



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 08:11 AM UTC

PDB ID : 1BGA / pdb_00001bga
Title : BETA-GLUCOSIDASE A FROM BACILLUS POLYMYXA
Authors : Sanz-Aparicio, J.; Hermoso, J.A.; Martinez-Ripoll, M.; Polaina, J.
Deposited on : 1997-04-04
Resolution : 2.40 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) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

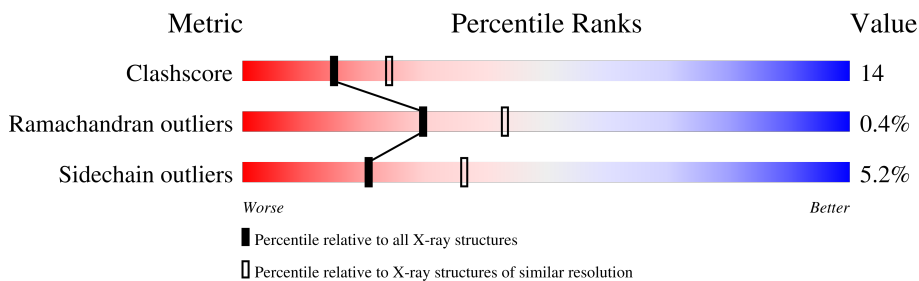
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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	190562	5391 (2.40-2.40)
Ramachandran outliers	187476	5320 (2.40-2.40)
Sidechain outliers	187428	5321 (2.40-2.40)

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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	447	
1	B	447	
1	C	447	
1	D	447	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 16117 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 A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	447	Total	C	N	O	S	0	0	0
			3644	2326	628	673	17			
1	B	447	Total	C	N	O	S	0	0	0
			3644	2326	628	673	17			
1	C	447	Total	C	N	O	S	0	0	0
			3644	2326	628	673	17			
1	D	447	Total	C	N	O	S	0	0	0
			3644	2326	628	673	17			

- Molecule 2 is water.

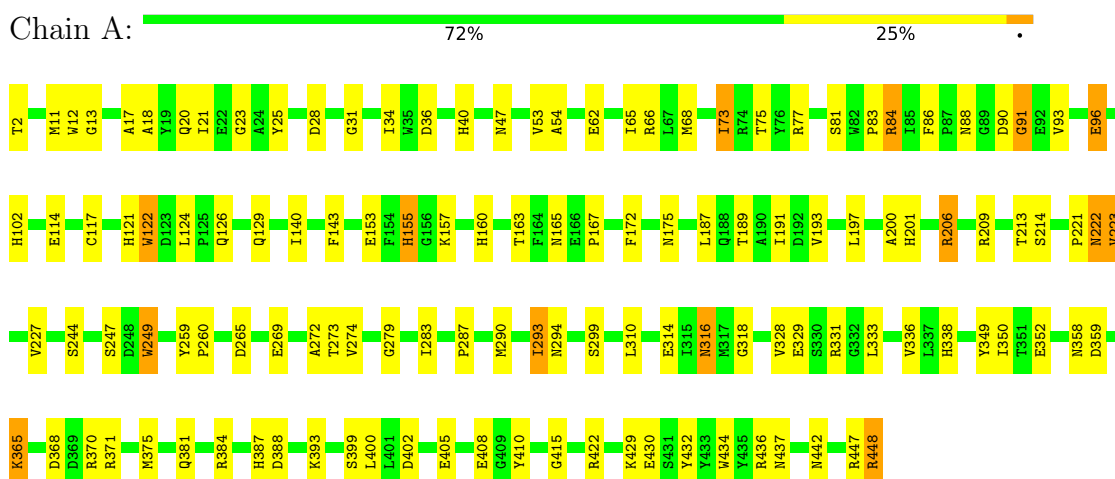
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	382	Total	O	0	0
			382	382		
2	B	396	Total	O	0	0
			396	396		
2	C	384	Total	O	0	0
			384	384		
2	D	379	Total	O	0	0
			379	379		

3 Residue-property plots

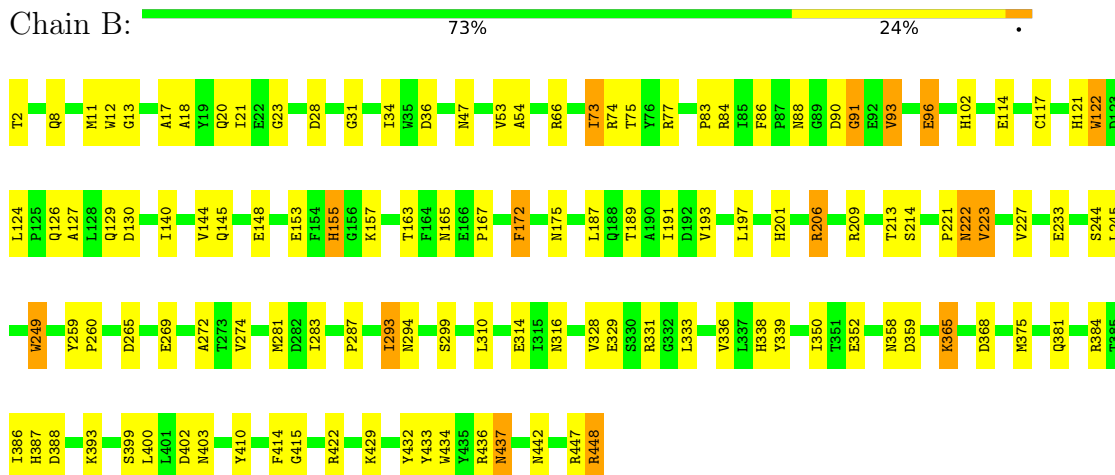
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded 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. 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.

