



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 07:05 PM GMT

PDB ID : 1E1E
Title : Crystal structure of a Monocot (Maize ZMGlu1) beta-glucosidase
Authors : Czjzek, M.; Cicek, M.; Bevan, D.R.; Henrissat, B.; Esen, A.
Deposited on : 2000-05-03
Resolution : 2.50 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 (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

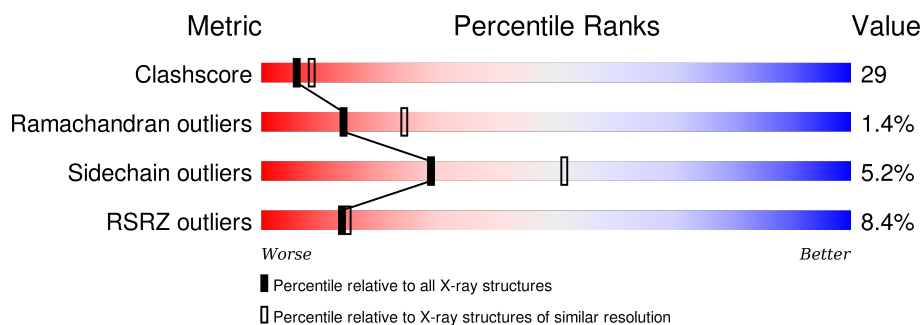
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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))
Clashscore	102246	4242 (2.50-2.50)
Ramachandran outliers	100387	4156 (2.50-2.50)
Sidechain outliers	100360	4158 (2.50-2.50)
RSRZ outliers	91569	3562 (2.50-2.50)

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	512	
1	B	512	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 8302 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 BETA-GLUCOSIDASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	490	Total	C	N	O	S	0	0	0
			3967	2544	656	749	18			
1	B	495	Total	C	N	O	S	0	0	0
			4004	2565	664	757	18			

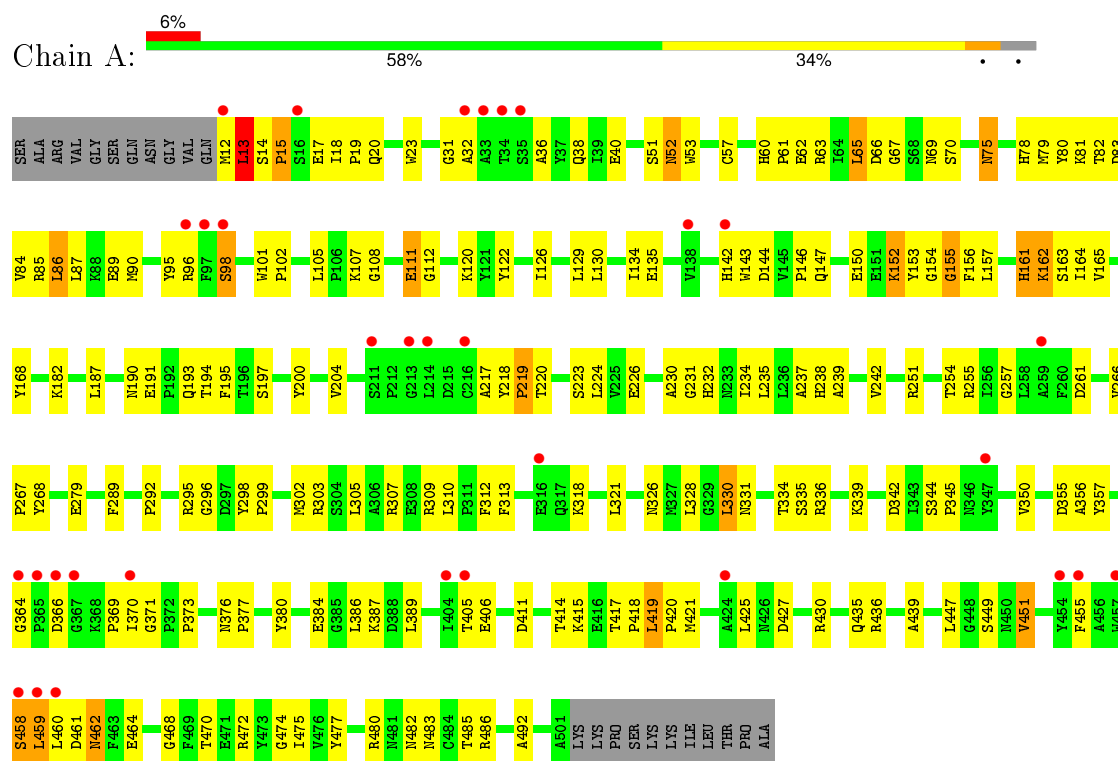
- Molecule 2 is water.

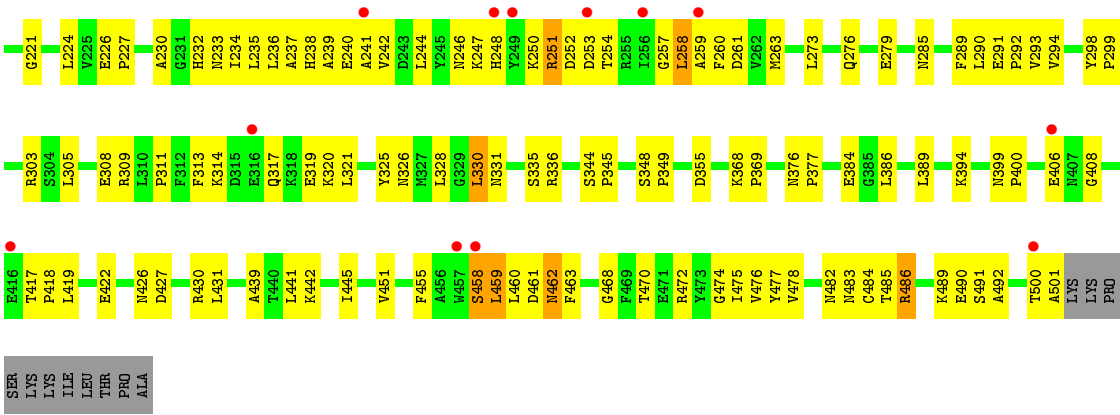
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	215	Total	O	0	0
			215	215		
2	B	116	Total	O	0	0
			116	116		

