:HB2	1.71	0.72
1:A:136:ASP:O	1:A:140:LYS:HB2	1.90	0.71
1:B:414:LEU:HD11	1:B:475:GLN:HA	1.73	0.71
1:B:456:LEU:HD13	1:B:457:GLN:N	1.99	0.71
1:A:129:TRP:HA	1:A:132:ILE:HD12	1.71	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:408:TYR:CZ	1:A:430:SER:HB3	2.25	0.71
1:A:456:LEU:CD1	1:A:458:ASP:H	2.04	0.70
1:B:209:ASP:OD1	1:B:212:ILE:HD13	1.92	0.70
1:A:136:ASP:HA	1:A:146:ALA:HB2	1.73	0.70
1:A:451:SER:HB3	1:A:465:TYR:O	1.92	0.70
2:B:673:GLC:C1	2:B:674:GLC:HO4	2.03	0.70
1:B:136:ASP:HA	1:B:146:ALA:HB2	1.73	0.69
1:A:18:ASN:HB2	1:A:296:ASP:OD2	1.93	0.69
1:B:18:ASN:HB2	1:B:296:ASP:OD2	1.91	0.69
1:A:460:ARG:HA	1:A:460:ARG:NE	2.06	0.68
1:A:150:ASN:HD22	1:A:210:TYR:HB2	1.58	0.68
1:A:172:GLU:CD	1:A:173:ASN:H	1.97	0.68
1:B:4:GLU:HG2	1:B:5:GLY:N	2.10	0.67
1:B:482:GLU:C	1:B:486:LYS:HE3	2.15	0.67
1:A:453:LYS:HD2	1:A:462:VAL:HG11	1.75	0.67
1:B:449:LEU:HD13	1:B:450:LEU:N	2.10	0.67
1:A:72:GLN:HA	1:A:72:GLN:HE21	1.59	0.67
1:A:140:LYS:HD2	1:A:144:LYS:O	1.94	0.67
1:A:316:ARG:HH11	1:A:316:ARG:HB2	1.60	0.67
1:A:466:VAL:HG12	1:A:470:GLN:HB3	1.76	0.67
1:B:159:PRO:HG3	1:B:257:PRO:HA	1.77	0.67
1:A:4:GLU:HG2	1:A:5:GLY:N	2.10	0.67
1:B:408:TYR:CZ	1:B:430:SER:HB3	2.30	0.67
1:B:244:VAL:CG2	1:B:316:ARG:HA	2.25	0.66
1:A:244:VAL:CG2	1:A:316:ARG:HA	2.26	0.66
1:B:316:ARG:HH11	1:B:316:ARG:HB2	1.60	0.66
1:A:316:ARG:HH11	1:A:316:ARG:CB	2.09	0.66
1:A:467:THR:HG22	1:A:468:ASP:N	2.09	0.66
1:B:72:GLN:HE21	1:B:72:GLN:HA	1.61	0.66
2:B:673:GLC:HO1	2:B:674:GLC:C4	2.08	0.66
1:B:150:ASN:HD22	1:B:210:TYR:HB2	1.61	0.66
1:B:217:PHE:HA	1:B:222:THR:HG22	1.76	0.66
1:A:217:PHE:HA	1:A:222:THR:HG22	1.76	0.66
1:A:449:LEU:HD13	1:A:450:LEU:N	2.09	0.66
1:B:307:TYR:O	1:B:311:LEU:HD13	1.96	0.66
1:B:140:LYS:HD2	1:B:144:LYS:O	1.95	0.66
1:A:356:THR:OG1	1:A:359:GLU:HG3	1.96	0.65
1:A:346:ALA:HB2	1:A:364:ALA:HB2	1.78	0.65
1:B:451:SER:HB3	1:B:465:TYR:O	1.97	0.65
1:A:307:TYR:O	1:A:311:LEU:HD13	1.96	0.65
1:B:316:ARG:HH11	1:B:316:ARG:CB	2.09	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:456:LEU:HD22	1:A:463:ILE:HD13	1.78	0.65
1:A:354:ARG:HG3	1:A:354:ARG:NH1	2.12	0.65
1:B:482:GLU:O	1:B:486:LYS:HE3	1.97	0.65
1:A:467:THR:HB	1:A:470:GLN:H	1.62	0.65
1:B:129:TRP:HA	1:B:132:ILE:CD1	2.27	0.65
1:A:411:ASN:ND2	1:B:380:ASN:HD22	1.95	0.65
1:B:164:ASP:O	1:B:187:GLY:HA3	1.97	0.65
1:B:172:GLU:CD	1:B:173:ASN:H	1.99	0.65
1:B:354:ARG:HG3	1:B:354:ARG:NH1	2.12	0.65
1:B:430:SER:C	1:B:432:PHE:H	2.00	0.65
1:B:466:VAL:HG12	1:B:470:GLN:HB3	1.80	0.64
1:A:159:PRO:HG3	1:A:257:PRO:HA	1.79	0.64
1:A:164:ASP:O	1:A:187:GLY:HA3	1.98	0.64
1:A:461:THR:HG22	1:A:461:THR:O	1.98	0.64
1:B:307:TYR:CE2	1:B:311:LEU:HD11	2.33	0.64
1:A:456:LEU:CD2	1:A:463:ILE:HD13	2.27	0.64
2:A:671:GLC:HO1	2:A:672:GLC:C4	2.10	0.64
1:B:467:THR:HB	1:B:470:GLN:H	1.62	0.64
1:A:316:ARG:HG3	1:A:316:ARG:NH1	2.10	0.63
1:B:467:THR:HG22	1:B:468:ASP:N	2.09	0.63
1:B:119:LYS:O	1:B:123:PRO:HG3	1.98	0.63
1:B:403:ASN:ND2	1:B:406:GLU:HG3	2.12	0.63
1:A:119:LYS:O	1:A:123:PRO:HG3	1.98	0.63
1:A:402:LEU:HD11	1:A:477:LEU:HD21	1.81	0.63
1:B:316:ARG:HG3	1:B:316:ARG:NH1	2.12	0.63
1:B:406:GLU:HB3	1:B:444:LEU:HD11	1.79	0.63
1:B:346:ALA:HB2	1:B:364:ALA:HB2	1.81	0.62
1:A:379:ILE:HG23	1:B:482:GLU:OE2	1.98	0.62
1:B:356:THR:OG1	1:B:359:GLU:HG3	1.98	0.62
1:B:414:LEU:CD1	1:B:478:ILE:HD12	2.19	0.62
1:B:453:LYS:HD2	1:B:462:VAL:HG11	1.82	0.62
1:A:430:SER:C	1:A:432:PHE:H	2.03	0.62
1:B:90:TYR:CE1	1:B:305:LYS:HG2	2.35	0.62
1:B:129:TRP:CD1	1:B:248:PRO:HB2	2.35	0.62
1:B:456:LEU:CD2	1:B:463:ILE:HD13	2.30	0.62
1:A:129:TRP:HA	1:A:132:ILE:CD1	2.29	0.62
1:A:237:THR:C	1:A:239:LYS:H	2.03	0.62
1:A:375:LYS:O	1:A:376:ILE:HB	1.99	0.61
1:A:405:GLU:HA	1:A:432:PHE:HZ	1.65	0.61
1:B:130:GLU:O	1:B:133:PRO:HD2	2.00	0.61
1:A:31:THR:HG21	1:A:33:ILE:HG12	1.82	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:90:TYR:CE1	1:A:305:LYS:HG2	2.36	0.61
1:A:466:VAL:CG1	1:A:470:GLN:HB3	2.31	0.61
1:B:461:THR:O	1:B:461:THR:HG22	1.99	0.61
1:A:130:GLU:O	1:A:133:PRO:HD2	2.01	0.61
1:A:307:TYR:CE2	1:A:311:LEU:HD11	2.35	0.60
1:A:450:LEU:O	1:A:450:LEU:HD22	2.01	0.60
1:A:403:ASN:ND2	1:A:406:GLU:HG3	2.16	0.60
1:B:237:THR:C	1:B:239:LYS:H	2.04	0.60
1:B:449:LEU:HD23	1:B:474:ILE:HG12	1.81	0.60
1:A:449:LEU:HD23	1:A:474:ILE:HG12	1.83	0.60
1:A:129:TRP:CD1	1:A:248:PRO:HB2	2.37	0.60
1:A:294:ASN:OD1	1:A:298:PRO:HA	2.02	0.60
1:A:64:HIS:HE1	1:A:330:MET:O	1.84	0.60
1:A:478:ILE:O	1:A:482:GLU:HB2	2.02	0.60
2:A:671:GLC:O1	2:A:672:GLC:C6	2.47	0.59
1:B:456:LEU:HD12	1:B:458:ASP:N	2.16	0.59
