



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 12:16 PM UTC

PDB ID : 3U5U / pdb_00003u5u
Title : Structures of Alkaloid Biosynthetic Glucosidases Decode Substrate Specificity
Authors : Xia, L.; Ruppert, M.; Wang, M.; Panjikar, S.; Lin, H.; Rajendran, C.; Barleben, L.; Stoeckigt, J.
Deposited on : 2011-10-11
Resolution : 2.20 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	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

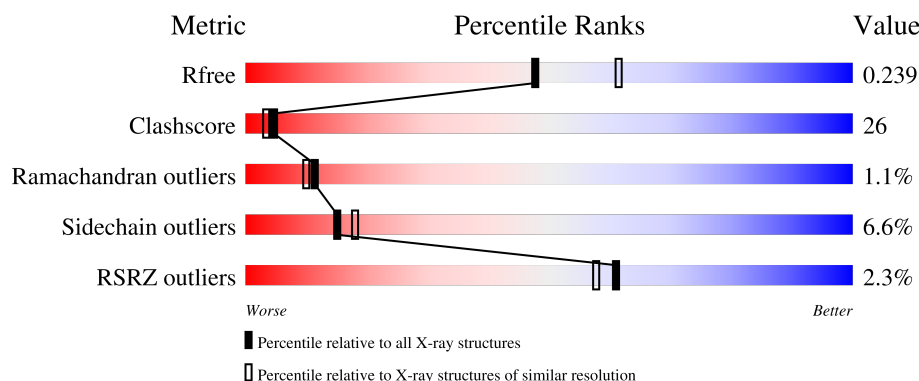
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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}	180053	6164 (2.20-2.20)
Clashscore	190562	6851 (2.20-2.20)
Ramachandran outliers	187476	6768 (2.20-2.20)
Sidechain outliers	187428	6769 (2.20-2.20)
RSRZ outliers	180081	6166 (2.20-2.20)

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	513	
1	B	513	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 7696 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 Raucaffricine-O-beta-D-glucosidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	470	Total	C	N	O	S	0	0	0
			3772	2413	643	703	13			
1	B	470	Total	C	N	O	S	0	0	0
			3772	2413	643	703	13			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	186	GLN	GLU	engineered mutation	UNP Q9SPP9
B	186	GLN	GLU	engineered mutation	UNP Q9SPP9

- Molecule 2 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	2	Total	Cl	0	0
			2	2		

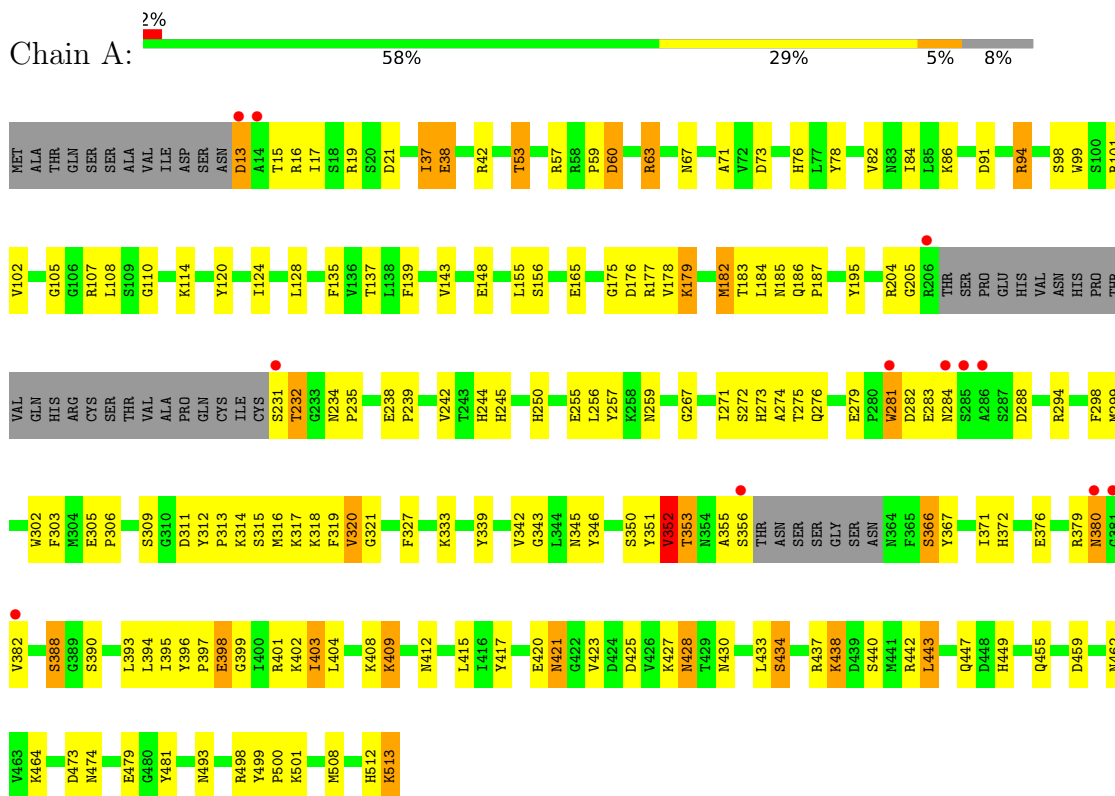
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	77	Total	O	0	0
			77	77		
3	B	73	Total	O	0	0
			73	73		