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: BETA-GLUCOSIDASE





4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	62.88Å 118.34Å 77.10Å 90.00° 90.30° 90.00°	Depositor
Resolution (Å)	27.00 – 2.50 29.17 – 2.30	Depositor EDS
% Data completeness (in resolution range)	98.2 (27.00-2.50) 97.6 (29.17-2.30)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	0.11	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.08 (at 2.31Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.256 , 0.322 0.274 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	DCC
Wilson B-factor (Å ²)	33.7	Xtriage
Anisotropy	0.283	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 47.2	EDS
Estimated twinning fraction	0.029 for h,-k,-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	1 of 50051 reflections (0.002%)	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	8302	wwPDB-VP
Average B, all atoms (Å ²)	49.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.23% 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, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

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	0.45	0/4088	0.63	0/5550
1	B	0.47	0/4125	0.62	0/5600
All	All	0.46	0/8213	0.63	0/11150

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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	3967	0	3759	175	0
1	B	4004	0	3793	273	0
2	A	215	0	0	33	0
2	B	116	0	0	36	0
All	All	8302	0	7552	443	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 29.

All (443) 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:376:ASN:HB2	1:A:377:PRO:HD2	1.46	0.98

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:77:TYR:HA	1:B:121:TYR:CZ	2.00	0.96
1:B:146:PRO:HG2	1:B:149:LEU:HG	1.48	0.94
1:A:461:ASP:HA	2:A:2198:HOH:O	1.67	0.94
1:B:49:GLY:O	1:B:102:PRO:HB2	1.65	0.94
1:B:236:LEU:HD12	2:B:2058:HOH:O	1.69	0.93
1:B:376:ASN:HB2	1:B:377:PRO:HD2	1.55	0.88
1:B:101:TRP:HA	1:B:171:PHE:CZ	2.10	0.86
1:A:436:ARG:CZ	2:A:2187:HOH:O	2.24	0.86
1:B:147:GLN:HE21	1:B:147:GLN:HA	1.40	0.85
1:A:482:ASN:HD22	1:A:483:ASN:H	1.20	0.85
1:B:51:SER:O	2:B:2024:HOH:O	1.95	0.84
1:A:482:ASN:ND2	1:A:483:ASN:H	1.76	0.84
1:B:34:THR:HG21	2:B:2032:HOH:O	1.79	0.83
1:B:77:TYR:HA	1:B:121:TYR:OH	1.79	0.82
1:A:95:TYR:HD2	1:A:129:LEU:HD11	1.45	0.82
1:B:482:ASN:ND2	1:B:483:ASN:H	1.78	0.82
1:B:149:LEU:HB3	1:B:153:TYR:HE1	1.45	0.81
1:B:119:ILE:H	1:B:119:ILE:HD13	1.45	0.81
1:B:110:LYS:HG2	1:B:170:TYR:CZ	2.15	0.81
1:B:460:LEU:HD22	2:B:2108:HOH:O	1.80	0.81
1:A:194:THR:CB	2:A:2110:HOH:O	2.29	0.81
1:A:384:GLU:HB3	2:A:2167:HOH:O	1.80	0.80
1:B:48:LYS:HD2	1:B:103:ARG:HG3	1.62	0.80
1:B:87:LEU:HD21	1:B:459:LEU:HG	1.64	0.80
1:A:87:LEU:HD21	1:A:459:LEU:HG	1.64	0.79
1:A:194:THR:HB	2:A:2110:HOH:O	1.82	0.78
1:A:251:ARG:HB2	1:A:254:THR:HG23	1.65	0.78
1:B:9:GLY:O	2:B:2003:HOH:O	2.02	0.77
1:A:12:MET:C	1:A:13:LEU:HD23	2.05	0.77
1:B:171:PHE:HE2	2:B:2046:HOH:O	1.69	0.75
1:B:119:ILE:HD13	1:B:119:ILE:N	2.02	0.74
1:B:408:GLY:HA3	2:B:2107:HOH:O	1.88	0.74
1:B:177:ASP:HA	2:B:2050:HOH:O	1.87	0.74
1:B:54:ASP:HB2	2:B:2024:HOH:O	1.88	0.74
1:B:482:ASN:HD22	1:B:483:ASN:H	1.34	0.74
1:B:19:PRO:HG3	1:B:439:ALA:HB2	1.68	0.74
1:B:171:PHE:CE2	2:B:2046:HOH:O	2.42	0.73
1:B:49:GLY:C	1:B:102:PRO:HB2	2.08	0.73
1:A:298:TYR:O	2:A:2139:HOH:O	2.06	0.73
1:A:162:LYS:HD3	2:A:2095:HOH:O	1.88	0.73
1:B:232:HIS:CE1	1:B:311:PRO:HB2	2.23	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:15:PRO:HG2	2:A:2001:HOH:O	1.89	0.72
1:B:101:TRP:CG	1:B:146:PRO:HD3	2.25	0.72
1:A:120:LYS:HE3	2:A:2067:HOH:O	1.88	0.72
1:B:173:LYS:HA	1:B:176:PHE:CD2	2.24	0.72
1:B:460:LEU:HB3	2:B:2108:HOH:O	1.88	0.72
1:A:427:ASP:OD2	1:A:430:ARG:HD2	1.90	0.72
1:A:52:ASN:N	1:A:52:ASN:HD22	1.86	0.72
1:A:82:THR:O	1:A:86:LEU:HD22	1.89	0.71
1:B:84:VAL:HG13	1:B:129:LEU:HD23	1.71	0.71
1:A:157:LEU:HD11	1:A:200:TYR:CE1	2.26	0.71
1:B:140:ILE:HG23	2:B:2042:HOH:O	1.90	0.71
1:A:370:ILE:O	2:A:2162:HOH:O	2.09	0.71
1:B:52:ASN:HD22	1:B:52:ASN:N	1.88	0.71
1:B:104:ILE:O	1:B:105:LEU:HD23	1.91	0.71
1:A:239:ALA:HB2	1:A:321:LEU:HD23	1.72	0.70
1:B:232:HIS:CE1	1:B:313:PHE:CE2	2.79	0.70
1:B:101:TRP:HE1	1:B:108:GLY:CA	2.03	0.70