1:B:459:GLU:CD	1:B:460:ARG:H	2.03	0.59
1:B:80:THR:O	1:B:80:THR:CG2	2.50	0.59
1:B:171:TYR:OH	1:B:174:GLY:HA2	2.02	0.59
1:B:163:ALA:HB2	1:B:255:SER:HA	1.84	0.59
1:B:199:ILE:HG23	1:B:204:MET:O	2.03	0.59
1:B:478:ILE:O	1:B:482:GLU:HB2	2.02	0.59
1:A:163:ALA:HB2	1:A:255:SER:HA	1.85	0.59
1:B:430:SER:O	1:B:432:PHE:N	2.35	0.59
1:B:450:LEU:HD22	1:B:450:LEU:O	2.02	0.59
1:A:406:GLU:HB3	1:A:444:LEU:HD11	1.83	0.59
2:B:673:GLC:O1	2:B:674:GLC:C6	2.48	0.59
1:A:198:LEU:O	1:A:203:HIS:HB2	2.02	0.59
1:B:47:PHE:CG	1:B:60:ILE:HD12	2.38	0.58
1:B:132:ILE:H	1:B:133:PRO:CD	2.17	0.58
1:B:294:ASN:OD1	1:B:298:PRO:HA	2.04	0.58
1:B:198:LEU:O	1:B:203:HIS:HB2	2.03	0.58
1:A:171:TYR:OH	1:A:174:GLY:HA2	2.04	0.58
1:B:31:THR:HG21	1:B:33:ILE:HG12	1.84	0.58
1:B:194:PHE:CZ	1:B:198:LEU:HD21	2.38	0.58
1:A:64:HIS:CE1	1:A:330:MET:O	2.56	0.58
1:A:450:LEU:HD13	1:A:451:SER:O	2.04	0.58
1:B:447:LEU:HD23	1:B:448:LYS:N	2.18	0.58
1:A:449:LEU:O	1:A:470:GLN:HG3	2.03	0.58
1:B:466:VAL:CG1	1:B:470:GLN:HB3	2.34	0.58
1:B:15:LYS:O	1:B:17:TYR:N	2.36	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:64:HIS:HE1	1:B:330:MET:O	1.86	0.57
1:A:428:LYS:HG3	1:A:429:CYS:N	2.19	0.57
1:A:447:LEU:HD23	1:A:448:LYS:N	2.19	0.57
1:B:450:LEU:HD13	1:B:451:SER:O	2.04	0.57
1:A:217:PHE:CE1	1:A:224:MET:HA	2.39	0.57
1:B:64:HIS:CE1	1:B:330:MET:O	2.58	0.57
1:B:175:LYS:NZ	1:B:418:SER:HA	2.20	0.57
1:A:132:ILE:H	1:A:133:PRO:CD	2.17	0.57
1:A:194:PHE:CZ	1:A:198:LEU:HD21	2.39	0.57
1:B:205:ASN:H	1:B:205:ASN:ND2	2.03	0.57
1:A:47:PHE:CG	1:A:60:ILE:HD12	2.40	0.57
1:A:2:ILE:N	1:A:2:ILE:HD12	2.20	0.56
1:A:205:ASN:ND2	1:A:205:ASN:H	2.03	0.56
1:B:149:PHE:O	1:B:151:LEU:CD1	2.54	0.56
1:B:314:ASP:OD1	1:B:316:ARG:HB2	2.05	0.56
1:B:428:LYS:HG3	1:B:429:CYS:N	2.19	0.56
1:A:117:TYR:CE2	1:A:125:PRO:HD3	2.40	0.56
1:A:199:ILE:HG23	1:A:204:MET:O	2.05	0.56
1:A:449:LEU:CD2	1:A:474:ILE:HG12	2.35	0.56
1:B:14:ASP:OD1	1:B:15:LYS:HG3	2.06	0.56
1:A:14:ASP:OD1	1:A:15:LYS:HG3	2.05	0.56
1:A:452:LYS:HG2	1:A:465:TYR:HB3	1.87	0.56
1:B:117:TYR:CE2	1:B:125:PRO:HD3	2.41	0.56
1:B:217:PHE:CE1	1:B:224:MET:HA	2.40	0.56
1:A:336:MET:O	1:A:339:PHE:HB3	2.05	0.56
1:A:430:SER:O	1:A:432:PHE:N	2.39	0.56
1:A:126:PRO:HD2	1:A:224:MET:HE1	1.88	0.56
1:A:149:PHE:O	1:A:151:LEU:CD1	2.53	0.56
1:B:405:GLU:HA	1:B:432:PHE:HZ	1.67	0.56
1:B:336:MET:O	1:B:339:PHE:HB3	2.06	0.55
1:A:33:ILE:O	1:A:33:ILE:HG13	2.07	0.55
1:B:127:LYS:HZ3	1:B:127:LYS:HB2	1.71	0.55
1:A:314:ASP:OD2	1:A:316:ARG:NH1	2.39	0.55
1:A:167:TYR:CE2	1:A:182:GLY:HA3	2.42	0.55
1:A:399:LYS:O	1:A:400:PHE:CD2	2.60	0.55
1:B:147:LEU:O	1:B:148:MET:HG2	2.07	0.55
1:A:31:THR:HG22	1:A:33:ILE:H	1.70	0.55
1:A:67:PHE:HB3	1:A:104:ILE:HD12	1.88	0.55
1:A:459:GLU:HG3	1:A:461:THR:OG1	2.06	0.55
1:B:343:VAL:O	1:B:347:VAL:HG23	2.07	0.55
1:A:64:HIS:CD2	1:A:261:VAL:H	2.24	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:80:THR:O	1:A:80:THR:CG2	2.51	0.55
1:B:457:GLN:HA	1:B:457:GLN:NE2	2.20	0.55
1:B:459:GLU:OE2	1:B:459:GLU:HA	2.06	0.55
2:A:671:GLC:O1	2:A:672:GLC:O4	2.10	0.55
1:A:15:LYS:O	1:A:17:TYR:N	2.38	0.55
1:B:31:THR:HG22	1:B:33:ILE:H	1.72	0.55
1:B:447:LEU:HB3	1:B:449:LEU:HD12	1.88	0.54
1:B:456:LEU:HD22	1:B:463:ILE:HD13	1.88	0.54
1:A:185:ASN:O	1:A:189:LYS:HG3	2.06	0.54
1:B:67:PHE:HB3	1:B:104:ILE:HD12	1.90	0.54
1:A:140:LYS:HA	1:A:144:LYS:O	2.08	0.54
1:B:126:PRO:HD2	1:B:224:MET:HE1	1.87	0.54
1:B:167:TYR:CE2	1:B:182:GLY:HA3	2.42	0.54
1:A:447:LEU:HB3	1:A:449:LEU:HD12	1.89	0.54
1:B:467:THR:CG2	1:B:468:ASP:H	2.04	0.54
1:A:127:LYS:HZ3	1:A:127:LYS:HB2	1.73	0.54
1:B:121:LEU:O	1:B:122:LEU:HB2	2.07	0.54
1:B:449:LEU:CD2	1:B:474:ILE:HG12	2.37	0.54
1:A:121:LEU:O	1:A:122:LEU:HB2	2.08	0.54
1:A:456:LEU:CD1	1:A:457:GLN:N	2.55	0.54
1:A:456:LEU:HD12	1:A:457:GLN:H	1.67	0.54
1:B:79:ILE:HG12	1:B:103:LEU:O	2.08	0.54
1:A:3:GLU:HB2	1:B:354:ARG:NE	2.23	0.53
1:B:64:HIS:CD2	1:B:261:VAL:H	2.25	0.53
1:B:456:LEU:CD1	1:B:457:GLN:N	2.61	0.53
1:A:205:ASN:N	1:A:205:ASN:HD22	2.06	0.53
2:B:673:GLC:C1	2:B:674:GLC:O4	2.51	0.53
1:B:205:ASN:N	1:B:205:ASN:HD22	2.06	0.53
1:B:2:ILE:HD12	1:B:2:ILE:N	2.24	0.53
1:B:33:ILE:O	1:B:33:ILE:HG13	2.09	0.53
1:A:79:ILE:HG12	1:A:103:LEU:O	2.08	0.53
1:A:405:GLU:HG3	1:A:432:PHE:CE2	2.43	0.53
1:B:185:ASN:O	1:B:189:LYS:HG3	2.07	0.53
1:A:467:THR:OG1	1:A:470:GLN:NE2	2.42	0.53
1:B:41:ASP:O	1:B:42:LYS:HB2	2.08	0.53
1:A:205:ASN:H	1:A:205:ASN:HD22	1.57	0.53
1:B:335:GLN:NE2	1:B:335:GLN:N	2.47	0.53
1:A:3:GLU:HB2	1:B:354:ARG:HE	1.72	0.52
1:A:41:ASP:O	1:A:42:LYS:HB2	2.09	0.52
1:A:314:ASP:OD1	1:A:316:ARG:HB2	2.08	0.52