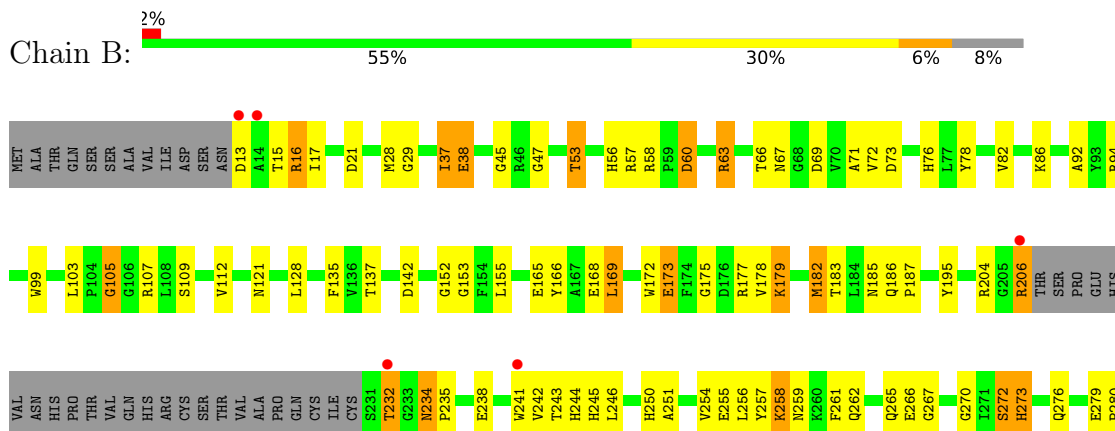
3 Residue-property plots

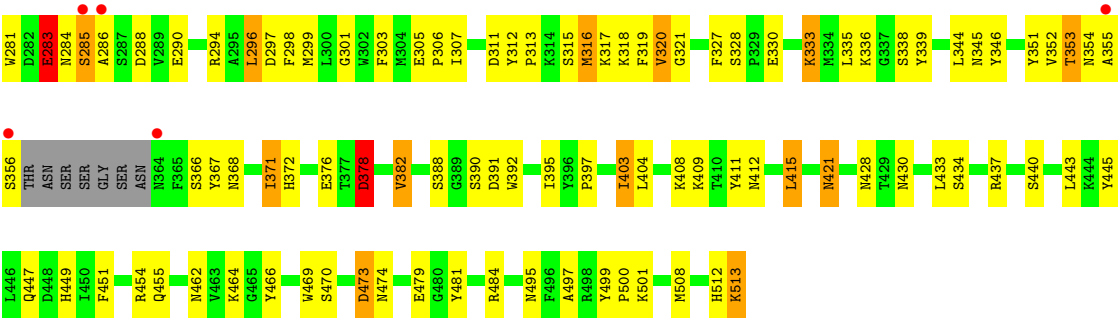
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: Raucaffricine-O-beta-D-glucosidase



• Molecule 1: Raucaffricine-O-beta-D-glucosidase





4 Data and refinement statistics

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α , β , γ	105.56Å 129.52Å 216.64Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	94.89 – 2.20 94.89 – 2.20	Depositor EDS
% Data completeness (in resolution range)	100.0 (94.89-2.20) 99.5 (94.89-2.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.11 (at 2.20Å)	Xtriage
Refinement program	REFMAC 5.5.0066	Depositor
R, R_{free}	0.220 , 0.267 (Not available) , 0.239	Depositor DCC
R_{free} test set	3758 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	35.8	Xtriage
Anisotropy	0.644	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 52.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	7696	wwPDB-VP
Average B, all atoms (Å ²)	39.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.44% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 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	1.05	2/3883 (0.1%)	1.14	16/5270 (0.3%)
1	B	1.02	2/3883 (0.1%)	1.16	25/5270 (0.5%)
All	All	1.03	4/7766 (0.1%)	1.15	41/10540 (0.4%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	112	VAL	CA-CB	-6.12	1.47	1.54
1	B	497	ALA	CA-C	-5.91	1.45	1.52
1	A	271	ILE	CA-CB	5.33	1.61	1.55
1	A	143	VAL	CA-CB	5.03	1.62	1.53

All (41) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	156	SER	CA-C-N	-10.52	108.78	120.45
1	A	156	SER	C-N-CA	-10.52	108.78	120.45
1	B	37	ILE	N-CA-C	9.07	119.25	111.90
1	B	105	GLY	N-CA-C	-7.11	103.43	115.80
1	A	37	ILE	N-CA-C	6.87	117.47	111.90
1	B	473	ASP	N-CA-C	-6.86	100.83	110.50
1	B	103	LEU	CA-C-N	-6.63	112.98	119.87
1	B	103	LEU	C-N-CA	-6.63	112.98	119.87
1	A	474	ASN	N-CA-C	6.62	117.32	108.38
1	A	320	VAL	N-CA-C	-6.61	106.35	112.96
1	B	58	ARG	CA-C-N	6.43	126.19	119.05
1	B	58	ARG	C-N-CA	6.43	126.19	119.05
1	B	72	VAL	N-CA-C	6.38	117.59	111.91
1	B	234	ASN	CA-C-N	6.22	125.90	119.56
1	B	234	ASN	C-N-CA	6.22	125.90	119.56

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	378	ASP	N-CA-C	5.92	118.86	109.50
1	B	474	ASN	N-CA-C	5.92	116.05	108.24
1	A	473	ASP	N-CA-C	-5.84	102.41	110.35
1	A	234	ASN	CA-C-N	5.83	125.51	119.56
1	A	234	ASN	C-N-CA	5.83	125.51	119.56
1	A	501	LYS	N-CA-C	-5.79	101.62	110.14
1	A	388	SER	N-CA-C	-5.69	101.22	109.31
1	B	47	GLY	CA-C-N	5.62	125.55	119.76
1	B	47	GLY	C-N-CA	5.62	125.55	119.76
1	B	501	LYS	N-CA-C	-5.53	102.28	110.46
1	A	352	VAL	N-CA-C	5.48	115.78	108.11
1	B	38	GLU	N-CA-C	5.45	116.90	111.07
1	B	173	GLU	N-CA-C	5.44	117.21	111.28
1	B	273	HIS	N-CA-C	5.39	118.02	109.24
1	B	495	ASN	CB-CA-C	-5.37	103.96	111.80
1	A	38	GLU	N-CA-C	5.35	117.55	111.02
1	B	388	SER	N-CA-C	-5.33	99.44	110.80
1	B	37	ILE	CB-CA-C	-5.30	106.21	111.30
1	B	272	SER	N-CA-C	5.28	117.00	108.34
1	B	382	VAL	N-CA-C	5.21	113.60	107.77
1	A	102	VAL	N-CA-C	5.21	115.98	110.72
1	A	342	VAL	CA-C-N	-5.20	117.76	122.80
1	A	342	VAL	C-N-CA	-5.20	117.76	122.80
1	B	45	GLY	N-CA-C	5.18	122.76	115.30
1	B	172	TRP	N-CA-C	-5.16	105.11	111.40
1	A	139	PHE	N-CA-C	5.09	116.70	108.26

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	3772	0	3577	183	0
1	B	3772	0	3577	200	0
2	B	2	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	77	0	0	8	0
3	B	73	0	0	7	0
All	All	7696	0	7154	379	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 26.