1:B:123:ARG:HG3	1:B:123:ARG:HH21	1.57	0.70
1:A:82:THR:HG22	1:A:85:ARG:NH2	2.06	0.69
1:B:240:GLU:HA	1:B:240:GLU:OE2	1.92	0.69
1:B:279:GLU:HA	1:B:279:GLU:OE1	1.92	0.69
1:B:55:HIS:N	2:B:2024:HOH:O	1.89	0.69
1:B:180:GLY:HA2	1:B:186:TRP:HZ2	1.56	0.69
1:B:244:LEU:HD12	1:B:248:HIS:HD2	1.57	0.69
1:A:107:LYS:HB2	1:A:112:GLY:HA3	1.75	0.69
1:B:149:LEU:HB3	1:B:153:TYR:CE1	2.26	0.68
1:B:147:GLN:NE2	1:B:147:GLN:HA	2.07	0.68
1:A:130:LEU:HD11	1:A:182:LYS:HB3	1.74	0.68
1:A:279:GLU:HA	1:A:279:GLU:OE1	1.93	0.68
1:A:153:TYR:CE2	1:A:163:SER:HB3	2.28	0.68
1:B:52:ASN:H	1:B:52:ASN:HD22	1.42	0.67
1:B:21:ARG:HB3	2:B:2011:HOH:O	1.94	0.67
1:B:114:ILE:CG2	1:B:119:ILE:HD11	2.24	0.67
1:B:88:LYS:HD3	1:B:132:ASN:HB3	1.77	0.67
1:B:101:TRP:HE1	1:B:108:GLY:HA2	1.60	0.67
1:B:442:LYS:HD3	1:B:442:LYS:O	1.95	0.66
1:B:107:LYS:HB2	1:B:112:GLY:HA3	1.77	0.66
1:B:150:GLU:OE2	1:B:155:GLY:HA3	1.95	0.66
1:B:173:LYS:CB	1:B:244:LEU:HD21	2.24	0.66
1:B:209:ARG:HH11	1:B:209:ARG:HG2	1.60	0.66
1:A:156:PHE:O	1:A:230:ALA:HA	1.95	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:14:SER:O	1:A:18:ILE:HG12	1.95	0.65
1:B:80:TYR:O	1:B:84:VAL:HG23	1.96	0.65
1:A:75:ASN:HD21	1:A:78:HIS:HD2	1.44	0.65
1:A:462:ASN:C	1:A:462:ASN:HD22	2.00	0.65
1:B:460:LEU:CB	2:B:2108:HOH:O	2.44	0.65
1:B:163:SER:O	1:B:167:ASP:OD2	2.15	0.64
1:A:303:ARG:HH22	1:A:312:PHE:HA	1.61	0.64
1:B:191:GLU:HG2	1:B:261:ASP:HB3	1.79	0.64
1:B:101:TRP:HA	1:B:171:PHE:CE1	2.32	0.64
1:A:191:GLU:CG	1:A:261:ASP:HB3	2.28	0.64
1:A:191:GLU:HG2	1:A:261:ASP:HB3	1.79	0.64
1:B:461:ASP:OD2	1:B:472:ARG:HB3	1.98	0.64
1:A:464:GLU:OE1	2:A:2201:HOH:O	2.15	0.63
1:B:460:LEU:CD2	2:B:2108:HOH:O	2.40	0.63
1:B:258:LEU:H	1:B:258:LEU:HD23	1.61	0.63
1:A:31:GLY:O	1:A:455:PHE:HA	1.99	0.62
1:A:193:GLN:HA	1:A:289:PHE:HE2	1.64	0.62
1:A:101:TRP:HB3	1:A:102:PRO:HD3	1.81	0.62
1:A:135:GLU:HG3	2:A:2025:HOH:O	2.00	0.61
1:A:312:PHE:CE2	1:B:345:PRO:HD3	2.34	0.61
1:B:289:PHE:C	1:B:292:PRO:HD2	2.21	0.61
1:B:95:TYR:OH	2:B:2032:HOH:O	2.15	0.61
1:A:13:LEU:O	1:A:14:SER:HB2	1.99	0.61
1:A:75:ASN:HB3	1:A:79:MET:CE	2.30	0.60
1:A:217:ALA:C	1:A:219:PRO:HD3	2.21	0.60
1:A:52:ASN:H	1:A:52:ASN:HD22	1.48	0.60
1:A:415:LYS:O	1:A:418:PRO:HD3	2.01	0.60
1:B:123:ARG:HH12	1:B:182:LYS:NZ	1.99	0.60
1:A:231:GLY:HA2	1:A:234:ILE:HD12	1.81	0.60
1:A:312:PHE:CE2	1:B:344:SER:HA	2.36	0.60
1:A:36:ALA:O	1:A:40:GLU:HB2	2.02	0.60
1:A:111:GLU:HG3	2:A:2064:HOH:O	2.00	0.60
1:B:211:SER:HA	1:B:221:GLY:O	2.02	0.60
1:B:52:ASN:N	1:B:145:VAL:O	2.34	0.60
1:B:250:LYS:HD3	1:B:251:ARG:H	1.66	0.59
1:B:22:ASP:N	2:B:2011:HOH:O	2.34	0.59
1:A:373:PRO:HG3	1:A:380:TYR:CE2	2.36	0.59
1:B:52:ASN:ND2	1:B:52:ASN:H	2.01	0.59
1:A:111:GLU:CG	2:A:2064:HOH:O	2.50	0.59
1:B:162:LYS:HA	1:B:165:VAL:HB	1.85	0.59
1:A:482:ASN:ND2	1:A:483:ASN:N	2.48	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:295:ARG:HD2	1:B:273:LEU:HD11	1.84	0.59
1:B:65:LEU:HD23	1:B:470:THR:HG21	1.84	0.59
1:B:179:PHE:C	1:B:181:ASP:H	2.06	0.59
1:B:478:VAL:CG2	2:B:2108:HOH:O	2.50	0.59
1:B:48:LYS:CD	1:B:103:ARG:HG3	2.30	0.58
1:B:174:VAL:O	1:B:177:ASP:HB2	2.03	0.58
1:B:124:ASN:HA	2:B:2038:HOH:O	2.03	0.58
1:B:123:ARG:HG3	1:B:123:ARG:NH2	2.18	0.58
1:B:20:GLN:O	1:B:23:TRP:HB2	2.03	0.57
1:B:459:LEU:HD13	1:B:460:LEU:HG	1.85	0.57
1:A:191:GLU:OE2	1:A:261:ASP:HB3	2.05	0.57
1:B:251:ARG:NH1	2:B:2062:HOH:O	2.37	0.57
1:B:145:VAL:HG13	1:B:146:PRO:HD2	1.86	0.57
1:A:472:ARG:HG2	2:A:2203:HOH:O	2.05	0.57
1:B:141:PHE:HD2	1:B:189:PHE:HD2	1.53	0.57
1:B:458:SER:O	1:B:474:GLY:HA2	2.04	0.56
1:A:60:HIS:NE2	1:A:218:TYR:HE1	2.02	0.56
1:B:173:LYS:HB2	1:B:244:LEU:HD21	1.86	0.56
1:B:251:ARG:HB3	2:B:2064:HOH:O	2.04	0.56
1:B:119:ILE:H	1:B:119:ILE:CD1	2.03	0.56
1:B:101:TRP:HE1	1:B:108:GLY:HA3	1.70	0.56
1:A:482:ASN:ND2	1:A:485:THR:OG1	2.38	0.56
1:B:250:LYS:O	1:B:251:ARG:HG2	2.05	0.56
1:A:168:TYR:CD2	1:A:237:ALA:HB1	2.40	0.56
1:A:449:SER:OG	1:A:451:VAL:HG22	2.05	0.56
1:A:459:LEU:HD13	1:A:460:LEU:HG	1.87	0.56
1:B:258:LEU:N	1:B:258:LEU:HD23	2.20	0.56
1:A:461:ASP:OD2	1:A:472:ARG:HB3	2.06	0.56
1:B:110:LYS:HG2	1:B:170:TYR:CE1	2.40	0.56
1:A:376:ASN:HB2	1:A:377:PRO:CD	2.26	0.56
1:B:51:SER:HB3	2:B:2023:HOH:O	2.05	0.55
1:B:49:GLY:O	1:B:102:PRO:CB	2.47	0.55