1:A:147:LEU:O	1:A:148:MET:HG2	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:2:ILE:HD11	1:B:54:GLY:O	2.09	0.52
1:B:212:ILE:HG22	1:B:213:ALA:N	2.24	0.52
1:A:396:THR:HG22	1:A:484:TYR:CD2	2.44	0.52
1:B:205:ASN:H	1:B:205:ASN:HD22	1.57	0.52
1:B:232:TRP:HB2	1:B:298:PRO:HG2	1.90	0.52
1:B:456:LEU:HD12	1:B:458:ASP:H	1.74	0.52
1:A:340:TRP:CD1	2:A:671:GLC:H4	2.45	0.52
1:B:379:ILE:O	1:B:383:VAL:HG23	2.10	0.52
1:B:13:GLY:O	1:B:17:TYR:HE2	1.93	0.52
1:B:429:CYS:O	1:B:430:SER:CB	2.57	0.52
1:A:232:TRP:HB2	1:A:298:PRO:HG2	1.92	0.51
1:A:311:LEU:O	1:A:317:ILE:HG13	2.10	0.51
1:B:288:GLU:O	1:B:291:GLU:HG2	2.09	0.51
1:B:445:LYS:HD2	1:B:453:LYS:HG2	1.92	0.51
1:A:385:ALA:O	1:A:389:VAL:HG23	2.10	0.51
1:B:314:ASP:OD2	1:B:316:ARG:NH1	2.39	0.51
1:A:15:LYS:NZ	2:A:672:GLC:O2	2.32	0.51
1:A:115:LEU:HB2	1:A:247:LEU:HD12	1.92	0.51
1:A:335:GLN:NE2	1:A:335:GLN:N	2.45	0.51
1:B:140:LYS:HA	1:B:144:LYS:O	2.09	0.51
1:A:130:GLU:H	1:A:130:GLU:CD	2.14	0.51
1:A:411:ASN:HD21	1:B:380:ASN:ND2	2.00	0.51
1:B:64:HIS:ND1	1:B:96:ALA:HB1	2.26	0.51
1:B:467:THR:OG1	1:B:470:GLN:NE2	2.44	0.51
1:A:2:ILE:HD11	1:A:54:GLY:O	2.11	0.51
1:A:13:GLY:O	1:A:17:TYR:HE2	1.94	0.51
1:A:451:SER:HB3	1:A:466:VAL:HA	1.93	0.51
1:B:14:ASP:O	1:B:230:TRP:HB2	2.11	0.51
1:A:114:SER:C	1:A:247:LEU:HD11	2.31	0.51
1:A:451:SER:CB	1:A:466:VAL:HA	2.41	0.51
1:B:120:ASP:C	1:B:121:LEU:HD12	2.31	0.51
1:A:3:GLU:HB3	1:B:354:ARG:HH21	1.76	0.51
1:A:86:GLN:HA	1:A:94:TRP:CZ2	2.46	0.51
1:A:172:GLU:OE1	1:A:173:ASN:N	2.44	0.50
1:B:151:LEU:HD13	1:B:208:THR:HB	1.93	0.50
1:A:343:VAL:O	1:A:347:VAL:HG23	2.10	0.50
1:B:115:LEU:HD12	1:B:116:ILE:N	2.26	0.50
1:A:14:ASP:O	1:A:230:TRP:HB2	2.12	0.50
1:A:217:PHE:CA	1:A:222:THR:HG22	2.40	0.50
1:A:429:CYS:O	1:A:430:SER:CB	2.59	0.50
1:B:217:PHE:CA	1:B:222:THR:HG22	2.42	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:64:HIS:HD2	1:A:261:VAL:H	1.58	0.50
1:B:175:LYS:HZ3	1:B:418:SER:HA	1.76	0.50
1:B:405:GLU:HG3	1:B:432:PHE:CE2	2.47	0.50
1:B:237:THR:C	1:B:239:LYS:N	2.65	0.50
1:A:131:GLU:O	1:A:131:GLU:HG3	2.12	0.50
1:B:115:LEU:HB2	1:B:247:LEU:HD12	1.94	0.50
1:B:255:SER:O	1:B:257:PRO:HD3	2.12	0.50
1:A:379:ILE:O	1:A:383:VAL:HG23	2.11	0.50
1:B:86:GLN:HA	1:B:94:TRP:CZ2	2.47	0.49
1:A:1:LYS:CE	1:B:354:ARG:HB3	2.18	0.49
1:A:456:LEU:CD1	1:A:458:ASP:OD1	2.60	0.49
1:A:295:LYS:HE2	1:A:295:LYS:N	2.27	0.49
1:B:130:GLU:CD	1:B:130:GLU:H	2.16	0.49
1:B:295:LYS:N	1:B:295:LYS:HE2	2.27	0.49
1:A:237:THR:C	1:A:239:LYS:N	2.65	0.49
1:A:47:PHE:N	1:A:48:PRO:HD2	2.27	0.49
1:A:288:GLU:O	1:A:291:GLU:HG2	2.13	0.49
1:A:379:ILE:HG13	1:A:380:ASN:N	2.27	0.49
1:B:47:PHE:N	1:B:48:PRO:HD2	2.27	0.49
1:A:414:LEU:HD11	1:A:475:GLN:CA	2.38	0.49
1:A:449:LEU:HD13	1:A:450:LEU:H	1.77	0.49
1:B:419:ASN:ND2	1:B:467:THR:O	2.46	0.49
1:A:151:LEU:HD13	1:A:208:THR:HB	1.94	0.49
1:B:114:SER:C	1:B:247:LEU:HD11	2.33	0.49
1:B:118:ASN:HB3	1:B:121:LEU:HB2	1.94	0.49
1:B:385:ALA:O	1:B:389:VAL:HG23	2.11	0.49
1:B:460:ARG:O	1:B:461:THR:OG1	2.26	0.49
1:A:244:VAL:HG21	1:A:316:ARG:CA	2.41	0.49
1:B:64:HIS:HD2	1:B:261:VAL:H	1.61	0.49
1:B:181:VAL:CG2	1:B:369:ALA:HB2	2.38	0.49
1:A:192:LEU:CD2	1:A:357:VAL:HG13	2.33	0.49
1:B:467:THR:CG2	1:B:468:ASP:N	2.73	0.49
1:A:445:LYS:HD2	1:A:453:LYS:HG2	1.95	0.48
1:B:172:GLU:OE1	1:B:173:ASN:N	2.46	0.48
1:A:115:LEU:HD12	1:A:116:ILE:N	2.28	0.48
1:A:212:ILE:HG22	1:A:213:ALA:N	2.27	0.48
1:A:452:LYS:CG	1:A:465:TYR:HB3	2.42	0.48
1:A:147:LEU:HD12	1:A:224:MET:O	2.13	0.48
1:B:244:VAL:HG21	1:B:316:ARG:CA	2.40	0.48
1:B:402:LEU:HD11	1:B:477:LEU:HD21	1.94	0.48
1:A:6:LYS:NZ	1:A:36:THR:HG21	2.28	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:255:SER:O	1:A:257:PRO:HD3	2.14	0.48
1:A:486:LYS:HD3	1:A:486:LYS:C	2.33	0.48
1:B:361:LEU:HA	1:B:364:ALA:HB3	1.95	0.48
1:A:64:HIS:ND1	1:A:96:ALA:HB1	2.28	0.48
1:B:129:TRP:HB3	1:B:194:PHE:CE2	2.49	0.48
1:B:430:SER:C	1:B:432:PHE:N	2.67	0.48
1:A:106:TYR:CE2	1:A:281:GLU:HG3	2.49	0.48
1:A:62:TRP:CD1	1:A:66:ARG:HG3	2.48	0.48
1:B:73:SER:HB2	1:B:75:LEU:HG	1.96	0.48
1:B:379:ILE:HG13	1:B:380:ASN:N	2.26	0.48
1:B:311:LEU:O	1:B:317:ILE:HG13	2.13	0.48
1:B:408:TYR:C	1:B:408:TYR:CD2	2.86	0.48
1:A:118:ASN:HB3	1:A:121:LEU:HB2	1.94	0.48
1:B:170:LYS:HB3	1:B:180:ASP:HB3	1.96	0.48
1:B:121:LEU:HD12	1:B:121:LEU:N	2.29	0.47
1:B:131:GLU:O	1:B:131:GLU:HG3	2.13	0.47
1:A:361:LEU:HA	1:A:364:ALA:HB3	1.95	0.47
1:A:448:LYS:N	1:A:448:LYS:HD2	2.30	0.47
1:A:450:LEU:O	1:A:450:LEU:HD13	2.14	0.47
1:A:45:GLU:O	1:A:48:PRO:HG2	2.14	0.47
1:A:120:ASP:C	1:A:121:LEU:HD12	2.35	0.47