All (379) 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:169:LEU:C	1:B:169:LEU:HD12	1.51	1.29
1:B:169:LEU:HD12	1:B:169:LEU:O	1.38	1.23
1:B:53:THR:HG22	1:B:57:ARG:HD2	1.21	1.20
1:A:313:PRO:HD2	1:A:316:MET:HE3	1.16	1.16
1:B:206:ARG:HH11	1:B:206:ARG:CG	1.60	1.12
1:A:313:PRO:CD	1:A:316:MET:HE3	1.81	1.10
1:A:283:GLU:OE2	1:A:379:ARG:NH2	1.86	1.08
1:B:313:PRO:HD2	1:B:316:MET:HE3	1.31	1.08
1:B:443:LEU:HD11	1:B:447:GLN:HE21	1.21	1.06
1:A:182:MET:CE	3:A:586:HOH:O	2.02	1.05
1:B:313:PRO:CD	1:B:316:MET:HE3	1.85	1.05
1:B:206:ARG:HG3	1:B:206:ARG:NH1	1.51	1.04
1:B:155:LEU:O	1:B:245:HIS:CE1	2.11	1.04
1:B:319:PHE:CD1	1:B:372:HIS:HD2	1.76	1.03
1:B:16:ARG:HG2	1:B:16:ARG:HH11	0.88	1.02
1:A:379:ARG:O	1:A:380:ASN:HB2	1.57	1.01
1:B:169:LEU:C	1:B:169:LEU:CD1	2.33	1.01
1:A:185:ASN:HD22	1:A:272:SER:HB2	1.22	0.99
1:B:16:ARG:HH11	1:B:16:ARG:CG	1.74	0.98
1:B:16:ARG:HG2	1:B:16:ARG:NH1	1.66	0.98
1:B:316:MET:O	1:B:320:VAL:HG23	1.64	0.97
1:A:185:ASN:HD22	1:A:272:SER:CB	1.77	0.97
1:A:182:MET:HE3	3:A:586:HOH:O	1.64	0.96
1:B:443:LEU:CD1	1:B:447:GLN:HE21	1.79	0.96
1:B:165:GLU:HG3	3:B:580:HOH:O	1.64	0.95
1:B:333:LYS:NZ	1:B:333:LYS:HB3	1.81	0.95
1:A:313:PRO:HG2	1:A:316:MET:HE2	1.51	0.93
1:B:333:LYS:HB3	1:B:333:LYS:HZ3	1.33	0.93
1:A:302:TRP:HA	1:A:316:MET:HE1	1.49	0.92
1:A:63:ARG:HH21	1:A:427:LYS:CE	1.83	0.92
1:A:443:LEU:O	1:A:447:GLN:HG3	1.68	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:443:LEU:CD1	1:A:447:GLN:HE21	1.85	0.89
1:A:313:PRO:CD	1:A:316:MET:CE	2.50	0.89
1:B:206:ARG:HH11	1:B:206:ARG:HG3	0.74	0.89
1:A:63:ARG:HH21	1:A:427:LYS:HE3	1.37	0.88
1:A:281:TRP:CD1	1:A:376:GLU:HG3	2.10	0.86
1:B:319:PHE:CD1	1:B:372:HIS:CD2	2.64	0.85
1:A:205:GLY:O	1:A:235:PRO:HG3	1.77	0.85
1:B:319:PHE:HD1	1:B:372:HIS:CD2	1.94	0.85
1:A:443:LEU:HD12	1:A:447:GLN:HE21	1.41	0.85
1:B:319:PHE:HD1	1:B:372:HIS:HD2	1.23	0.85
1:A:276:GLN:H	1:A:299:MET:HE1	1.42	0.84
1:A:428:ASN:OD1	1:A:430:ASN:HB2	1.78	0.83
1:B:294:ARG:HD2	1:B:371:ILE:O	1.80	0.82
1:B:368:ASN:O	1:B:371:ILE:HG13	1.80	0.82
1:A:409:LYS:NZ	1:A:409:LYS:HB3	1.94	0.81
1:A:313:PRO:HG2	1:A:316:MET:CE	2.11	0.81
1:A:281:TRP:O	1:A:281:TRP:CE3	2.33	0.80
1:B:17:ILE:HD12	1:B:21:ASP:OD2	1.83	0.79
1:A:351:TYR:HB2	1:A:376:GLU:O	1.82	0.79
1:A:398:GLU:CD	1:A:398:GLU:H	1.91	0.79
1:B:169:LEU:O	1:B:169:LEU:CD1	2.27	0.79
1:A:63:ARG:NH2	1:A:427:LYS:CE	2.46	0.78
1:A:155:LEU:O	1:A:245:HIS:CE1	2.37	0.78
1:B:313:PRO:HD2	1:B:316:MET:CE	2.13	0.78
1:A:409:LYS:HB3	1:A:409:LYS:HZ2	1.45	0.78
1:B:443:LEU:HD11	1:B:447:GLN:NE2	1.97	0.78
1:A:155:LEU:O	1:A:245:HIS:HE1	1.66	0.78
1:B:73:ASP:OD1	1:B:76:HIS:HD2	1.67	0.78
1:A:256:LEU:C	1:A:256:LEU:HD23	2.10	0.77
1:B:155:LEU:O	1:B:245:HIS:HE1	1.66	0.77
1:B:186:GLN:HE21	1:B:345:ASN:HD22	1.32	0.77
1:A:185:ASN:ND2	1:A:272:SER:CB	2.48	0.77
1:A:276:GLN:N	1:A:299:MET:HE1	2.00	0.77
1:B:175:GLY:O	1:B:179:LYS:HE3	1.85	0.77
1:B:53:THR:HG22	1:B:57:ARG:CD	2.10	0.77
1:A:283:GLU:CD	1:A:379:ARG:HH22	1.93	0.76
1:B:313:PRO:CD	1:B:316:MET:CE	2.63	0.76
1:B:378:ASP:HB3	1:B:382:VAL:C	2.10	0.76
1:A:294:ARG:HD2	1:A:371:ILE:O	1.84	0.76
1:B:204:ARG:HH12	1:B:238:GLU:CD	1.92	0.76
1:A:382:VAL:O	3:A:576:HOH:O	2.04	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:53:THR:HG22	1:A:57:ARG:HD2	1.68	0.76
1:B:204:ARG:NH1	1:B:238:GLU:OE1	2.19	0.75
1:A:73:ASP:OD1	1:A:76:HIS:HD2	1.70	0.75
1:B:13:ASP:HB3	1:B:16:ARG:HD2	1.69	0.75
1:B:121:ASN:OD1	1:B:177:ARG:NH2	2.17	0.75
1:A:305:GLU:N	1:A:306:PRO:CD	2.50	0.74
1:A:499:TYR:CD2	1:A:500:PRO:HD2	2.22	0.74
1:A:512:HIS:O	1:A:513:LYS:HD3	1.88	0.73
1:A:415:LEU:HD12	1:A:462:ASN:ND2	2.02	0.73
1:B:137:THR:OG1	1:B:182:MET:HE3	1.88	0.73
1:A:281:TRP:CE3	1:A:281:TRP:C	2.67	0.73
1:A:313:PRO:CG	1:A:316:MET:CE	2.67	0.73
1:B:443:LEU:O	1:B:447:GLN:HG3	1.89	0.73
1:B:53:THR:CG2	1:B:57:ARG:HD2	2.12	0.72
1:A:409:LYS:NZ	1:A:409:LYS:CB	2.49	0.72
1:B:155:LEU:O	1:B:245:HIS:ND1	2.22	0.72
1:A:316:MET:O	1:A:320:VAL:HG23	1.90	0.71
1:A:281:TRP:C	1:A:281:TRP:HE3	1.99	0.71
1:A:114:LYS:HE2	3:A:565:HOH:O	1.90	0.71
1:B:284:ASN:O	1:B:286:ALA:N	2.24	0.70
1:B:313:PRO:HG2	1:B:316:MET:CE	2.22	0.70
1:A:244:HIS:HD2	1:A:312:TYR:OH	1.75	0.70