1:B:21:ARG:C	1:B:23:TRP:H	2.10	0.55
1:B:25:PRO:HB2	1:B:27:ASP:OD1	2.07	0.55
1:A:52:ASN:ND2	1:A:52:ASN:H	2.05	0.55
1:A:90:MET:HE1	1:A:475:ILE:HD12	1.88	0.55
1:A:52:ASN:ND2	1:A:52:ASN:N	2.55	0.55
1:B:247:LYS:HA	2:B:2060:HOH:O	2.07	0.55
1:B:179:PHE:O	1:B:181:ASP:N	2.40	0.55
1:B:224:LEU:O	1:B:309:ARG:HD2	2.06	0.55
1:B:239:ALA:HB1	1:B:320:LYS:HB3	1.87	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:83:ASP:O	1:A:87:LEU:HG	2.06	0.54
1:A:142:HIS:NE2	1:A:190:ASN:ND2	2.55	0.54
1:B:173:LYS:HE2	1:B:174:VAL:CG2	2.37	0.54
1:B:160:SER:O	1:B:161:HIS:HB2	2.07	0.54
1:B:462:ASN:HD22	1:B:462:ASN:C	2.09	0.54
1:B:209:ARG:HG2	1:B:209:ARG:NH1	2.23	0.54
1:B:290:LEU:O	1:B:294:VAL:HG23	2.08	0.54
1:A:419:LEU:HD23	1:A:420:PRO:HD2	1.89	0.54
1:A:344:SER:HB2	1:A:345:PRO:HD2	1.89	0.54
1:A:130:LEU:CD1	1:A:182:LYS:HB3	2.38	0.54
1:A:60:HIS:HE2	1:A:218:TYR:HE1	1.54	0.54
1:A:86:LEU:HD21	1:A:486:ARG:HD3	1.88	0.54
1:A:421:MET:O	1:A:425:LEU:HG	2.08	0.54
1:B:184:LYS:C	1:B:185:ASN:HD22	2.11	0.54
1:B:19:PRO:CG	1:B:439:ALA:HB2	2.36	0.54
1:B:226:GLU:HB2	1:B:227:PRO:HD3	1.91	0.54
1:B:427:ASP:HB2	1:B:430:ARG:HB3	1.89	0.54
1:A:373:PRO:HG3	1:A:380:TYR:HE2	1.73	0.53
1:B:49:GLY:N	1:B:102:PRO:O	2.40	0.53
1:B:77:TYR:CA	1:B:121:TYR:OH	2.54	0.53
1:B:46:ASP:O	1:B:115:ASN:OD1	2.26	0.53
1:A:312:PHE:CD2	1:B:345:PRO:HD3	2.44	0.53
1:A:191:GLU:OE1	2:A:2107:HOH:O	2.19	0.53
1:B:232:HIS:ND1	1:B:311:PRO:HB2	2.23	0.52
1:B:52:ASN:ND2	1:B:52:ASN:N	2.56	0.52
1:B:459:LEU:HD13	1:B:460:LEU:CD2	2.39	0.52
1:B:426:ASN:HA	1:B:490:GLU:HG2	1.92	0.52
1:A:387:LYS:HD2	1:A:447:LEU:HD12	1.91	0.52
1:A:14:SER:HB3	1:A:17:GLU:HB2	1.91	0.52
1:A:414:THR:HG22	1:A:470:THR:HB	1.91	0.52
1:B:75:ASN:HD21	1:B:78:HIS:CD2	2.28	0.52
1:B:122:TYR:O	1:B:126:ILE:HG13	2.10	0.52
1:B:196:THR:HG22	1:B:230:ALA:HB3	1.90	0.52
1:B:97:PHE:CZ	1:B:138:VAL:HG22	2.44	0.52
1:A:330:LEU:HG	1:A:389:LEU:HD21	1.91	0.52
1:A:135:GLU:CG	2:A:2025:HOH:O	2.56	0.52
1:B:172:ALA:O	1:B:175:CYS:HB2	2.10	0.52
1:B:123:ARG:HH12	1:B:182:LYS:HZ2	1.58	0.52
1:B:478:VAL:HG23	2:B:2108:HOH:O	2.11	0.51
1:A:200:TYR:HB3	1:A:226:GLU:HB3	1.93	0.51
1:B:141:PHE:HD2	1:B:189:PHE:CD2	2.28	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:303:ARG:HG2	1:B:303:ARG:HH11	1.74	0.51
1:A:326:ASN:HA	2:A:2151:HOH:O	2.09	0.51
1:A:147:GLN:NE2	1:A:150:GLU:HB3	2.24	0.51
1:A:477:TYR:O	1:A:486:ARG:HA	2.11	0.51
1:B:427:ASP:OD1	1:B:427:ASP:N	2.42	0.51
1:B:60:HIS:HA	1:B:62:GLU:OE1	2.11	0.51
1:A:218:TYR:O	1:A:220:THR:N	2.36	0.51
1:B:24:PHE:N	1:B:24:PHE:CD1	2.78	0.51
1:A:342:ASP:HB3	2:A:2155:HOH:O	2.10	0.51
1:B:173:LYS:HA	1:B:176:PHE:HD2	1.72	0.51
1:B:101:TRP:HB3	1:B:102:PRO:HD3	1.93	0.51
1:B:119:ILE:O	1:B:123:ARG:HB2	2.10	0.51
1:B:173:LYS:HE2	1:B:174:VAL:HG23	1.93	0.51
1:A:194:THR:O	1:A:195:PHE:C	2.48	0.51
1:A:235:LEU:HD21	1:A:289:PHE:HD1	1.76	0.51
1:B:252:ASP:N	2:B:2064:HOH:O	2.38	0.51
1:B:303:ARG:NH1	1:B:303:ARG:HG2	2.24	0.51
1:B:431:LEU:HD13	1:B:491:SER:HA	1.92	0.51
1:B:173:LYS:HG3	1:B:174:VAL:N	2.26	0.50
1:A:371:GLY:HA2	2:A:2079:HOH:O	2.09	0.50
1:B:146:PRO:O	1:B:148:ALA:N	2.45	0.50
1:A:251:ARG:HB2	1:A:254:THR:CG2	2.39	0.50
1:A:51:SER:HB3	1:A:102:PRO:HG2	1.93	0.50
1:A:61:PRO:O	1:A:67:GLY:HA2	2.11	0.50
1:B:100:SER:HB2	2:B:2018:HOH:O	2.11	0.50
1:B:31:GLY:HA2	1:B:92:MET:SD	2.51	0.50
1:A:164:ILE:HG23	1:A:165:VAL:N	2.26	0.50
1:B:235:LEU:O	1:B:321:LEU:HD21	2.12	0.50
1:B:105:LEU:C	1:B:107:LYS:H	2.14	0.50
1:A:303:ARG:HH11	1:A:303:ARG:HG2	1.77	0.50
1:B:251:ARG:HH11	1:B:251:ARG:HG3	1.75	0.50
1:B:263:MET:HE1	2:B:2065:HOH:O	2.11	0.50
1:A:364:GLY:HA3	2:A:2160:HOH:O	2.12	0.50
1:B:246:ASN:HA	1:B:250:LYS:HG2	1.94	0.50
1:B:251:ARG:HB2	1:B:254:THR:HG23	1.93	0.50
1:A:89:GLU:HB3	2:A:2211:HOH:O	2.11	0.50
1:B:48:LYS:CG	1:B:103:ARG:HG3	2.42	0.49
1:B:35:SER:HB3	1:B:38:GLN:OE1	2.11	0.49
1:B:291:GLU:OE2	1:B:299:PRO:HA	2.12	0.49
1:B:293:VAL:O	1:B:325:TYR:HE2	1.95	0.49
1:B:241:ALA:O	1:B:244:LEU:HB3	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:417:THR:O	1:A:417:THR:HG22	2.13	0.49
1:B:305:LEU:HD13	1:B:355:ASP:O	2.12	0.49
1:B:107:LYS:CB	1:B:112:GLY:HA3	2.43	0.49
1:B:20:GLN:HB2	1:B:23:TRP:CD1	2.48	0.49
1:A:152:LYS:HD2	1:A:153:TYR:CD2	2.47	0.49