Note EDS was not executed.

• Molecule 1: BETA-GLUCOSIDASE A

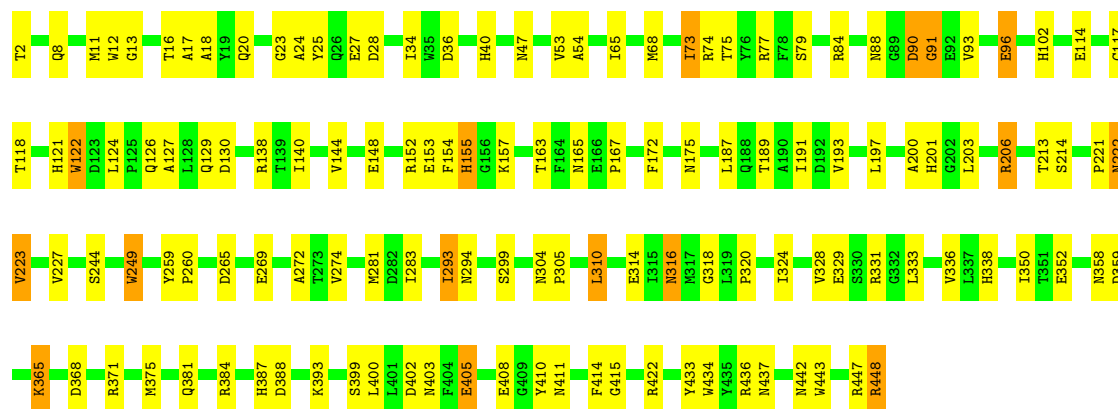


• Molecule 1: BETA-GLUCOSIDASE A

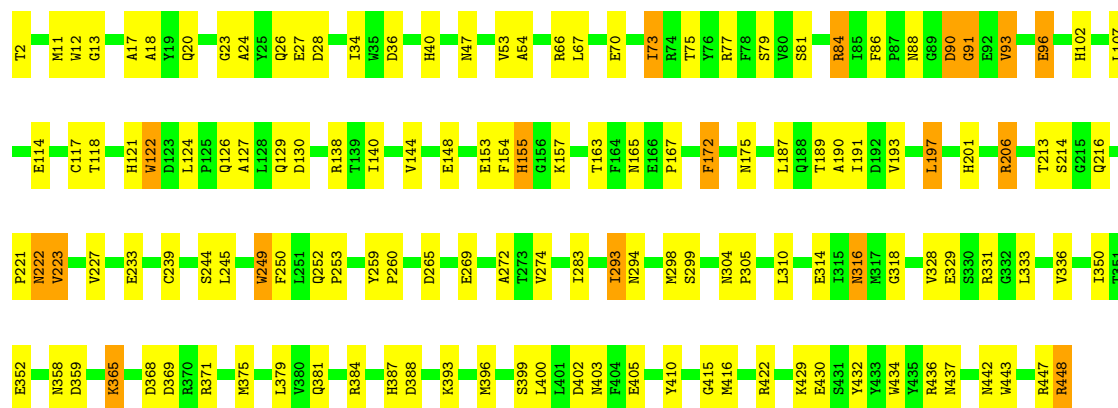


• Molecule 1: BETA-GLUCOSIDASE A





• Molecule 1: BETA-GLUCOSIDASE A



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 42 21 2	Depositor
Cell constants a, b, c, α , β , γ	205.46 Å 205.46 Å 155.86 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	8.00 – 2.40	Depositor
% Data completeness (in resolution range)	78.7 (8.00-2.40)	Depositor
R_{merge}	0.08	Depositor
R_{sym}	0.08	Depositor
Refinement program	X-PLOR 3.843	Depositor
R, R_{free}	0.200 , 0.270	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	16117	wwPDB-VP
Average B, all atoms (Å ²)	19.0	wwPDB-VP

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	0.55	0/3754	1.00	19/5107 (0.4%)
1	B	0.55	0/3754	1.00	18/5107 (0.4%)
1	C	0.55	0/3754	0.99	17/5107 (0.3%)
1	D	0.53	0/3754	1.00	19/5107 (0.4%)
All	All	0.55	0/15016	1.00	73/20428 (0.4%)

There are no bond length outliers.