1:A:281:TRP:HD1	1:A:376:GLU:CG	2.04	0.70
1:A:256:LEU:HD23	1:A:256:LEU:O	1.92	0.69
1:A:281:TRP:CD1	1:A:376:GLU:CG	2.76	0.69
1:B:186:GLN:HG2	1:B:345:ASN:ND2	2.08	0.68
1:B:53:THR:HG21	1:B:57:ARG:NH1	2.09	0.68
1:A:379:ARG:O	1:A:380:ASN:CB	2.38	0.68
1:B:73:ASP:OD1	1:B:76:HIS:CD2	2.46	0.68
1:A:183:THR:OG1	1:A:250:HIS:HD2	1.77	0.68
1:B:378:ASP:HB3	1:B:382:VAL:O	1.94	0.68
1:A:185:ASN:ND2	1:A:272:SER:HB3	2.08	0.67
1:B:183:THR:OG1	1:B:250:HIS:HD2	1.77	0.67
1:B:137:THR:OG1	1:B:182:MET:CE	2.42	0.67
1:B:204:ARG:NH1	1:B:238:GLU:CD	2.52	0.67
1:A:17:ILE:HD12	1:A:21:ASP:OD2	1.95	0.67
1:A:137:THR:OG1	1:A:182:MET:HE2	1.95	0.67
1:A:273:HIS:HA	3:A:588:HOH:O	1.94	0.67
1:B:255:GLU:HG3	1:B:259:ASN:ND2	2.10	0.67
1:B:351:TYR:HB2	1:B:376:GLU:O	1.94	0.67
1:A:63:ARG:NH2	1:A:427:LYS:HE3	2.10	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:256:LEU:C	1:B:256:LEU:HD23	2.19	0.66
1:A:186:GLN:HG3	1:A:345:ASN:HD22	1.61	0.66
1:B:142:ASP:OD1	3:B:539:HOH:O	2.12	0.66
1:A:433:LEU:O	1:A:437:ARG:HG2	1.95	0.66
1:B:185:ASN:HD21	1:B:345:ASN:HD21	1.44	0.66
1:A:165:GLU:OE1	1:A:165:GLU:HA	1.94	0.66
1:B:443:LEU:CD1	1:B:447:GLN:NE2	2.57	0.65
1:A:73:ASP:OD1	1:A:76:HIS:CD2	2.50	0.65
1:A:305:GLU:N	1:A:306:PRO:HD2	2.11	0.65
1:B:186:GLN:NE2	1:B:345:ASN:HD22	1.94	0.65
1:A:204:ARG:NH1	1:A:238:GLU:OE1	2.30	0.64
1:B:244:HIS:NE2	1:B:327:PHE:CE1	2.65	0.64
1:B:382:VAL:O	3:B:547:HOH:O	2.14	0.64
1:B:186:GLN:HG2	1:B:345:ASN:HD22	1.62	0.64
1:B:284:ASN:O	1:B:285:SER:C	2.38	0.64
1:A:185:ASN:HD21	1:A:345:ASN:HD21	1.47	0.63
1:B:433:LEU:O	1:B:437:ARG:HG2	1.97	0.63
1:A:53:THR:HG21	1:A:57:ARG:NH1	2.13	0.63
1:A:345:ASN:HB3	1:A:420:GLU:HB2	1.80	0.63
1:B:178:VAL:C	1:B:179:LYS:HD2	2.24	0.63
1:A:401:ARG:HH21	1:A:459:ASP:CG	2.08	0.62
1:B:378:ASP:CB	1:B:382:VAL:O	2.48	0.62
1:A:175:GLY:O	1:A:179:LYS:HE3	2.00	0.62
1:B:328:SER:OG	1:B:330:GLU:HG2	2.00	0.62
1:A:409:LYS:HZ2	1:A:409:LYS:CB	2.11	0.61
1:B:185:ASN:HD22	1:B:272:SER:HB3	1.64	0.61
1:A:443:LEU:CD1	1:A:447:GLN:NE2	2.61	0.61
1:B:451:PHE:CE2	1:B:455:GLN:NE2	2.68	0.61
1:A:148:GLU:OE1	3:A:534:HOH:O	2.16	0.61
1:A:53:THR:HG22	1:A:57:ARG:CD	2.30	0.61
1:A:279:GLU:O	1:A:351:TYR:HA	2.01	0.61
1:A:455:GLN:HA	1:A:455:GLN:OE1	2.00	0.61
1:B:428:ASN:OD1	1:B:430:ASN:HB2	2.01	0.60
1:A:443:LEU:O	1:A:443:LEU:HD12	2.01	0.60
1:A:396:TYR:OH	1:A:402:LYS:NZ	2.35	0.60
1:B:298:PHE:O	1:B:367:TYR:OH	2.20	0.60
1:A:53:THR:HG21	1:A:57:ARG:CZ	2.31	0.59
1:B:313:PRO:CG	1:B:316:MET:CE	2.80	0.59
1:B:169:LEU:HD11	1:B:173:GLU:HG3	1.84	0.59
1:B:391:ASP:OD1	1:B:392:TRP:N	2.36	0.59
1:A:355:ALA:O	1:A:356:SER:C	2.44	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:421:ASN:HD21	1:A:449:HIS:HB3	1.67	0.58
1:B:339:TYR:CD1	1:B:339:TYR:C	2.81	0.58
1:A:256:LEU:C	1:A:256:LEU:CD2	2.76	0.58
1:B:232:THR:HG23	1:B:232:THR:O	2.02	0.58
1:B:244:HIS:CD2	1:B:327:PHE:CE1	2.92	0.58
1:B:305:GLU:HB3	1:B:306:PRO:HD3	1.86	0.58
1:A:302:TRP:CA	1:A:316:MET:HE1	2.30	0.58
1:B:276:GLN:N	1:B:299:MET:HE1	2.19	0.58
1:A:235:PRO:HB2	1:A:366:SER:HB2	1.84	0.57
1:A:128:LEU:HD11	1:A:177:ARG:HB3	1.86	0.57
1:B:256:LEU:HD23	1:B:256:LEU:O	2.04	0.57
1:B:313:PRO:HG2	1:B:316:MET:HE2	1.85	0.57
1:B:279:GLU:O	1:B:351:TYR:HA	2.03	0.57
1:B:288:ASP:OD1	1:B:353:THR:OG1	2.21	0.57
1:A:42:ARG:HH11	1:A:42:ARG:HG3	1.69	0.57
1:B:185:ASN:ND2	1:B:345:ASN:HD21	2.03	0.56
1:B:319:PHE:CE1	1:B:372:HIS:HD2	2.23	0.56
1:A:53:THR:CG2	1:A:57:ARG:CZ	2.82	0.56
1:B:178:VAL:O	1:B:179:LYS:HD2	2.06	0.56
1:B:315:SER:O	1:B:319:PHE:HD2	1.88	0.56
1:A:273:HIS:ND1	3:A:588:HOH:O	2.01	0.56
1:A:13:ASP:OD2	1:A:16:ARG:HG3	2.05	0.55
1:A:275:THR:HA	1:A:299:MET:HE3	1.87	0.55
1:A:19:ARG:O	1:A:19:ARG:HG2	2.06	0.55
1:B:254:VAL:O	1:B:258:LYS:HB2	2.06	0.55
1:B:454:ARG:HD2	1:B:454:ARG:O	2.06	0.55
1:A:63:ARG:HH21	1:A:427:LYS:HE2	1.67	0.55
1:B:305:GLU:HG3	1:B:311:ASP:O	2.06	0.55
1:A:398:GLU:CD	1:A:398:GLU:N	2.64	0.55
1:A:59:PRO:HG2	1:B:430:ASN:O	2.07	0.55
1:A:231:SER:OG	1:A:232:THR:N	2.36	0.55
1:A:60:ASP:HA	1:B:430:ASN:OD1	2.07	0.55
1:A:298:PHE:O	1:A:367:TYR:OH	2.22	0.55
1:B:128:LEU:HD11	1:B:177:ARG:HB3	1.89	0.55
1:B:186:GLN:CG	1:B:345:ASN:HD22	2.20	0.54
1:B:346:TYR:C	1:B:346:TYR:CD2	2.85	0.54
1:A:415:LEU:HD12	1:A:462:ASN:HD22	1.69	0.54