1:A:57:CYS:HB3	1:A:69:ASN:HB3	1.94	0.48
1:B:232:HIS:CE1	1:B:313:PHE:HE2	2.31	0.48
1:A:60:HIS:HB3	1:A:62:GLU:OE2	2.13	0.48
1:B:195:PHE:O	1:B:199:SER:HB2	2.13	0.48
1:B:54:ASP:CB	2:B:2024:HOH:O	2.56	0.48
1:B:173:LYS:HB3	1:B:244:LEU:HD21	1.95	0.48
1:B:184:LYS:C	1:B:185:ASN:ND2	2.66	0.48
1:B:187:LEU:HA	1:B:257:GLY:O	2.13	0.48
1:B:149:LEU:HD23	1:B:149:LEU:N	2.27	0.48
1:B:482:ASN:ND2	1:B:485:THR:OG1	2.46	0.48
1:B:191:GLU:CG	1:B:261:ASP:HB3	2.43	0.48
1:A:480:ARG:NH1	2:A:2207:HOH:O	2.47	0.48
1:B:54:ASP:N	2:B:2024:HOH:O	2.45	0.48
1:A:289:PHE:C	1:A:292:PRO:HD2	2.33	0.48
1:B:477:TYR:O	1:B:486:ARG:HA	2.12	0.48
1:A:20:GLN:O	1:A:23:TRP:HB2	2.13	0.48
1:B:107:LYS:O	1:B:149:LEU:HD21	2.14	0.48
1:B:482:ASN:ND2	1:B:483:ASN:N	2.55	0.48
1:B:83:ASP:OD1	1:B:460:LEU:HD11	2.13	0.48
1:B:101:TRP:CD2	1:B:146:PRO:HD3	2.47	0.48
1:B:101:TRP:HB3	1:B:102:PRO:CD	2.43	0.48
1:B:190:ASN:HA	1:B:259:ALA:HB3	1.94	0.48
1:B:173:LYS:HG3	1:B:174:VAL:H	1.78	0.48
1:B:66:ASP:OD1	1:B:468:GLY:HA3	2.14	0.48
1:A:411:ASP:HA	2:A:2178:HOH:O	2.13	0.48
1:A:60:HIS:NE2	1:A:218:TYR:CE1	2.81	0.47
1:B:142:HIS:NE2	1:B:190:ASN:ND2	2.62	0.47
1:B:77:TYR:O	1:B:121:TYR:CE1	2.68	0.47
1:A:193:GLN:HA	1:A:289:PHE:CE2	2.48	0.47
1:A:82:THR:HG22	1:A:85:ARG:HH22	1.77	0.47
1:A:38:GLN:O	1:A:462:ASN:HB2	2.14	0.47
1:B:368:LYS:HB3	1:B:369:PRO:HD2	1.97	0.47
1:B:258:LEU:N	1:B:258:LEU:CD2	2.78	0.47
1:B:399:ASN:N	1:B:400:PRO:CD	2.78	0.47
1:B:168:TYR:C	1:B:170:TYR:N	2.68	0.47
1:A:52:ASN:HD22	1:A:53:TRP:H	1.63	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:96:ARG:NH1	1:A:405:THR:HB	2.30	0.47
1:A:356:ALA:O	1:A:357:TYR:C	2.53	0.47
1:B:114:ILE:HG22	1:B:119:ILE:HD11	1.97	0.47
1:B:153:TYR:CD2	1:B:163:SER:HB3	2.49	0.47
1:B:105:LEU:HD11	1:B:171:PHE:HA	1.96	0.47
1:B:230:ALA:O	1:B:234:ILE:HG13	2.14	0.47
1:A:312:PHE:HE2	1:B:344:SER:HA	1.79	0.47
1:A:339:LYS:HE3	2:A:2153:HOH:O	2.15	0.47
1:B:105:LEU:HD12	1:B:108:GLY:HA2	1.97	0.46
1:A:266:VAL:HG13	1:A:267:PRO:HD2	1.97	0.46
1:B:54:ASP:CA	2:B:2024:HOH:O	2.64	0.46
1:A:80:TYR:O	1:A:84:VAL:HG23	2.15	0.46
1:B:149:LEU:CB	1:B:153:TYR:HE1	2.23	0.46
1:B:49:GLY:HA3	1:B:106:PRO:HA	1.98	0.46
1:A:191:GLU:HB3	2:A:2110:HOH:O	2.15	0.46
1:B:34:THR:CG2	2:B:2032:HOH:O	2.52	0.46
1:B:38:GLN:O	1:B:462:ASN:HB2	2.16	0.46
1:B:52:ASN:HD22	1:B:53:TRP:H	1.64	0.46
1:B:146:PRO:C	1:B:148:ALA:N	2.66	0.46
1:A:142:HIS:O	1:A:143:TRP:HB2	2.16	0.46
1:B:165:VAL:HG13	1:B:237:ALA:HA	1.98	0.45
1:A:95:TYR:CD2	1:A:129:LEU:HD11	2.37	0.45
1:A:486:ARG:HG3	1:A:486:ARG:HH11	1.79	0.45
1:B:115:ASN:O	1:B:119:ILE:HD11	2.16	0.45
1:B:298:TYR:HB3	1:B:299:PRO:HD2	1.99	0.45
1:A:105:LEU:O	1:A:108:GLY:N	2.45	0.45
1:B:317:GLN:C	1:B:319:GLU:H	2.19	0.45
1:B:417:THR:N	1:B:418:PRO:HD3	2.32	0.45
1:B:106:PRO:O	1:B:107:LYS:HD3	2.16	0.45
1:B:194:THR:O	1:B:198:PHE:HB2	2.17	0.45
1:A:66:ASP:OD1	1:A:468:GLY:HA3	2.15	0.45
1:A:144:ASP:OD2	1:A:144:ASP:N	2.48	0.45
1:A:436:ARG:NE	2:A:2187:HOH:O	2.44	0.45
1:B:442:LYS:HD3	1:B:442:LYS:C	2.36	0.45
1:A:96:ARG:HH12	1:A:406:GLU:HG3	1.81	0.45
1:A:98:SER:HB3	2:A:2081:HOH:O	2.17	0.45
1:B:335:SER:O	1:B:336:ARG:HG2	2.17	0.45
1:B:251:ARG:HB2	1:B:254:THR:CG2	2.47	0.45
1:A:18:ILE:HD12	1:A:435:GLN:NE2	2.32	0.45
1:A:475:ILE:O	1:A:492:ALA:HB2	2.17	0.45
1:B:459:LEU:CD1	1:B:460:LEU:HG	2.46	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:172:ALA:O	1:B:175:CYS:N	2.46	0.44
1:A:268:TYR:CD2	1:A:339:LYS:HD2	2.52	0.44
1:B:168:TYR:O	1:B:170:TYR:N	2.50	0.44
1:B:118:GLY:C	1:B:120:LYS:H	2.20	0.44
1:A:255:ARG:HD3	2:A:2129:HOH:O	2.16	0.44
1:B:156:PHE:O	1:B:233:ASN:ND2	2.41	0.44
1:B:289:PHE:O	1:B:292:PRO:HD2	2.18	0.44
1:B:161:HIS:O	1:B:165:VAL:HG21	2.17	0.44
1:B:105:LEU:HD23	1:B:114:ILE:HG12	2.00	0.44
1:B:115:ASN:O	1:B:119:ILE:CD1	2.66	0.44
1:B:123:ARG:NH2	1:B:127:ASN:HD21	2.15	0.44
1:A:459:LEU:O	1:A:459:LEU:HD22	2.18	0.44
1:A:239:ALA:HB2	1:A:321:LEU:CD2	2.45	0.44
1:A:303:ARG:NH2	1:A:312:PHE:HA	2.28	0.44
1:A:194:THR:O	1:A:197:SER:N	2.51	0.44
1:A:299:PRO:HD2	1:A:302:MET:SD	2.58	0.44
1:B:384:GLU:OE2	2:B:2094:HOH:O	2.21	0.44
1:A:200:TYR:O	1:A:223:SER:HA	2.18	0.44
1:B:114:ILE:CG2	1:B:119:ILE:CD1	2.94	0.43
1:B:147:GLN:CA	1:B:147:GLN:NE2	2.74	0.43
1:A:472:ARG:HA	2:A:2203:HOH:O	2.18	0.43