1:A:130:GLU:CD	1:A:130:GLU:N	2.68	0.47
1:A:453:LYS:O	1:A:453:LYS:HG3	2.14	0.47
1:B:449:LEU:HD13	1:B:450:LEU:H	1.77	0.47
1:A:406:GLU:OE1	1:A:443:LYS:HD2	2.15	0.47
1:B:6:LYS:NZ	1:B:36:THR:HG21	2.29	0.47
1:A:408:TYR:C	1:A:408:TYR:CD2	2.87	0.47
1:B:398:LYS:HG3	1:B:399:LYS:N	2.19	0.47
1:B:453:LYS:HG3	1:B:453:LYS:O	2.15	0.47
1:A:116:ILE:HG12	1:A:244:VAL:HG12	1.97	0.47
1:A:295:LYS:NZ	1:A:295:LYS:HA	2.30	0.47
1:A:454:ARG:NH1	1:A:454:ARG:HB3	2.29	0.47
1:B:149:PHE:O	1:B:151:LEU:HD12	2.15	0.47
1:B:217:PHE:HE1	1:B:224:MET:HA	1.80	0.47
1:B:454:ARG:HB3	1:B:454:ARG:NH1	2.30	0.46
1:A:129:TRP:HB3	1:A:194:PHE:CE2	2.49	0.46
1:A:154:PRO:HG2	2:A:671:GLC:O6	2.15	0.46
1:B:116:ILE:HG12	1:B:244:VAL:HG12	1.97	0.46
1:B:340:TRP:HA	1:B:340:TRP:CE3	2.50	0.46
1:B:20:LEU:N	1:B:293:VAL:HG22	2.30	0.46
1:B:45:GLU:O	1:B:48:PRO:HG2	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:62:TRP:CD1	1:B:66:ARG:HG3	2.50	0.46
1:B:456:LEU:HB3	1:B:459:GLU:H	1.81	0.46
1:B:483:GLU:HA	1:B:486:LYS:CG	2.40	0.46
1:B:147:LEU:HD12	1:B:224:MET:O	2.15	0.46
1:A:249:THR:HB	1:A:253:GLN:O	2.16	0.46
1:B:398:LYS:CG	1:B:399:LYS:H	2.16	0.46
1:A:430:SER:C	1:A:432:PHE:N	2.69	0.46
1:B:482:GLU:O	1:B:486:LYS:HG2	2.16	0.46
1:A:2:ILE:HD12	1:A:2:ILE:H	1.81	0.46
1:A:73:SER:HB2	1:A:75:LEU:HG	1.97	0.46
1:A:149:PHE:O	1:A:151:LEU:HD12	2.14	0.46
1:B:4:GLU:HG2	1:B:5:GLY:H	1.81	0.46
1:B:205:ASN:ND2	1:B:205:ASN:N	2.62	0.46
1:B:396:THR:O	1:B:400:PHE:O	2.33	0.46
1:A:217:PHE:HE1	1:A:224:MET:HA	1.79	0.45
1:A:452:LYS:HZ3	1:A:465:TYR:HD2	1.63	0.45
1:B:413:ILE:O	1:B:416:SER:HB3	2.16	0.45
1:A:149:PHE:CD1	1:A:204:MET:HE1	2.52	0.45
1:A:244:VAL:CG2	1:A:316:ARG:HG2	2.46	0.45
1:A:394:ARG:NH2	1:B:431:GLU:HB2	2.30	0.45
1:B:421:ILE:HG22	1:B:422:SER:N	2.32	0.45
1:A:394:ARG:NH1	1:B:431:GLU:HG3	2.31	0.45
1:A:421:ILE:HG22	1:A:422:SER:N	2.32	0.45
1:B:277:LYS:O	1:B:281:GLU:HB2	2.17	0.45
1:B:484:TYR:N	1:B:484:TYR:CD1	2.85	0.45
1:A:255:SER:O	1:A:257:PRO:CD	2.65	0.45
1:B:106:TYR:CE2	1:B:281:GLU:HG3	2.52	0.45
1:B:244:VAL:CG2	1:B:316:ARG:HG2	2.47	0.45
1:B:255:SER:O	1:B:257:PRO:CD	2.65	0.45
1:B:472:ALA:O	1:B:476:LYS:HG3	2.17	0.45
1:A:157:THR:O	1:A:161:ILE:HG13	2.17	0.45
1:A:205:ASN:ND2	1:A:205:ASN:N	2.63	0.45
1:A:405:GLU:HG3	1:A:432:PHE:CZ	2.51	0.45
1:A:413:ILE:O	1:A:416:SER:HB3	2.16	0.45
1:A:467:THR:CG2	1:A:468:ASP:H	2.05	0.45
1:B:448:LYS:N	1:B:448:LYS:HD2	2.31	0.45
1:B:467:THR:OG1	1:B:470:GLN:HB2	2.16	0.45
1:A:121:LEU:HD12	1:A:121:LEU:N	2.32	0.45
1:B:445:LYS:C	1:B:447:LEU:N	2.70	0.45
1:B:452:LYS:HG2	1:B:465:TYR:HB3	1.98	0.45
1:A:472:ALA:O	1:A:476:LYS:HG3	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:340:TRP:HA	1:A:340:TRP:CE3	2.51	0.44
1:B:249:THR:HB	1:B:253:GLN:O	2.18	0.44
1:B:450:LEU:O	1:B:450:LEU:HD13	2.17	0.44
1:A:244:VAL:HG21	1:A:316:ARG:CG	2.48	0.44
1:A:484:TYR:N	1:A:484:TYR:CD1	2.85	0.44
1:B:295:LYS:HA	1:B:295:LYS:NZ	2.32	0.44
1:B:314:ASP:HB3	1:B:317:ILE:HG12	1.99	0.44
1:A:117:TYR:N	1:A:117:TYR:CD1	2.86	0.44
1:A:454:ARG:HB3	1:A:454:ARG:HH11	1.83	0.44
1:B:4:GLU:CG	1:B:5:GLY:N	2.80	0.44
1:B:130:GLU:CD	1:B:130:GLU:N	2.70	0.44
1:B:406:GLU:OE1	1:B:443:LYS:HD2	2.17	0.44
1:B:454:ARG:HB3	1:B:454:ARG:HH11	1.83	0.44
1:A:287:ASP:OD1	1:A:307:TYR:HB2	2.18	0.44
1:A:445:LYS:C	1:A:447:LEU:N	2.71	0.44
1:B:356:THR:O	1:B:357:VAL:C	2.55	0.44
1:A:20:LEU:N	1:A:293:VAL:HG22	2.32	0.44
1:A:380:ASN:ND2	1:B:411:ASN:HD21	2.05	0.44
1:B:18:ASN:O	1:B:21:ALA:HB3	2.17	0.44
1:B:428:LYS:NZ	1:B:428:LYS:HB3	2.33	0.44
1:B:478:ILE:O	1:B:481:LEU:HD12	2.18	0.44
1:A:10:TRP:CG	1:A:57:PRO:HB3	2.52	0.44
1:B:287:ASP:OD1	1:B:307:TYR:HB2	2.18	0.44
1:B:158:TRP:HB3	1:B:159:PRO:HD3	2.00	0.43
1:B:244:VAL:HG21	1:B:316:ARG:CG	2.48	0.43
1:B:449:LEU:O	1:B:470:GLN:HG3	2.18	0.43
1:B:149:PHE:CD1	1:B:204:MET:HE1	2.53	0.43
1:A:170:LYS:HB3	1:A:180:ASP:HB3	1.99	0.43
1:A:277:LYS:O	1:A:281:GLU:HB2	2.17	0.43
1:A:482:GLU:OE2	1:B:379:ILE:HG23	2.18	0.43
1:B:476:LYS:O	1:B:480:GLU:HB2	2.19	0.43
1:A:18:ASN:O	1:A:21:ALA:HB3	2.19	0.43
2:A:671:GLC:O1	2:A:672:GLC:C4	2.63	0.43
1:A:394:ARG:HH12	1:B:431:GLU:HG3	1.83	0.43
1:B:67:PHE:CD1	1:B:67:PHE:N	2.87	0.43
1:A:67:PHE:CD1	1:A:67:PHE:N	2.87	0.43
1:A:193:THR:HA	1:A:357:VAL:HG21	2.00	0.43
1:A:250:PHE:C	1:A:252:GLY:N	2.72	0.43
1:A:375:LYS:NZ	1:B:487:ASN:OD1	2.40	0.43
1:B:117:TYR:CD1	1:B:117:TYR:N	2.87	0.43
1:B:405:GLU:HG3	1:B:432:PHE:CZ	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:447:LEU:HD23	1:B:448:LYS:H	1.81	0.43
1:A:48:PRO:HA	1:A:75:LEU:CD1	2.47	0.43