1:B:403:ILE:CG2	1:B:404:LEU:N	2.70	0.54
1:B:473:ASP:OD2	1:B:484:ARG:NH1	2.35	0.54
1:A:512:HIS:O	1:A:513:LYS:HB2	2.07	0.54
1:B:294:ARG:NH1	1:B:372:HIS:O	2.41	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:63:ARG:NH2	1:A:427:LYS:HE2	2.22	0.53
1:A:425:ASP:OD1	1:A:442:ARG:NH1	2.39	0.53
1:A:281:TRP:CD1	1:A:376:GLU:CB	2.91	0.53
1:B:251:ALA:HB2	1:B:335:LEU:HD23	1.90	0.53
1:A:257:TYR:OH	1:A:267:GLY:HA3	2.09	0.53
1:B:168:GLU:HB2	1:B:256:LEU:HD11	1.90	0.53
1:B:415:LEU:HD12	1:B:462:ASN:ND2	2.24	0.53
1:A:346:TYR:C	1:A:346:TYR:CD2	2.86	0.53
1:B:37:ILE:HG13	1:B:38:GLU:N	2.24	0.53
1:A:178:VAL:C	1:A:179:LYS:HD2	2.33	0.53
1:A:512:HIS:O	1:A:513:LYS:CB	2.56	0.53
1:A:42:ARG:HG3	1:A:42:ARG:NH1	2.24	0.53
1:B:152:GLY:O	1:B:153:GLY:C	2.51	0.53
1:A:281:TRP:HD1	1:A:376:GLU:CB	2.21	0.53
1:A:512:HIS:C	1:A:513:LYS:HD3	2.34	0.53
1:B:206:ARG:CG	1:B:206:ARG:NH1	2.32	0.52
1:B:15:THR:HG22	1:B:447:GLN:OE1	2.09	0.52
1:A:78:TYR:O	1:A:82:VAL:HG23	2.11	0.51
1:A:244:HIS:HE1	3:A:579:HOH:O	1.93	0.51
1:B:451:PHE:CZ	1:B:455:GLN:NE2	2.79	0.51
1:A:343:GLY:HA2	1:A:417:TYR:O	2.11	0.50
1:B:243:THR:HG23	1:B:303:PHE:CZ	2.47	0.50
1:B:99:TRP:HA	1:B:166:TYR:CE1	2.46	0.50
1:A:281:TRP:O	1:A:281:TRP:HE3	1.84	0.50
1:A:204:ARG:HH12	1:A:238:GLU:CD	2.20	0.50
1:A:421:ASN:HD21	1:A:449:HIS:CB	2.24	0.50
1:A:19:ARG:O	1:A:19:ARG:CG	2.59	0.50
1:A:120:TYR:O	1:A:124:ILE:HG13	2.12	0.50
1:A:319:PHE:HD1	1:A:372:HIS:HD2	1.59	0.50
1:A:401:ARG:NE	1:A:459:ASP:OD2	2.40	0.50
1:B:187:PRO:HB2	1:B:303:PHE:CE1	2.47	0.50
1:B:185:ASN:HD22	1:B:272:SER:CB	2.25	0.49
1:B:195:TYR:CE2	1:B:242:VAL:HG21	2.47	0.49
1:B:508:MET:O	1:B:512:HIS:HB2	2.12	0.49
1:A:98:SER:O	1:A:101:ARG:N	2.39	0.49
1:B:258:LYS:HG3	1:B:262:GLN:OE1	2.12	0.49
1:B:142:ASP:CG	3:B:539:HOH:O	2.53	0.49
1:B:273:HIS:CE1	1:B:303:PHE:HB3	2.47	0.49
1:B:512:HIS:ND1	1:B:513:LYS:HD3	2.28	0.49
1:B:186:GLN:N	1:B:187:PRO:CD	2.76	0.49
1:A:244:HIS:NE2	1:A:327:PHE:CE1	2.81	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:393:LEU:C	1:A:393:LEU:HD23	2.38	0.48
1:A:398:GLU:N	1:A:398:GLU:OE1	2.46	0.48
1:B:256:LEU:C	1:B:256:LEU:CD2	2.85	0.48
1:B:204:ARG:NH1	1:B:238:GLU:OE2	2.25	0.48
1:B:255:GLU:CG	1:B:259:ASN:ND2	2.76	0.48
1:B:296:LEU:O	1:B:297:ASP:C	2.56	0.48
1:A:37:ILE:HG13	1:A:38:GLU:N	2.28	0.48
1:A:317:LYS:O	1:A:321:GLY:HA2	2.13	0.48
1:A:294:ARG:NH1	1:A:372:HIS:O	2.45	0.48
1:B:179:LYS:HD2	1:B:179:LYS:N	2.29	0.48
1:B:257:TYR:OH	1:B:267:GLY:HA3	2.14	0.48
1:A:67:ASN:OD1	1:A:67:ASN:C	2.57	0.48
1:A:345:ASN:CB	1:A:420:GLU:HB2	2.44	0.48
1:B:105:GLY:O	1:B:107:ARG:N	2.45	0.47
1:A:281:TRP:NE1	1:A:376:GLU:HG3	2.29	0.47
1:B:276:GLN:H	1:B:299:MET:HE1	1.79	0.47
1:B:512:HIS:C	1:B:513:LYS:HD3	2.40	0.47
1:B:355:ALA:O	1:B:356:SER:C	2.56	0.47
1:A:244:HIS:CD2	1:A:312:TYR:OH	2.63	0.47
1:B:38:GLU:OE2	3:B:534:HOH:O	2.20	0.47
1:B:94:ARG:HA	1:B:135:PHE:O	2.13	0.47
1:A:279:GLU:O	1:A:352:VAL:N	2.43	0.47
1:B:256:LEU:HD21	1:B:261:PHE:HE2	1.79	0.47
1:A:15:THR:HG22	1:A:447:GLN:OE1	2.15	0.47
1:A:388:SER:HB2	1:A:423:VAL:CG2	2.44	0.47
1:A:38:GLU:OE1	1:A:101:ARG:NH2	2.43	0.47
1:A:282:ASP:OD1	1:A:284:ASN:HB2	2.14	0.47
1:B:445:TYR:CZ	1:B:449:HIS:CE1	3.03	0.47
1:A:317:LYS:O	1:A:321:GLY:N	2.47	0.47
1:B:250:HIS:CE1	1:B:338:SER:O	2.67	0.47
1:A:281:TRP:HD1	1:A:376:GLU:HB2	1.80	0.46
1:A:186:GLN:HG3	1:A:345:ASN:ND2	2.29	0.46
1:A:315:SER:O	1:A:319:PHE:HD2	1.98	0.46
1:B:63:ARG:HH11	1:B:63:ARG:HG2	1.80	0.46
1:B:421:ASN:ND2	1:B:466:TYR:OH	2.46	0.46
1:A:195:TYR:CE2	1:A:242:VAL:HG21	2.51	0.46
1:A:395:ILE:HG22	1:A:397:PRO:HD3	1.98	0.46
1:B:63:ARG:HG2	1:B:63:ARG:NH1	2.29	0.46
1:A:288:ASP:OD1	1:A:353:THR:OG1	2.32	0.46
1:B:333:LYS:NZ	1:B:333:LYS:CB	2.60	0.46
1:A:114:LYS:HA	1:A:114:LYS:HD3	1.83	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:86:LYS:HB3	1:A:86:LYS:HE3	1.60	0.46
1:A:508:MET:O	1:A:512:HIS:HB2	2.16	0.46
1:A:105:GLY:O	1:A:107:ARG:N	2.43	0.46
1:A:179:LYS:HD2	1:A:179:LYS:N	2.30	0.46
1:A:187:PRO:HB2	1:A:303:PHE:CE1	2.51	0.46
1:A:238:GLU:O	1:A:239:PRO:C	2.55	0.46
1:B:279:GLU:HG3	1:B:280:PRO:HD2	1.98	0.46
1:B:391:ASP:OD1	1:B:391:ASP:C	2.59	0.46
1:B:317:LYS:O	1:B:321:GLY:N	2.47	0.45