1:A:60:HIS:C	1:A:62:GLU:H	2.21	0.43
1:A:369:PRO:C	1:A:371:GLY:H	2.21	0.43
1:B:200:TYR:HA	1:B:209:ARG:O	2.19	0.43
1:A:19:PRO:HA	1:A:23:TRP:CZ3	2.53	0.43
1:B:394:LYS:HA	1:B:399:ASN:HA	2.01	0.43
1:A:101:TRP:N	1:A:102:PRO:CD	2.81	0.43
1:B:308:GLU:HG2	1:B:309:ARG:N	2.32	0.43
1:A:65:LEU:HD23	1:A:470:THR:HG21	1.99	0.43
1:A:19:PRO:HG3	1:A:439:ALA:HB2	2.00	0.43
1:A:309:ARG:CB	1:A:309:ARG:HH11	2.32	0.43
1:B:331:ASN:CG	1:B:406:GLU:HB2	2.39	0.43
1:B:158:ASP:HB3	1:B:164:ILE:HG22	2.01	0.43
1:B:169:THR:O	1:B:173:LYS:HB3	2.17	0.43
1:B:459:LEU:HD22	1:B:459:LEU:O	2.19	0.43
1:A:161:HIS:O	1:A:162:LYS:HB2	2.18	0.43
1:B:31:GLY:O	1:B:455:PHE:HA	2.19	0.43
1:A:331:ASN:CG	1:A:406:GLU:HB2	2.39	0.43
1:B:215:ASP:CG	1:B:215:ASP:O	2.56	0.43
1:A:232:HIS:CE1	1:A:313:PHE:CE2	3.06	0.43
1:B:276:GLN:NE2	2:B:2071:HOH:O	2.45	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:348:SER:HA	1:B:349:PRO:HD3	1.84	0.43
1:B:123:ARG:HH22	1:B:127:ASN:HD21	1.66	0.43
1:B:149:LEU:HD22	1:B:153:TYR:OH	2.19	0.43
1:A:63:ARG:HH21	1:A:217:ALA:HA	1.83	0.43
1:B:335:SER:O	1:B:336:ARG:NH1	2.52	0.43
1:A:20:GLN:HB2	1:A:23:TRP:CD1	2.54	0.42
1:B:55:HIS:ND1	1:B:147:GLN:OE1	2.52	0.42
1:B:74:ALA:O	1:B:75:ASN:C	2.57	0.42
1:B:330:LEU:HG	1:B:389:LEU:HD21	1.99	0.42
1:A:122:TYR:O	1:A:126:ILE:HD12	2.19	0.42
1:B:260:PHE:CZ	1:B:290:LEU:HA	2.55	0.42
1:B:164:ILE:HA	1:B:167:ASP:OD2	2.19	0.42
1:A:376:ASN:CB	1:A:377:PRO:HD2	2.28	0.42
1:B:38:GLN:HG2	1:B:463:PHE:O	2.20	0.42
1:B:142:HIS:CE1	1:B:190:ASN:ND2	2.87	0.42
1:A:305:LEU:HD13	1:A:355:ASP:O	2.19	0.42
1:A:32:ALA:CB	1:A:459:LEU:HB2	2.50	0.42
1:B:251:ARG:NH2	1:B:253:ASP:OD1	2.52	0.42
1:B:51:SER:HB3	1:B:102:PRO:HG3	2.02	0.42
1:B:52:ASN:ND2	1:B:145:VAL:H	2.17	0.42
1:B:19:PRO:HA	1:B:23:TRP:CZ3	2.55	0.42
1:A:155:GLY:N	2:A:2086:HOH:O	2.52	0.42
1:B:376:ASN:CB	1:B:377:PRO:HD2	2.36	0.42
1:A:298:TYR:CD2	1:A:310:LEU:HD21	2.54	0.42
1:B:61:PRO:O	1:B:67:GLY:HA2	2.19	0.42
1:A:101:TRP:CD1	1:A:146:PRO:HG2	2.55	0.42
1:B:173:LYS:CG	1:B:174:VAL:N	2.82	0.42
1:A:462:ASN:C	1:A:462:ASN:ND2	2.72	0.42
1:B:200:TYR:C	1:B:227:PRO:HG3	2.41	0.41
1:B:217:ALA:C	1:B:218:TYR:HD1	2.23	0.41
1:B:238:HIS:O	1:B:242:VAL:HG23	2.20	0.41
1:B:14:SER:HB2	1:B:17:GLU:HG3	2.02	0.41
1:A:63:ARG:NH1	2:A:2038:HOH:O	2.53	0.41
1:B:263:MET:CE	2:B:2065:HOH:O	2.66	0.41
1:B:486:ARG:H	1:B:486:ARG:HG2	1.55	0.41
1:A:96:ARG:NH1	1:A:406:GLU:HG3	2.35	0.41
1:B:314:LYS:HG3	1:B:317:GLN:OE1	2.20	0.41
1:B:76:SER:O	1:B:121:TYR:OH	2.34	0.41
1:B:60:HIS:NE2	1:B:218:TYR:HE1	2.18	0.41
1:B:103:ARG:O	1:B:104:ILE:HD13	2.20	0.41
1:B:179:PHE:C	1:B:181:ASP:N	2.72	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:80:TYR:HD1	1:B:80:TYR:H	1.67	0.41
1:A:335:SER:O	1:A:336:ARG:NH1	2.53	0.41
1:A:187:LEU:HA	1:A:257:GLY:O	2.21	0.41
1:A:193:GLN:HB3	1:A:261:ASP:OD2	2.21	0.41
1:A:154:GLY:O	1:A:155:GLY:C	2.59	0.41
1:B:123:ARG:HD2	1:B:123:ARG:HA	1.91	0.41
1:B:483:ASN:O	1:B:484:CYS:HB2	2.21	0.41
1:B:170:TYR:HD1	1:B:173:LYS:HZ3	1.64	0.41
1:A:217:ALA:O	1:A:219:PRO:HD3	2.20	0.41
1:A:334:THR:OG1	1:A:335:SER:N	2.54	0.41
1:A:335:SER:O	1:A:336:ARG:HG2	2.21	0.41
1:A:296:GLY:O	1:A:318:LYS:HG2	2.21	0.41
1:A:458:SER:O	1:A:474:GLY:HA2	2.21	0.41
1:A:129:LEU:HD23	1:A:134:ILE:HD12	2.03	0.41
1:B:263:MET:HE2	2:B:2028:HOH:O	2.21	0.41
1:B:214:LEU:HD23	1:B:214:LEU:HA	1.82	0.41
1:A:224:LEU:HD13	1:A:350:VAL:O	2.21	0.41
1:B:459:LEU:O	1:B:476:VAL:HB	2.22	0.40
1:B:165:VAL:O	1:B:165:VAL:HG12	2.21	0.40
1:A:238:HIS:CE1	1:A:242:VAL:HG21	2.55	0.40
1:B:500:THR:O	1:B:501:ALA:C	2.58	0.40
1:B:475:ILE:O	1:B:492:ALA:HB2	2.22	0.40
1:B:153:TYR:N	1:B:153:TYR:CD1	2.69	0.40
1:B:474:GLY:O	1:B:489:LYS:HD2	2.22	0.40
1:B:246:ASN:HA	1:B:250:LYS:CG	2.51	0.40
1:A:187:LEU:HA	1:A:187:LEU:HD23	1.95	0.40
1:B:458:SER:C	1:B:460:LEU:N	2.74	0.40
1:A:32:ALA:HB1	1:A:459:LEU:HB2	2.03	0.40
1:A:152:LYS:HD2	1:A:153:TYR:HD2	1.87	0.40
1:B:193:GLN:HA	1:B:289:PHE:HE2	1.85	0.40
1:B:441:LEU:O	1:B:445:ILE:HG13	2.22	0.40
1:A:81:LYS:HB2	2:A:2049:HOH:O	2.22	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	488/512 (95%)	430 (88%)	50 (10%)	8 (2%)	12	21
1	B	493/512 (96%)	425 (86%)	62 (13%)	6 (1%)	16	29
All	All	981/1024 (96%)	855 (87%)	112 (11%)	14 (1%)	14	24