All (73) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	21	ILE	N-CA-C	8.11	118.93	112.12
1	B	358	ASN	N-CA-C	7.80	122.18	113.21
1	A	358	ASN	N-CA-C	7.71	122.08	113.21
1	D	358	ASN	N-CA-C	7.71	122.07	113.21
1	A	21	ILE	N-CA-C	7.68	118.57	112.12
1	C	358	ASN	N-CA-C	7.57	122.16	113.15
1	A	402	ASP	N-CA-C	-7.31	100.19	110.50
1	D	402	ASP	N-CA-C	-7.19	100.36	110.50
1	C	402	ASP	N-CA-C	-7.15	100.42	110.50
1	B	117	CYS	N-CA-C	7.11	120.27	108.96
1	B	36	ASP	N-CA-C	-7.04	103.53	111.14
1	A	36	ASP	N-CA-C	-6.90	103.69	111.07
1	C	117	CYS	N-CA-C	6.85	119.85	108.96
1	B	402	ASP	N-CA-C	-6.77	100.95	110.50
1	D	36	ASP	N-CA-C	-6.75	103.84	111.07
1	D	117	CYS	N-CA-C	6.73	119.55	109.25
1	A	117	CYS	N-CA-C	6.59	119.44	108.96
1	B	415	GLY	N-CA-C	6.54	121.85	112.82
1	A	400	LEU	N-CA-C	-6.44	104.34	111.36
1	B	400	LEU	N-CA-C	-6.43	104.35	111.36
1	C	36	ASP	N-CA-C	-6.39	104.23	111.07
1	A	415	GLY	N-CA-C	6.31	121.53	112.82
1	A	388	ASP	N-CA-C	-6.30	105.35	113.16

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	415	GLY	N-CA-C	6.27	121.47	112.82
1	A	122	TRP	N-CA-C	6.24	123.07	113.28
1	C	388	ASP	N-CA-C	-6.23	105.43	113.16
1	B	388	ASP	N-CA-C	-6.22	105.45	113.16
1	B	122	TRP	N-CA-C	6.18	122.99	113.28
1	D	400	LEU	N-CA-C	-6.18	104.62	111.36
1	D	244	SER	N-CA-C	6.13	118.77	111.71
1	B	84	ARG	N-CA-C	-6.12	105.95	113.41
1	A	244	SER	N-CA-C	6.08	118.70	111.71
1	C	172	PHE	N-CA-C	6.04	119.12	111.69
1	C	122	TRP	N-CA-C	6.03	122.74	113.28
1	C	400	LEU	N-CA-C	-6.02	104.80	111.36
1	D	122	TRP	N-CA-C	6.01	122.72	113.28
1	A	84	ARG	N-CA-C	-5.99	106.11	113.41
1	D	172	PHE	N-CA-C	5.86	118.55	111.40
1	B	244	SER	N-CA-C	5.86	118.44	111.71
1	C	415	GLY	N-CA-C	5.86	120.90	112.82
1	C	244	SER	N-CA-C	5.82	118.40	111.71
1	D	388	ASP	N-CA-C	-5.74	106.05	113.16
1	D	393	LYS	N-CA-C	5.71	120.31	113.23
1	D	18	ALA	N-CA-C	5.69	117.96	111.02
1	A	18	ALA	N-CA-C	5.67	117.94	111.02
1	A	172	PHE	N-CA-C	5.63	118.62	111.69
1	B	393	LYS	N-CA-C	5.57	120.14	113.23
1	A	222	ASN	N-CA-C	-5.54	101.44	110.20
1	A	393	LYS	N-CA-C	5.51	120.06	113.23
1	B	222	ASN	N-CA-C	-5.46	101.58	110.20
1	D	416	MET	N-CA-C	-5.45	106.48	113.23
1	B	172	PHE	N-CA-C	5.41	118.34	111.69
1	B	18	ALA	N-CA-C	5.40	117.60	111.02
1	B	86	PHE	CA-C-N	5.34	125.66	119.47
1	B	86	PHE	C-N-CA	5.34	125.66	119.47
1	C	403	ASN	N-CA-C	5.32	115.16	108.45
1	A	25	TYR	N-CA-C	5.32	118.87	112.38
1	C	350	ILE	N-CA-C	-5.28	99.88	107.37
1	D	403	ASN	N-CA-C	5.26	115.08	108.45
1	A	350	ILE	N-CA-C	-5.26	99.91	107.37
1	C	393	LYS	N-CA-C	5.24	119.73	113.23
1	D	222	ASN	N-CA-C	-5.22	101.45	109.76
1	D	86	PHE	CA-C-N	5.20	125.50	119.47
1	D	86	PHE	C-N-CA	5.20	125.50	119.47
1	D	84	ARG	N-CA-C	-5.18	106.11	112.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	84	ARG	N-CA-C	-5.18	106.12	112.90
1	C	18	ALA	N-CA-C	5.15	117.31	111.02
1	B	350	ILE	N-CA-C	-5.12	100.09	107.37
1	A	86	PHE	CA-C-N	5.11	125.15	119.32
1	A	86	PHE	C-N-CA	5.11	125.15	119.32
1	C	222	ASN	N-CA-C	-5.11	101.64	109.76
1	D	350	ILE	N-CA-C	-5.06	100.19	107.37
1	C	25	TYR	N-CA-C	5.03	118.52	112.38

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	3644	0	3419	99	0
1	B	3644	0	3419	89	0
1	C	3644	0	3419	98	0
1	D	3644	0	3419	110	0
2	A	382	0	0	32	0
2	B	396	0	0	23	0
2	C	384	0	0	27	0
2	D	379	0	0	34	0
All	All	16117	0	13676	387	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 14.