1:A:179:LYS:HA	1:A:179:LYS:HE2	2.01	0.43
1:A:356:THR:O	1:A:357:VAL:C	2.56	0.43
1:A:392:PHE:HD1	1:A:485:ILE:HG23	1.83	0.43
1:A:467:THR:OG1	1:A:470:GLN:HB2	2.17	0.43
1:B:306:SER:OG	1:B:307:TYR:N	2.52	0.43
1:B:484:TYR:N	1:B:484:TYR:HD1	2.17	0.43
1:A:156:PHE:O	1:A:159:PRO:HD2	2.18	0.43
1:B:307:TYR:CZ	1:B:311:LEU:HD11	2.52	0.43
1:A:239:LYS:HD2	1:A:239:LYS:HA	1.86	0.43
1:A:411:ASN:HB2	1:B:379:ILE:HD11	2.01	0.43
1:B:10:TRP:CG	1:B:57:PRO:HB3	2.53	0.43
1:B:250:PHE:C	1:B:252:GLY:N	2.71	0.43
1:A:88:LYS:C	1:A:89:LEU:HD12	2.39	0.42
1:A:453:LYS:HA	1:A:463:ILE:O	2.19	0.42
1:A:454:ARG:O	1:A:455:SER:C	2.57	0.42
1:B:461:THR:O	1:B:462:VAL:C	2.58	0.42
1:A:258:PHE:CG	1:A:330:MET:HG2	2.54	0.42
1:B:459:GLU:CG	1:B:460:ARG:N	2.83	0.42
1:A:4:GLU:CG	1:A:5:GLY:N	2.79	0.42
1:A:154:PRO:HB3	1:A:343:VAL:HG12	2.01	0.42
1:A:428:LYS:NZ	1:A:428:LYS:HB3	2.33	0.42
1:B:258:PHE:CG	1:B:330:MET:HG2	2.55	0.42
1:A:86:GLN:HA	1:A:94:TRP:HZ2	1.84	0.42
1:A:307:TYR:CZ	1:A:311:LEU:HD11	2.54	0.42
1:A:314:ASP:HB3	1:A:317:ILE:HG12	2.01	0.42
1:B:157:THR:O	1:B:161:ILE:HG13	2.19	0.42
1:B:172:GLU:CD	1:B:173:ASN:N	2.71	0.42
1:B:296:ASP:OD1	1:B:297:LYS:HG2	2.20	0.42
1:B:392:PHE:HD1	1:B:485:ILE:HG23	1.84	0.42
1:B:451:SER:CB	1:B:466:VAL:HA	2.49	0.42
1:B:454:ARG:O	1:B:455:SER:C	2.57	0.42
1:A:67:PHE:HD1	1:A:67:PHE:H	1.67	0.42
1:A:141:ALA:C	1:A:143:GLY:H	2.23	0.42
1:A:172:GLU:CD	1:A:173:ASN:N	2.70	0.42
1:A:456:LEU:HD11	1:A:458:ASP:OD1	2.19	0.42
1:B:150:ASN:ND2	1:B:210:TYR:HB2	2.32	0.42
1:A:258:PHE:HB3	1:A:330:MET:CG	2.50	0.42
1:A:296:ASP:OD1	1:A:297:LYS:HG2	2.20	0.42
1:A:337:SER:O	1:A:341:TYR:HD2	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:427:ALA:HB2	1:A:437:LEU:HD11	2.02	0.42
1:A:476:LYS:O	1:A:480:GLU:HB2	2.19	0.42
1:A:484:TYR:N	1:A:484:TYR:HD1	2.17	0.42
1:B:2:ILE:HD12	1:B:2:ILE:H	1.84	0.42
1:A:372:PHE:O	1:A:373:MET:HB3	2.19	0.42
1:A:396:THR:O	1:A:400:PHE:O	2.38	0.42
1:B:179:LYS:HE2	1:B:179:LYS:HA	2.01	0.42
1:A:270:SER:O	1:A:273:LYS:NZ	2.45	0.42
1:B:258:PHE:HB3	1:B:330:MET:CG	2.49	0.42
1:B:19:GLY:HA3	1:B:293:VAL:HA	2.02	0.42
1:B:402:LEU:HD12	1:B:481:LEU:HD23	2.00	0.42
1:B:39:HIS:O	1:B:40:PRO:C	2.58	0.41
1:B:167:TYR:O	1:B:182:GLY:O	2.38	0.41
1:B:244:VAL:HG21	1:B:316:ARG:CB	2.50	0.41
1:A:51:ALA:HA	1:A:55:ASP:O	2.20	0.41
1:B:141:ALA:C	1:B:143:GLY:H	2.24	0.41
1:B:396:THR:HG22	1:B:484:TYR:CD2	2.55	0.41
1:A:4:GLU:HG2	1:A:5:GLY:H	1.83	0.41
1:A:167:TYR:O	1:A:182:GLY:O	2.38	0.41
1:A:460:ARG:HA	1:A:460:ARG:HE	1.81	0.41
1:A:19:GLY:HA3	1:A:293:VAL:HA	2.02	0.41
1:A:467:THR:HB	1:A:470:GLN:N	2.32	0.41
1:B:67:PHE:HD1	1:B:67:PHE:H	1.68	0.41
1:B:132:ILE:N	1:B:133:PRO:CD	2.82	0.41
1:B:193:THR:HA	1:B:357:VAL:HG21	2.03	0.41
1:A:48:PRO:HA	1:A:75:LEU:HD13	2.02	0.41
1:A:232:TRP:CH2	1:A:316:ARG:HB3	2.54	0.41
1:A:244:VAL:HG21	1:A:316:ARG:CB	2.51	0.41
1:A:414:LEU:CD1	1:A:478:ILE:HD12	2.25	0.41
1:A:478:ILE:O	1:A:481:LEU:HD12	2.20	0.41
1:B:94:TRP:CZ3	1:B:107:PRO:HD3	2.55	0.41
1:B:451:SER:HB3	1:B:466:VAL:HA	2.02	0.41
1:A:158:TRP:N	1:A:159:PRO:CD	2.84	0.41
1:A:201:ASN:HB2	1:A:203:HIS:CD2	2.56	0.41
1:B:38:GLU:C	1:B:40:PRO:HD3	2.41	0.41
1:B:172:GLU:OE1	1:B:172:GLU:N	2.53	0.41
1:A:172:GLU:OE1	1:A:172:GLU:N	2.53	0.41
1:A:246:VAL:HA	1:A:323:ASN:HD21	1.86	0.41
1:B:192:LEU:CD2	1:B:357:VAL:HG13	2.34	0.41
1:B:487:ASN:N	1:B:487:ASN:HD22	2.19	0.41
1:A:39:HIS:O	1:A:40:PRO:C	2.58	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:94:TRP:CZ3	1:A:107:PRO:HD3	2.56	0.41
1:B:51:ALA:HA	1:B:55:ASP:O	2.20	0.41
1:B:155:TYR:CD2	2:B:674:GLC:H61	2.56	0.41
1:B:270:SER:O	1:B:273:LYS:NZ	2.46	0.41
1:B:86:GLN:HA	1:B:94:TRP:HZ2	1.86	0.41
1:B:164:ASP:O	1:B:187:GLY:CA	2.68	0.41
1:B:380:ASN:O	1:B:384:ASN:HB2	2.21	0.41
1:A:1:LYS:HB3	1:A:1:LYS:HZ3	1.86	0.41
1:B:344:ARG:HE	1:B:344:ARG:HB2	1.77	0.41
1:A:3:GLU:CB	1:B:354:ARG:HH21	2.34	0.40
1:B:6:LYS:HZ1	1:B:36:THR:HG21	1.86	0.40
1:B:447:LEU:HB3	1:B:449:LEU:CD1	2.51	0.40
1:B:457:GLN:C	1:B:459:GLU:N	2.75	0.40
1:A:461:THR:O	1:A:462:VAL:C	2.59	0.40
1:B:429:CYS:O	1:B:430:SER:HB3	2.20	0.40
1:B:455:SER:C	1:B:456:LEU:O	2.59	0.40
1:A:429:CYS:O	1:A:430:SER:HB3	2.21	0.40
1:A:132:ILE:O	1:A:133:PRO:C	2.59	0.40
1:B:246:VAL:HA	1:B:323:ASN:HD21	1.86	0.40
1:A:79:ILE:HD13	1:A:105:ALA:C	2.42	0.40
1:A:148:MET:HB2	1:A:222:THR:HG21	2.03	0.40
1:B:397:LYS:O	1:B:398:LYS:O	2.40	0.40
1:B:487:ASN:N	1:B:487:ASN:ND2	2.70	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	485/487 (100%)	403 (83%)	57 (12%)	25 (5%)	2 1
1	B	485/487 (100%)	409 (84%)	53 (11%)	23 (5%)	2 1