All (14) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	155	GLY
1	A	162	LYS
1	A	307	ARG
1	B	180	GLY
1	A	15	PRO
1	B	75	ASN
1	B	147	GLN
1	A	13	LEU
1	A	161	HIS
1	A	219	PRO
1	A	65	LEU
1	B	68	SER
1	B	104	ILE
1	B	106	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	423/441 (96%)	405 (96%)	18 (4%)	35	61
1	B	427/441 (97%)	401 (94%)	26 (6%)	23	42
All	All	850/882 (96%)	806 (95%)	44 (5%)	29	51

All (44) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	13	LEU
1	A	52	ASN
1	A	70	SER
1	A	75	ASN
1	A	86	LEU
1	A	98	SER
1	A	111	GLU
1	A	152	LYS
1	A	204	VAL
1	A	328	LEU
1	A	330	LEU
1	A	366	ASP
1	A	386	LEU
1	A	419	LEU
1	A	451	VAL
1	A	458	SER
1	A	459	LEU
1	A	462	ASN
1	B	52	ASN
1	B	75	ASN
1	B	86	LEU
1	B	109	THR
1	B	119	ILE
1	B	144	ASP
1	B	153	TYR
1	B	156	PHE
1	B	162	LYS
1	B	167	ASP
1	B	173	LYS
1	B	181	ASP
1	B	251	ARG
1	B	258	LEU
1	B	285	ASN
1	B	326	ASN
1	B	328	LEU
1	B	330	LEU
1	B	386	LEU
1	B	419	LEU
1	B	422	GLU
1	B	451	VAL
1	B	458	SER
1	B	459	LEU
1	B	462	ASN