All (387) 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:D:75:THR:HG22	1:D:114:GLU:HB2	1.44	0.99
1:C:75:THR:HG22	1:C:114:GLU:HB2	1.48	0.96
1:A:75:THR:HG22	1:A:114:GLU:HB2	1.47	0.96
1:B:75:THR:HG22	1:B:114:GLU:HB2	1.48	0.94

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:324:ILE:HG21	2:C:750:HOH:O	1.69	0.91
1:A:140:ILE:HA	2:A:807:HOH:O	1.69	0.90
1:C:448:ARG:OXT	1:C:448:ARG:HD2	1.72	0.90
1:D:448:ARG:HD2	1:D:448:ARG:OXT	1.72	0.90
1:C:200:ALA:HA	2:C:809:HOH:O	1.71	0.88
1:B:448:ARG:OXT	1:B:448:ARG:HD2	1.72	0.88
1:A:448:ARG:OXT	1:A:448:ARG:HD2	1.72	0.88
1:D:405:GLU:O	1:D:405:GLU:HG3	1.77	0.82
1:C:375:MET:SD	2:C:765:HOH:O	2.39	0.80
1:B:281:MET:HE3	2:B:803:HOH:O	1.84	0.76
1:D:191:ILE:HG13	2:D:816:HOH:O	1.85	0.75
1:A:375:MET:SD	2:A:751:HOH:O	2.45	0.75
1:B:387:HIS:HE1	2:B:450:HOH:O	1.70	0.74
1:D:90:ASP:HB2	2:D:645:HOH:O	1.87	0.73
1:A:102:HIS:HD2	1:A:157:LYS:HZ3	1.36	0.73
1:B:414:PHE:HB2	2:B:535:HOH:O	1.88	0.72
1:C:102:HIS:HD2	1:C:157:LYS:HZ3	1.34	0.72
1:A:223:VAL:HG22	2:A:760:HOH:O	1.87	0.72
1:B:102:HIS:HD2	1:B:157:LYS:HZ3	1.38	0.72
1:B:144:VAL:HB	2:B:472:HOH:O	1.91	0.71
1:B:121:HIS:HD2	2:B:748:HOH:O	1.73	0.71
1:D:375:MET:SD	2:D:809:HOH:O	2.48	0.71
1:D:197:LEU:HD11	2:D:761:HOH:O	1.90	0.70
1:A:201:HIS:HE1	2:A:829:HOH:O	1.75	0.69
1:A:66:ARG:HD2	2:A:739:HOH:O	1.93	0.69
1:C:414:PHE:HZ	2:C:750:HOH:O	1.75	0.69
1:A:143:PHE:HB3	2:A:807:HOH:O	1.92	0.69
1:C:387:HIS:HE1	2:C:478:HOH:O	1.76	0.69
1:D:11:MET:SD	1:D:75:THR:HG21	2.32	0.69
1:A:381:GLN:HE22	1:A:384:ARG:HH11	1.40	0.69
1:B:11:MET:SD	1:B:75:THR:HG21	2.32	0.69
1:A:11:MET:SD	1:A:75:THR:HG21	2.33	0.69
1:C:23:GLY:HA3	1:C:53:VAL:O	1.93	0.68
1:C:102:HIS:HD2	1:C:157:LYS:NZ	1.91	0.68
1:D:365:LYS:NZ	1:D:365:LYS:HB3	2.08	0.68
1:D:436:ARG:HD2	2:D:549:HOH:O	1.93	0.68
1:B:381:GLN:HE22	1:B:384:ARG:HH11	1.39	0.68
1:A:365:LYS:NZ	1:A:365:LYS:HB3	2.09	0.67
1:D:381:GLN:HE22	1:D:384:ARG:HH11	1.40	0.67
1:C:11:MET:SD	1:C:75:THR:HG21	2.34	0.67
1:A:28:ASP:HB3	1:A:96:GLU:HG2	1.77	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:88:ASN:HD22	1:D:91:GLY:H	1.42	0.66
1:C:381:GLN:HE22	1:C:384:ARG:HH11	1.41	0.66
1:B:88:ASN:HD22	1:B:91:GLY:H	1.43	0.66
1:C:90:ASP:HB2	2:C:450:HOH:O	1.95	0.66
1:D:102:HIS:HD2	1:D:157:LYS:NZ	1.94	0.66
1:A:88:ASN:HD22	1:A:91:GLY:H	1.43	0.66
1:A:102:HIS:HD2	1:A:157:LYS:NZ	1.93	0.66
1:C:299:SER:HB2	1:C:314:GLU:HG3	1.78	0.65
1:B:28:ASP:HB3	1:B:96:GLU:HG2	1.76	0.65
1:C:365:LYS:NZ	1:C:365:LYS:HB3	2.12	0.65
1:D:387:HIS:HE1	2:D:557:HOH:O	1.78	0.65
1:D:28:ASP:HB3	1:D:96:GLU:HG2	1.79	0.65
1:C:28:ASP:HB3	1:C:96:GLU:HG2	1.77	0.65
1:C:414:PHE:CZ	2:C:750:HOH:O	2.47	0.65
1:D:102:HIS:HD2	1:D:157:LYS:HZ3	1.43	0.65
1:A:121:HIS:HD2	2:A:499:HOH:O	1.79	0.65