1:B:255:GLU:HG3	1:B:259:ASN:HD21	1.79	0.45
1:B:455:GLN:OE1	1:B:455:GLN:HA	2.16	0.45
1:A:276:GLN:H	1:A:299:MET:CE	2.22	0.45
1:B:408:LYS:O	1:B:408:LYS:HG2	2.17	0.45
1:A:155:LEU:HD23	1:A:155:LEU:HA	1.86	0.45
1:A:305:GLU:OE2	1:A:309:SER:OG	2.28	0.45
1:B:186:GLN:N	1:B:272:SER:O	2.35	0.45
1:B:316:MET:HE2	1:B:316:MET:HB2	1.73	0.45
1:B:469:TRP:HA	1:B:470:SER:HA	1.64	0.45
1:A:393:LEU:HD23	1:A:394:LEU:N	2.32	0.45
1:B:297:ASP:OD2	1:B:315:SER:OG	2.27	0.45
1:B:186:GLN:HE21	1:B:345:ASN:ND2	2.07	0.45
1:B:305:GLU:N	1:B:306:PRO:CD	2.80	0.45
1:A:71:ALA:HA	1:A:481:TYR:OH	2.17	0.45
1:A:94:ARG:HA	1:A:135:PHE:O	2.16	0.45
1:B:183:THR:OG1	1:B:250:HIS:CD2	2.65	0.45
1:B:479:GLU:OE2	1:B:479:GLU:HA	2.17	0.45
1:A:346:TYR:OH	1:A:399:GLY:HA3	2.16	0.45
1:A:427:LYS:O	1:A:428:ASN:HB2	2.17	0.45
1:B:317:LYS:HB2	1:B:317:LYS:HE3	1.78	0.45
1:A:281:TRP:CD1	1:A:376:GLU:HB2	2.52	0.45
1:A:305:GLU:HB3	1:A:306:PRO:HD3	1.98	0.45
1:B:499:TYR:CD2	1:B:500:PRO:HD2	2.52	0.45
1:B:86:LYS:HE3	1:B:86:LYS:HB3	1.82	0.44
1:B:403:ILE:HD12	1:B:403:ILE:HA	1.74	0.44
1:B:513:LYS:HA	1:B:513:LYS:HD2	1.39	0.44
1:A:415:LEU:CD1	1:A:462:ASN:ND2	2.78	0.44
1:B:78:TYR:O	1:B:82:VAL:HG23	2.17	0.44
1:B:344:LEU:HD12	1:B:404:LEU:HD23	1.99	0.44
1:A:255:GLU:HG3	1:A:259:ASN:ND2	2.33	0.44
1:A:305:GLU:HG3	1:A:311:ASP:O	2.18	0.44
1:B:234:ASN:HA	1:B:235:PRO:HD2	1.72	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:443:LEU:O	1:A:447:GLN:CG	2.54	0.44
1:A:339:TYR:CD1	1:A:339:TYR:C	2.96	0.44
1:A:434:SER:O	1:A:438:LYS:HE2	2.18	0.43
1:B:298:PHE:CG	1:B:371:ILE:HG23	2.53	0.43
1:B:17:ILE:O	1:B:17:ILE:HG23	2.18	0.43
1:B:71:ALA:HA	1:B:481:TYR:OH	2.18	0.43
1:B:53:THR:CG2	1:B:57:ARG:NH1	2.78	0.43
1:B:512:HIS:O	1:B:513:LYS:HB2	2.19	0.43
1:A:186:GLN:HG2	1:A:274:ALA:HB2	1.99	0.43
1:B:403:ILE:HG22	1:B:404:LEU:N	2.33	0.43
1:A:493:ASN:OD1	1:B:66:THR:HG22	2.18	0.43
1:B:464:LYS:HA	1:B:464:LYS:HD2	1.53	0.43
1:A:513:LYS:HA	1:A:513:LYS:HD2	1.37	0.43
1:B:53:THR:CG2	1:B:57:ARG:CZ	2.97	0.43
1:A:403:ILE:CG2	1:A:404:LEU:N	2.82	0.42
1:B:257:TYR:OH	1:B:267:GLY:CA	2.67	0.42
1:B:56:HIS:CE1	1:B:69:ASP:OD1	2.72	0.42
1:B:243:THR:HA	1:B:246:LEU:HD12	2.00	0.42
1:B:454:ARG:HD2	1:B:454:ARG:C	2.43	0.42
1:A:108:LEU:C	1:A:110:GLY:N	2.76	0.42
1:B:165:GLU:CB	3:B:580:HOH:O	2.66	0.42
1:B:279:GLU:O	1:B:352:VAL:N	2.41	0.42
1:B:313:PRO:HD3	1:B:316:MET:HE3	1.91	0.42
1:B:335:LEU:O	1:B:336:LYS:C	2.61	0.42
1:B:421:ASN:HD21	1:B:449:HIS:CB	2.32	0.42
1:B:445:TYR:C	1:B:445:TYR:CD2	2.97	0.42
1:A:464:LYS:HD3	1:A:464:LYS:HA	1.55	0.42
1:A:108:LEU:C	1:A:110:GLY:H	2.28	0.42
1:B:99:TRP:HB2	3:B:574:HOH:O	2.18	0.42
1:B:288:ASP:C	1:B:290:GLU:N	2.75	0.42
1:B:411:TYR:O	1:B:412:ASN:CB	2.64	0.42
1:B:434:SER:OG	2:B:514:CL:CL	2.75	0.41
1:A:98:SER:O	1:A:99:TRP:C	2.63	0.41
1:A:176:ASP:CG	1:A:177:ARG:HD3	2.45	0.41
1:B:301:GLY:HA2	1:B:411:TYR:OH	2.20	0.41
1:B:29:GLY:HA3	1:B:92:ALA:O	2.21	0.41
1:B:67:ASN:OD1	1:B:67:ASN:C	2.64	0.41
1:A:84:ILE:CD1	1:A:498:ARG:HG2	2.51	0.41
1:A:430:ASN:OD1	1:B:60:ASP:HA	2.20	0.41
1:B:241:TRP:O	1:B:244:HIS:N	2.53	0.41
1:B:283:GLU:H	1:B:283:GLU:HG2	1.60	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:281:TRP:CE2	1:B:376:GLU:HG3	2.56	0.41
1:A:408:LYS:O	1:A:412:ASN:HA	2.21	0.41
1:A:257:TYR:OH	1:A:267:GLY:CA	2.69	0.41
1:A:479:GLU:OE2	1:A:479:GLU:HA	2.20	0.41
1:B:244:HIS:HD2	1:B:312:TYR:OH	2.04	0.41
1:B:378:ASP:CB	1:B:382:VAL:C	2.86	0.41
1:B:28:MET:HE3	1:B:28:MET:HB3	1.96	0.41
1:B:142:ASP:OD1	1:B:142:ASP:N	2.52	0.41
1:B:395:ILE:HG22	1:B:397:PRO:HD3	2.03	0.41
1:B:451:PHE:O	1:B:455:GLN:HG2	2.21	0.41
1:A:53:THR:HG22	1:A:57:ARG:NE	2.36	0.40
1:A:438:LYS:HB2	1:A:438:LYS:HE3	1.42	0.40
1:A:15:THR:HA	1:A:447:GLN:OE1	2.21	0.40
1:B:107:ARG:H	1:B:107:ARG:HG2	1.72	0.40
1:B:265:GLN:O	1:B:266:GLU:HB2	2.21	0.40
1:B:328:SER:HG	1:B:330:GLU:HG2	1.87	0.40
1:B:63:ARG:HH11	1:B:63:ARG:CG	2.35	0.40
1:B:182:MET:HA	1:B:270:GLY:O	2.21	0.40
1:A:305:GLU:H	1:A:306:PRO:CD	2.30	0.40
1:A:428:ASN:C	1:A:430:ASN:H	2.29	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	464/513 (90%)	435 (94%)	24 (5%)	5 (1%)	11	10
1	B	464/513 (90%)	425 (92%)	34 (7%)	5 (1%)	11	10
All	All	928/1026 (90%)	860 (93%)	58 (6%)	10 (1%)	11	10