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Mol	Chain	Res	Type
1	B	486	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (29) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	52	ASN
1	A	75	ASN
1	A	124	ASN
1	A	132	ASN
1	A	246	ASN
1	A	276	GLN
1	A	435	GLN
1	A	450	ASN
1	A	452	GLN
1	A	462	ASN
1	A	481	ASN
1	A	482	ASN
1	A	499	ASN
1	B	52	ASN
1	B	75	ASN
1	B	78	HIS
1	B	115	ASN
1	B	127	ASN
1	B	190	ASN
1	B	193	GLN
1	B	232	HIS
1	B	248	HIS
1	B	276	GLN
1	B	450	ASN
1	B	452	GLN
1	B	462	ASN
1	B	481	ASN
1	B	482	ASN
1	B	499	ASN

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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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	490/512 (95%)	0.36	32 (6%)	22 25	7, 45, 75, 94	1 (0%)
1	B	495/512 (96%)	0.61	51 (10%)	9 9	8, 52, 86, 99	1 (0%)
All	All	985/1024 (96%)	0.49	83 (8%)	14 14	7, 48, 83, 99	2 (0%)

All (83) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	458	SER	8.1
1	B	141	PHE	4.5
1	B	458	SER	4.5
1	A	457	TRP	3.9
1	A	459	LEU	3.9
1	B	148	ALA	3.7
1	B	153	TYR	3.7
1	A	97	PHE	3.6
1	A	213	GLY	3.6
1	B	316	GLU	3.6
1	B	98	SER	3.6
1	B	35	SER	3.4
1	B	99	ILE	3.4
1	B	113	GLY	3.3
1	B	142	HIS	3.2
1	B	109	THR	3.2
1	A	35	SER	3.1
1	A	211	SER	3.0
1	B	112	GLY	3.0
1	B	49	GLY	3.0
1	B	164	ILE	3.0
1	A	32	ALA	3.0
1	A	34	THR	2.9
1	B	47	GLY	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	33	ALA	2.8
1	A	214	LEU	2.7
1	A	370	ILE	2.7
1	B	500	THR	2.7
1	B	59	ASN	2.7
1	B	140	ILE	2.6
1	A	366	ASP	2.6
1	B	406	GLU	2.6
1	A	364	GLY	2.6
1	A	12	MET	2.6
1	A	367	GLY	2.6
1	B	144	ASP	2.6
1	B	111	GLU	2.6
1	B	60	HIS	2.6
1	B	416	GLU	2.5
1	B	241	ALA	2.5
1	A	142	HIS	2.5
1	B	139	THR	2.5
1	A	16	SER	2.5
1	B	259	ALA	2.5
1	B	182	LYS	2.4
1	B	189	PHE	2.4
1	A	316	GLU	2.4
1	B	190	ASN	2.4
1	B	216	CYS	2.4
1	A	405	THR	2.4
1	B	175	CYS	2.4
1	B	168	TYR	2.4
1	B	132	ASN	2.4
1	B	171	PHE	2.4
1	A	216	CYS	2.3
1	B	256	ILE	2.3
1	A	424	ALA	2.3
1	B	61	PRO	2.3
1	B	108	GLY	2.3
1	B	48	LYS	2.3
1	A	138	VAL	2.3
1	A	365	PRO	2.3
1	B	143	TRP	2.3
1	B	248	HIS	2.2
1	B	253	ASP	2.2
1	B	457	TRP	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	455	PHE	2.2
1	B	188	THR	2.2
1	B	131	GLU	2.1
1	B	97	PHE	2.1
1	B	187	LEU	2.1
1	A	259	ALA	2.1
1	B	100	SER	2.1
1	A	347	TYR	2.1
1	B	249	TYR	2.1
1	A	404	ILE	2.1
1	A	454	TYR	2.1
1	A	460	LEU	2.0
1	A	96	ARG	2.0
1	B	32	ALA	2.0
1	B	101	TRP	2.0
1	A	98	SER	2.0
1	B	147	GLN	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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.