1:B:299:SER:HB2	1:B:314:GLU:HG3	1.79	0.65
1:B:365:LYS:HB3	1:B:365:LYS:NZ	2.12	0.64
1:A:13:GLY:HA2	1:A:73:ILE:HG13	1.79	0.64
1:D:23:GLY:HA3	1:D:53:VAL:O	1.97	0.64
1:B:23:GLY:HA3	1:B:53:VAL:O	1.96	0.64
1:C:88:ASN:HD22	1:C:91:GLY:H	1.44	0.63
1:B:102:HIS:HD2	1:B:157:LYS:NZ	1.95	0.63
1:A:40:HIS:HD2	2:A:732:HOH:O	1.80	0.63
1:D:201:HIS:HE1	2:D:637:HOH:O	1.80	0.63
1:A:436:ARG:HD2	2:A:577:HOH:O	1.99	0.63
1:A:73:ILE:HG21	2:A:794:HOH:O	1.98	0.63
1:A:247:SER:HB3	2:A:760:HOH:O	1.99	0.62
1:A:17:ALA:HB3	1:A:20:GLN:HE21	1.64	0.62
1:A:23:GLY:HA3	1:A:53:VAL:O	1.99	0.62
1:C:223:VAL:HG11	1:C:336:VAL:HG11	1.81	0.62
1:C:17:ALA:HB3	1:C:20:GLN:HE21	1.63	0.62
1:A:299:SER:HB2	1:A:314:GLU:HG3	1.82	0.62
1:B:12:TRP:HE1	1:B:442:ASN:HD22	1.47	0.62
1:B:17:ALA:HB3	1:B:20:GLN:HE21	1.64	0.62
1:D:13:GLY:HA2	1:D:73:ILE:HG13	1.82	0.61
1:A:279:GLY:HA2	2:A:639:HOH:O	2.01	0.61
1:D:17:ALA:HB3	1:D:20:GLN:HE21	1.65	0.61
1:A:223:VAL:HG11	1:A:336:VAL:HG11	1.82	0.61
1:C:12:TRP:HE1	1:C:442:ASN:HD22	1.49	0.61
1:D:299:SER:HB2	1:D:314:GLU:HG3	1.81	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:16:THR:HG22	2:C:563:HOH:O	2.01	0.60
1:D:12:TRP:HE1	1:D:442:ASN:HD22	1.49	0.60
1:A:12:TRP:HE1	1:A:442:ASN:HD22	1.49	0.60
1:D:88:ASN:HD22	1:D:91:GLY:N	2.00	0.60
1:B:233:GLU:HG3	2:B:482:HOH:O	2.02	0.60
1:C:13:GLY:HA2	1:C:73:ILE:HG13	1.84	0.60
1:D:223:VAL:HG11	1:D:336:VAL:HG11	1.83	0.59
1:B:88:ASN:HD22	1:B:91:GLY:N	2.00	0.59
1:D:66:ARG:NH1	2:D:518:HOH:O	2.36	0.59
1:A:88:ASN:HD22	1:A:91:GLY:N	2.01	0.59
1:C:203:LEU:HD12	2:C:809:HOH:O	2.03	0.59
1:A:447:ARG:HH12	1:D:47:ASN:HD22	1.50	0.59
1:D:67:LEU:HD23	2:D:518:HOH:O	2.02	0.58
1:B:223:VAL:HG11	1:B:336:VAL:HG11	1.84	0.58
1:D:163:THR:OG1	1:D:201:HIS:HD2	1.86	0.58
1:C:88:ASN:HD22	1:C:91:GLY:N	2.01	0.57
1:A:365:LYS:HB3	1:A:365:LYS:HZ3	1.67	0.57
1:A:436:ARG:HD3	2:A:548:HOH:O	2.04	0.57
1:B:222:ASN:HA	1:B:294:ASN:HB2	1.86	0.57
1:B:13:GLY:HA2	1:B:73:ILE:HG13	1.87	0.56
1:C:163:THR:OG1	1:C:201:HIS:HD2	1.87	0.56
1:D:365:LYS:HB3	1:D:365:LYS:HZ3	1.69	0.56
1:C:381:GLN:HE21	1:C:381:GLN:HA	1.70	0.56
1:D:121:HIS:HD2	2:D:650:HOH:O	1.88	0.56
1:D:436:ARG:HD3	2:D:674:HOH:O	2.04	0.56
1:D:443:TRP:HZ3	2:D:505:HOH:O	1.87	0.56
1:B:201:HIS:HE1	2:B:492:HOH:O	1.88	0.56
1:C:281:MET:HE3	2:C:709:HOH:O	2.05	0.56
1:B:338:HIS:HD2	2:B:627:HOH:O	1.88	0.56
1:D:190:ALA:HB3	2:D:816:HOH:O	2.06	0.56
1:A:290:MET:HG2	2:A:788:HOH:O	2.05	0.56
1:B:88:ASN:ND2	1:B:91:GLY:H	2.04	0.56
1:D:329:GLU:OE2	1:D:331:ARG:HD3	2.06	0.56
1:D:88:ASN:ND2	1:D:91:GLY:H	2.04	0.55
1:D:250:PHE:CD1	2:D:761:HOH:O	2.53	0.55
1:C:411:ASN:HB3	2:C:686:HOH:O	2.06	0.55
1:A:163:THR:OG1	1:A:201:HIS:HD2	1.90	0.54
1:A:329:GLU:OE2	1:A:331:ARG:HD3	2.07	0.54
1:C:88:ASN:ND2	1:C:91:GLY:H	2.05	0.54