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	232	THR
1	A	380	ASN
1	B	285	SER
1	A	421	ASN
1	A	428	ASN
1	A	60	ASP
1	B	60	ASP
1	B	283	GLU
1	B	296	LEU
1	B	421	ASN

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	396/435 (91%)	371 (94%)	25 (6%)	16	19
1	B	396/435 (91%)	369 (93%)	27 (7%)	14	17
All	All	792/870 (91%)	740 (93%)	52 (7%)	15	18

All (52) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	13	ASP
1	A	53	THR
1	A	63	ARG
1	A	91	ASP
1	A	94	ARG
1	A	179	LYS
1	A	182	MET
1	A	184	LEU
1	A	281	TRP
1	A	314	LYS
1	A	318	LYS
1	A	333	LYS
1	A	350	SER
1	A	352	VAL

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Mol	Chain	Res	Type
1	A	353	THR
1	A	366	SER
1	A	390	SER
1	A	398	GLU
1	A	403	ILE
1	A	409	LYS
1	A	434	SER
1	A	438	LYS
1	A	440	SER
1	A	443	LEU
1	A	513	LYS
1	B	16	ARG
1	B	53	THR
1	B	63	ARG
1	B	109	SER
1	B	169	LEU
1	B	179	LYS
1	B	182	MET
1	B	206	ARG
1	B	232	THR
1	B	258	LYS
1	B	283	GLU
1	B	307	ILE
1	B	316	MET
1	B	318	LYS
1	B	320	VAL
1	B	333	LYS
1	B	353	THR
1	B	354	ASN
1	B	366	SER
1	B	371	ILE
1	B	378	ASP
1	B	390	SER
1	B	403	ILE
1	B	409	LYS
1	B	415	LEU
1	B	440	SER
1	B	513	LYS