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	970/974 (100%)	812 (84%)	110 (11%)	48 (5%)	2 1

All (48) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	168	ALA
1	A	398	LYS
1	A	400	PHE
1	A	462	VAL
1	A	467	THR
1	B	168	ALA
1	B	398	LYS
1	B	399	LYS
1	B	462	VAL
1	B	467	THR
1	A	16	GLY
1	A	122	LEU
1	A	373	MET
1	A	430	SER
1	A	431	GLU
1	A	432	PHE
1	A	455	SER
1	A	456	LEU
1	B	16	GLY
1	B	122	LEU
1	B	430	SER
1	B	431	GLU
1	B	432	PHE
1	B	455	SER
1	B	456	LEU
1	A	357	VAL
1	A	3	GLU
1	A	132	ILE
1	A	163	ALA
1	A	239	LYS
1	A	374	SER
1	A	376	ILE
1	B	3	GLU
1	B	132	ILE
1	B	163	ALA
1	B	239	LYS
1	B	357	VAL

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Mol	Chain	Res	Type
1	A	172	GLU
1	A	458	ASP
1	B	172	GLU
1	B	461	THR
1	A	449	LEU
1	B	449	LEU
1	B	270	SER
1	B	40	PRO
1	A	40	PRO
1	A	270	SER
1	B	91	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	405/405 (100%)	374 (92%)	31 (8%)	13	16
1	B	405/405 (100%)	376 (93%)	29 (7%)	14	18
All	All	810/810 (100%)	750 (93%)	60 (7%)	13	17