1:A:88:ASN:ND2	1:A:91:GLY:H	2.05	0.54
1:D:40:HIS:HD2	2:D:653:HOH:O	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:365:LYS:HB3	1:B:365:LYS:HZ3	1.72	0.54
1:B:381:GLN:NE2	1:B:381:GLN:HA	2.23	0.54
1:C:40:HIS:HD2	2:C:530:HOH:O	1.90	0.54
1:D:381:GLN:HA	1:D:381:GLN:HE21	1.73	0.54
1:B:102:HIS:CD2	1:B:157:LYS:NZ	2.76	0.54
1:B:122:TRP:CD1	1:B:122:TRP:N	2.76	0.54
1:B:163:THR:OG1	1:B:201:HIS:HD2	1.91	0.54
1:D:138:ARG:HD2	2:D:626:HOH:O	2.07	0.54
1:B:209:ARG:NH1	2:B:823:HOH:O	2.41	0.54
1:C:74:ARG:HD2	2:C:701:HOH:O	2.06	0.54
1:C:381:GLN:HA	1:C:381:GLN:NE2	2.23	0.54
1:B:339:TYR:HD2	2:B:741:HOH:O	1.91	0.54
1:A:102:HIS:CD2	1:A:157:LYS:NZ	2.76	0.53
1:B:223:VAL:CG1	1:B:336:VAL:HG21	2.39	0.53
1:B:381:GLN:HA	1:B:381:GLN:HE21	1.72	0.53
1:D:172:PHE:HE1	2:D:816:HOH:O	1.91	0.53
1:A:160:HIS:HD2	2:A:483:HOH:O	1.92	0.53
1:A:223:VAL:HA	2:A:760:HOH:O	2.08	0.53
1:B:102:HIS:HE1	1:B:153:GLU:OE1	1.90	0.53
1:A:381:GLN:HE21	1:A:381:GLN:HA	1.73	0.53
1:B:448:ARG:HD2	1:B:448:ARG:C	2.34	0.53
1:D:223:VAL:CG1	1:D:336:VAL:HG21	2.39	0.53
1:D:381:GLN:HA	1:D:381:GLN:NE2	2.24	0.53
1:C:222:ASN:HA	1:C:294:ASN:HB2	1.91	0.53
1:A:206:ARG:NH2	1:A:283:ILE:HG12	2.24	0.53
1:C:338:HIS:HD2	2:C:613:HOH:O	1.91	0.53
1:A:222:ASN:HA	1:A:294:ASN:HB2	1.91	0.53
1:A:223:VAL:CG1	1:A:336:VAL:HG21	2.39	0.53
1:A:381:GLN:HA	1:A:381:GLN:NE2	2.24	0.53
1:C:102:HIS:CD2	1:C:157:LYS:NZ	2.74	0.52
1:D:329:GLU:HG2	1:D:331:ARG:HG2	1.90	0.52
1:A:265:ASP:O	1:A:269:GLU:HG2	2.09	0.52
1:C:405:GLU:HA	1:C:405:GLU:OE1	2.07	0.52
1:D:206:ARG:NH2	1:D:283:ILE:HG12	2.24	0.52
1:B:223:VAL:HG13	1:B:336:VAL:HG21	1.91	0.52
1:A:47:ASN:HD22	1:B:447:ARG:HH12	1.56	0.52
1:B:12:TRP:HE1	1:B:442:ASN:ND2	2.08	0.52
1:C:102:HIS:HE1	1:C:153:GLU:OE1	1.93	0.52
1:D:222:ASN:HA	1:D:294:ASN:HB2	1.91	0.52
1:D:371:ARG:HD3	2:D:562:HOH:O	2.09	0.52
1:A:102:HIS:HE1	1:A:153:GLU:OE1	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:448:ARG:HD2	1:D:448:ARG:C	2.34	0.52
1:C:329:GLU:HG2	1:C:331:ARG:HG2	1.92	0.52
1:B:403:ASN:ND2	2:B:749:HOH:O	2.42	0.52
1:D:102:HIS:HE1	1:D:153:GLU:OE1	1.93	0.52
1:C:47:ASN:HD22	1:D:447:ARG:HH12	1.57	0.52
1:D:265:ASP:O	1:D:269:GLU:HG2	2.09	0.52
1:C:138:ARG:HD2	2:C:718:HOH:O	2.10	0.51
1:A:122:TRP:CD1	1:A:122:TRP:N	2.77	0.51
1:B:155:HIS:O	1:B:214:SER:OG	2.27	0.51
1:C:206:ARG:NH2	1:C:283:ILE:HG12	2.25	0.51
1:C:74:ARG:CD	2:C:701:HOH:O	2.58	0.51
1:C:365:LYS:HB3	1:C:365:LYS:HZ3	1.75	0.51
1:C:448:ARG:HD2	1:C:448:ARG:C	2.34	0.51
1:B:206:ARG:NH2	1:B:283:ILE:HG12	2.25	0.51
1:C:155:HIS:O	1:C:214:SER:OG	2.28	0.51
1:B:93:VAL:HG23	2:B:496:HOH:O	2.11	0.51
1:B:436:ARG:HD3	2:B:515:HOH:O	2.10	0.51
1:A:273:THR:HA	2:A:759:HOH:O	2.11	0.51
1:D:233:GLU:HG3	2:D:463:HOH:O	2.11	0.51