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	76	HIS
1	A	83	ASN
1	A	185	ASN
1	A	244	HIS
1	A	250	HIS
1	A	276	GLN
1	A	284	ASN
1	A	372	HIS
1	A	421	ASN
1	A	447	GLN
1	A	462	ASN
1	B	76	HIS
1	B	83	ASN
1	B	180	HIS
1	B	186	GLN
1	B	250	HIS
1	B	259	ASN
1	B	273	HIS
1	B	276	GLN
1	B	345	ASN
1	B	354	ASN
1	B	364	ASN
1	B	372	HIS
1	B	380	ASN
1	B	421	ASN
1	B	447	GLN
1	B	462	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

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	470/513 (91%)	0.06	12 (2%) 57 54	18, 36, 58, 70	0
1	B	470/513 (91%)	0.11	10 (2%) 63 60	20, 38, 58, 68	0
All	All	940/1026 (91%)	0.09	22 (2%) 61 58	18, 37, 58, 70	0

All (22) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	206	ARG	6.1
1	A	206	ARG	5.6
1	A	281	TRP	4.4
1	A	382	VAL	3.4
1	B	356	SER	3.1
1	A	381	GLY	3.0
1	A	13	ASP	3.0
1	A	231	SER	2.8
1	B	232	THR	2.6
1	A	356	SER	2.5
1	A	380	ASN	2.4
1	B	364	ASN	2.3
1	B	14	ALA	2.3
1	B	285	SER	2.2
1	B	355	ALA	2.2
1	A	284	ASN	2.1
1	A	14	ALA	2.1
1	A	285	SER	2.1
1	B	286	ALA	2.1
1	B	13	ASP	2.1
1	A	286	ALA	2.1
1	B	241	TRP	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 oligosaccharides 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($\text{\AA}^2$)	Q<0.9
2	CL	B	515	1/1	0.95	0.20	45,45,45,45	0
2	CL	B	514	1/1	0.96	0.24	42,42,42,42	0

6.5 Other polymers [i](#)

There are no such residues in this entry.