All (60) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	LYS
1	A	30	ASP
1	A	33	ILE
1	A	36	THR
1	A	72	GLN
1	A	91	PRO
1	A	127	LYS
1	A	142	LYS
1	A	172	GLU
1	A	205	ASN
1	A	229	PRO
1	A	236	ASP

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Mol	Chain	Res	Type
1	A	241	ASN
1	A	258	PHE
1	A	271	PRO
1	A	295	LYS
1	A	316	ARG
1	A	325	GLN
1	A	335	GLN
1	A	394	ARG
1	A	399	LYS
1	A	420	GLU
1	A	425	GLU
1	A	428	LYS
1	A	443	LYS
1	A	449	LEU
1	A	450	LEU
1	A	453	LYS
1	A	458	ASP
1	A	470	GLN
1	A	481	LEU
1	B	1	LYS
1	B	30	ASP
1	B	33	ILE
1	B	36	THR
1	B	72	GLN
1	B	91	PRO
1	B	127	LYS
1	B	142	LYS
1	B	172	GLU
1	B	205	ASN
1	B	229	PRO
1	B	236	ASP
1	B	241	ASN
1	B	258	PHE
1	B	295	LYS
1	B	316	ARG
1	B	325	GLN
1	B	335	GLN
1	B	375	LYS
1	B	394	ARG
1	B	420	GLU
1	B	425	GLU
1	B	428	LYS