1:A:124:LEU:HD23	1:A:129:GLN:HE21	1.76	0.50
1:A:223:VAL:HG13	1:A:336:VAL:HG21	1.92	0.50
1:C:122:TRP:N	1:C:122:TRP:CD1	2.78	0.50
1:B:329:GLU:OE2	1:B:331:ARG:HD3	2.11	0.50
1:C:329:GLU:OE2	1:C:331:ARG:HD3	2.10	0.50
1:D:249:TRP:CZ3	2:D:627:HOH:O	2.54	0.50
1:A:12:TRP:HE1	1:A:442:ASN:ND2	2.09	0.50
1:C:265:ASP:O	1:C:269:GLU:HG2	2.11	0.50
1:D:369:ASP:HB2	2:D:745:HOH:O	2.11	0.50
1:A:167:PRO:HD2	1:A:221:PRO:HA	1.93	0.50
1:A:387:HIS:HE1	2:A:505:HOH:O	1.94	0.50
1:B:155:HIS:CD2	1:B:213:THR:HA	2.46	0.50
1:C:436:ARG:HD2	2:C:667:HOH:O	2.11	0.50
1:D:201:HIS:CE1	2:D:637:HOH:O	2.59	0.50
1:A:77:ARG:NH2	1:A:352:GLU:HG3	2.27	0.50
1:C:223:VAL:CG1	1:C:336:VAL:HG21	2.42	0.50
1:D:73:ILE:HG21	2:D:810:HOH:O	2.12	0.50
1:A:316:ASN:C	1:A:316:ASN:HD22	2.20	0.49
1:B:329:GLU:HG2	1:B:331:ARG:HG2	1.93	0.49
1:A:329:GLU:HG2	1:A:331:ARG:HG2	1.93	0.49
1:A:442:ASN:ND2	2:A:636:HOH:O	2.44	0.49
1:B:265:ASP:O	1:B:269:GLU:HG2	2.11	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:155:HIS:O	1:A:214:SER:OG	2.30	0.49
1:B:77:ARG:NH2	1:B:352:GLU:HG3	2.27	0.49
1:C:316:ASN:C	1:C:316:ASN:HD22	2.20	0.49
1:A:191:ILE:HD12	1:A:272:ALA:HB1	1.95	0.49
1:D:102:HIS:CD2	1:D:157:LYS:NZ	2.76	0.49
1:D:122:TRP:N	1:D:122:TRP:CD1	2.78	0.49
1:D:223:VAL:HG13	1:D:336:VAL:HG21	1.93	0.49
1:A:155:HIS:CD2	1:A:213:THR:HA	2.46	0.49
1:B:66:ARG:HG3	2:B:755:HOH:O	2.12	0.49
1:C:54:ALA:HA	1:C:410:TYR:OH	2.12	0.49
1:C:8:GLN:NE2	2:C:696:HOH:O	2.45	0.49
1:D:316:ASN:C	1:D:316:ASN:HD22	2.21	0.49
1:B:34:ILE:HA	1:B:126:GLN:NE2	2.28	0.49
1:C:12:TRP:HE1	1:C:442:ASN:ND2	2.10	0.49
1:C:124:LEU:HD23	1:C:129:GLN:HE21	1.77	0.49
1:C:191:ILE:HD12	1:C:272:ALA:HB1	1.94	0.49
1:D:155:HIS:O	1:D:214:SER:OG	2.31	0.49
1:A:287:PRO:HD2	2:A:791:HOH:O	2.13	0.49
1:B:54:ALA:HA	1:B:410:TYR:OH	2.12	0.49
1:C:371:ARG:HD3	2:C:670:HOH:O	2.12	0.49
1:A:448:ARG:HD2	1:A:448:ARG:C	2.34	0.49
1:C:155:HIS:CD2	1:C:213:THR:HA	2.48	0.49
1:D:70:GLU:HB3	2:D:515:HOH:O	2.11	0.49
1:C:77:ARG:NH2	1:C:352:GLU:HG3	2.28	0.48
1:B:124:LEU:HD23	1:B:129:GLN:HE21	1.77	0.48
1:B:191:ILE:HD12	1:B:272:ALA:HB1	1.96	0.48
1:C:320:PRO:HD2	2:C:655:HOH:O	2.14	0.48
1:C:167:PRO:HD2	1:C:221:PRO:HA	1.95	0.48
1:A:54:ALA:HA	1:A:410:TYR:OH	2.14	0.48
1:B:167:PRO:HD2	1:B:221:PRO:HA	1.95	0.48
1:D:155:HIS:CD2	1:D:213:THR:HA	2.48	0.48
1:D:239:CYS:HA	2:D:754:HOH:O	2.13	0.48
1:A:359:ASP:OD2	1:A:368:ASP:HA	2.14	0.48
1:A:209:ARG:NH1	2:A:791:HOH:O	2.46	0.47
1:C:443:TRP:HZ3	2:C:467:HOH:O	1.97	0.47
1:D:359:ASP:OD2	1:D:368:ASP:HA	2.15	0.47
1:B:386:ILE:HB	2:B:799:HOH:O	2.13	0.47
1:B:316:ASN:C	1:B:316:ASN:HD22	2.22	0.47
1:D:12:TRP:HE1	1:D:442:ASN:ND2	2.11	0.47
1:D:26:GLN:HG2	2:D:620:HOH:O	2.15	0.47