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Mol	Chain	Res	Type
1	B	443	LYS
1	B	449	LEU
1	B	450	LEU
1	B	453	LYS
1	B	470	GLN
1	B	481	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (27) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	39	HIS
1	A	64	HIS
1	A	72	GLN
1	A	205	ASN
1	A	218	ASN
1	A	323	ASN
1	A	325	GLN
1	A	335	GLN
1	A	380	ASN
1	A	411	ASN
1	A	419	ASN
1	A	457	GLN
1	A	470	GLN
1	B	39	HIS
1	B	64	HIS
1	B	72	GLN
1	B	205	ASN
1	B	218	ASN
1	B	323	ASN
1	B	325	GLN
1	B	335	GLN
1	B	349	ASN
1	B	384	ASN
1	B	388	GLN
1	B	419	ASN
1	B	457	GLN
1	B	470	GLN

5.3.3 RNA

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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

4 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	GLC	A	671	-	12,12,12	0.42	0	17,17,17	0.65	0
2	GLC	B	674	-	12,12,12	0.67	0	17,17,17	0.77	1 (5%)
2	GLC	A	672	-	12,12,12	0.39	0	17,17,17	0.60	0
2	GLC	B	673	-	12,12,12	0.42	0	17,17,17	0.58	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	GLC	A	671	-	-	0/2/22/22	0/1/1/1
2	GLC	B	674	-	-	0/2/22/22	0/1/1/1
2	GLC	A	672	-	-	0/2/22/22	0/1/1/1
2	GLC	B	673	-	-	0/2/22/22	0/1/1/1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	674	GLC	O4-C4-C3	-2.31	105.00	110.35

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 14 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	671	GLC	7	0
2	B	674	GLC	6	0
2	A	672	GLC	6	0
2	B	673	GLC	5	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	487/487 (100%)	0.88	78 (16%) 1 2	21, 72, 109, 127	0
1	B	487/487 (100%)	0.77	65 (13%) 3 4	27, 69, 108, 127	0
All	All	974/974 (100%)	0.83	143 (14%) 2 3	21, 71, 109, 127	0

All (143) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	147	LEU	9.2
1	A	143	GLY	9.0
1	A	429	CYS	7.9
1	B	224	MET	6.1
1	A	239	LYS	5.7
1	A	435	TYR	5.6
1	A	139	LEU	5.4
1	B	225	THR	5.4
1	B	217	PHE	5.2
1	B	223	ALA	5.1
1	A	147	LEU	5.0
1	B	241	ASN	4.7
1	B	116	ILE	4.6
1	B	398	LYS	4.5
1	A	372	PHE	4.4
1	B	141	ALA	4.3
1	B	183	VAL	4.3
1	B	435	TYR	4.2
1	B	222	THR	4.2
1	A	428	LYS	4.2
1	A	450	LEU	4.0
1	A	161	ILE	3.9
1	B	161	ILE	3.9
1	B	148	MET	3.9

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Mol	Chain	Res	Type	RSRZ
1	B	237	THR	3.8
1	A	436	TYR	3.8
1	B	140	LYS	3.8
1	A	424	LYS	3.8
1	B	448	LYS	3.8
1	A	124	ASN	3.7
1	A	452	LYS	3.5
1	A	202	LYS	3.5
1	A	207	ASP	3.4
1	A	465	TYR	3.4
1	B	160	LEU	3.4
1	A	224	MET	3.4
1	B	137	LYS	3.3
1	B	146	ALA	3.3
1	A	123	PRO	3.3
1	B	400	PHE	3.3
1	A	354	ARG	3.2
1	A	341	TYR	3.2
1	A	356	THR	3.2
1	A	200	LYS	3.2
1	B	129	TRP	3.1
1	B	436	TYR	3.1
1	A	399	LYS	3.1
1	A	449	LEU	3.1
1	A	116	ILE	3.0
1	A	448	LYS	3.0
1	B	204	MET	3.0
1	B	145	SER	3.0
1	B	433	LYS	2.9
1	B	123	PRO	2.9
1	B	262	LEU	2.9
1	A	225	THR	2.9
1	A	134	ALA	2.9
1	A	144	LYS	2.9
1	B	452	LYS	2.9
1	A	241	ASN	2.9
1	A	351	ALA	2.9
1	A	172	GLU	2.8
1	A	146	ALA	2.8
1	A	204	MET	2.8
1	A	443	LYS	2.8
1	A	220	GLY	2.8

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Mol	Chain	Res	Type	RSRZ
1	B	460	ARG	2.8
1	A	223	ALA	2.7
1	A	374	SER	2.7
1	B	465	TYR	2.7
1	A	217	PHE	2.7
1	A	456	LEU	2.7
1	A	211	SER	2.7
1	A	237	THR	2.7
1	A	444	LEU	2.7
1	A	137	LYS	2.7
1	A	141	ALA	2.7
1	A	487	ASN	2.6
1	A	363	ALA	2.6
1	B	115	LEU	2.6
1	B	171	TYR	2.6
1	A	129	TRP	2.6
1	A	136	ASP	2.6
1	B	149	PHE	2.6
1	B	192	LEU	2.6
1	A	145	SER	2.6
1	A	205	ASN	2.6
1	A	280	LEU	2.6
1	A	17	TYR	2.6
1	A	373	MET	2.6
1	A	203	HIS	2.6
1	B	53	THR	2.5
1	A	192	LEU	2.5
1	B	121	LEU	2.5
1	A	427	ALA	2.5
1	B	409	ILE	2.5
1	B	239	LYS	2.5
1	A	120	ASP	2.5
1	B	343	VAL	2.5
1	B	264	ALA	2.5
1	A	358	ASP	2.5
1	B	424	LYS	2.5
1	B	135	LEU	2.5
1	A	117	TYR	2.5
1	B	124	ASN	2.5
1	A	410	LEU	2.5
1	A	242	TYR	2.4
1	A	175	LYS	2.4

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Mol	Chain	Res	Type	RSRZ
1	B	485	ILE	2.4
1	B	487	ASN	2.4
1	B	119	LYS	2.4
1	B	157	THR	2.4
1	B	172	GLU	2.3
1	A	236	ASP	2.3
1	B	394	ARG	2.3
1	A	67	PHE	2.3
1	A	486	LYS	2.3
1	B	59	ILE	2.3
1	B	200	LYS	2.3
1	B	449	LEU	2.2
1	A	142	LYS	2.2
1	B	458	ASP	2.2
1	A	32	GLY	2.2
1	A	458	ASP	2.2
1	A	485	ILE	2.2
1	A	433	LYS	2.2
1	B	480	GLU	2.2
1	A	222	THR	2.2
1	B	236	ASP	2.2
1	B	410	LEU	2.2
1	A	13	GLY	2.1
1	A	118	ASN	2.1
1	A	148	MET	2.1
1	B	354	ARG	2.1
1	B	202	LYS	2.1
1	A	229	PRO	2.1
1	B	464	VAL	2.1
1	B	444	LEU	2.1
1	B	451	SER	2.1
1	A	226	ILE	2.0
1	B	238	SER	2.0
1	B	117	TYR	2.0
1	B	226	ILE	2.0

6.2 Non-standard residues in protein, DNA, RNA chains

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

6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	GLC	A	672	12/12	0.88	0.20	71,77,84,84	0
2	GLC	A	671	12/12	0.89	0.17	53,64,76,78	0
2	GLC	B	674	12/12	0.92	0.12	31,50,58,64	0
2	GLC	B	673	12/12	0.94	0.12	30,35,44,44	0

6.5 Other polymers [i](#)

There are no such residues in this entry.