1:D:54:ALA:HA	1:D:410:TYR:OH	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:124:LEU:HD23	1:D:129:GLN:HE21	1.80	0.47
1:B:145:GLN:N	2:B:472:HOH:O	2.47	0.47
1:D:216:GLN:NE2	2:D:711:HOH:O	2.46	0.47
1:B:201:HIS:CE1	2:B:492:HOH:O	2.66	0.46
1:C:34:ILE:HA	1:C:126:GLN:NE2	2.30	0.46
1:A:338:HIS:HD2	2:A:618:HOH:O	1.98	0.46
1:C:223:VAL:HG13	1:C:336:VAL:HG21	1.97	0.46
1:B:8:GLN:NE2	2:B:641:HOH:O	2.48	0.46
1:D:93:VAL:HG23	2:D:766:HOH:O	2.14	0.46
1:C:12:TRP:CD1	2:C:701:HOH:O	2.69	0.46
1:C:203:LEU:HB2	2:C:809:HOH:O	2.14	0.46
1:D:34:ILE:HA	1:D:126:GLN:NE2	2.31	0.46
1:A:13:GLY:HA2	1:A:73:ILE:CG1	2.43	0.45
1:D:13:GLY:HA2	1:D:73:ILE:CG1	2.45	0.45
1:B:293:ILE:HD13	1:B:293:ILE:HA	1.81	0.45
1:D:155:HIS:CD2	1:D:214:SER:H	2.34	0.45
1:A:34:ILE:HA	1:A:126:GLN:NE2	2.31	0.45
1:A:201:HIS:CE1	2:A:829:HOH:O	2.58	0.45
1:A:405:GLU:HB3	1:A:408:GLU:HB2	1.98	0.45
1:A:189:THR:O	1:A:193:VAL:HG23	2.16	0.45
1:A:62:GLU:HG3	2:A:492:HOH:O	2.16	0.45
1:A:290:MET:HE2	2:A:788:HOH:O	2.17	0.45
1:C:152:ARG:NH1	2:C:508:HOH:O	2.47	0.45
1:C:359:ASP:OD2	1:C:368:ASP:HA	2.17	0.45
1:B:287:PRO:HD2	2:B:823:HOH:O	2.15	0.45
1:C:13:GLY:HA2	1:C:73:ILE:CG1	2.46	0.45
1:D:127:ALA:O	1:D:130:ASP:HB2	2.17	0.45
1:D:298:MET:HE1	1:D:331:ARG:NH1	2.32	0.45
1:D:66:ARG:HG2	2:D:518:HOH:O	2.15	0.45
1:A:375:MET:HE3	1:A:434:TRP:CZ3	2.52	0.45
1:C:155:HIS:CD2	1:C:214:SER:H	2.34	0.45
1:B:74:ARG:HG3	2:B:794:HOH:O	2.16	0.45
1:B:172:PHE:CZ	1:B:245:LEU:HD11	2.52	0.45
1:B:359:ASP:OD2	1:B:368:ASP:HA	2.17	0.45
1:D:375:MET:HE3	1:D:434:TRP:CZ3	2.52	0.45
1:C:293:ILE:HD13	1:C:293:ILE:HA	1.83	0.44
1:C:375:MET:HE3	1:C:434:TRP:CZ3	2.53	0.44
1:D:191:ILE:HD12	1:D:272:ALA:HB1	1.98	0.44
1:A:77:ARG:HH21	1:A:352:GLU:HG3	1.83	0.44
1:D:77:ARG:NH2	1:D:352:GLU:HG3	2.32	0.44
1:D:316:ASN:ND2	1:D:318:GLY:H	2.15	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:396:MET:SD	2:D:791:HOH:O	2.61	0.44
1:D:167:PRO:HD2	1:D:221:PRO:HA	1.99	0.44
1:A:200:ALA:CB	2:A:807:HOH:O	2.65	0.44
1:B:140:ILE:O	1:B:144:VAL:HG23	2.17	0.44
1:B:259:TYR:CE2	1:B:274:VAL:HG11	2.53	0.44
1:B:436:ARG:NH1	2:B:795:HOH:O	2.51	0.44
1:C:121:HIS:HD2	2:C:586:HOH:O	2.00	0.44
1:A:293:ILE:HD13	1:A:293:ILE:HA	1.83	0.43
1:D:442:ASN:ND2	2:D:554:HOH:O	2.51	0.43
1:A:259:TYR:CE2	1:A:274:VAL:HG11	2.54	0.43
1:D:252:GLN:HB3	1:D:253:PRO:HD3	2.00	0.43
1:A:370:ARG:HD3	2:A:592:HOH:O	2.18	0.43
1:A:371:ARG:HD3	2:A:623:HOH:O	2.18	0.43
1:C:127:ALA:O	1:C:130:ASP:HB2	2.18	0.43
1:D:249:TRP:CD1	1:D:260:PRO:HD2	2.54	0.43
1:B:189:THR:O	1:B:193:VAL:HG23	2.18	0.43
1:A:200:ALA:HB2	2:A:807:HOH:O	2.17	0.43
1:B:249:TRP:CD1	1:B:260:PRO:HD2	2.54	0.43
1:C:79:SER:HA	1:C:118:THR:O	2.19	0.43
1:C:77:ARG:HH21	1:C:352:GLU:HG3	1.83	0.42
1:D:189:THR:O	1:D:193:VAL:HG23	2.19	0.42
1:D:259:TYR:CE2	1:D:274:VAL:HG11	2.54	0.42
1:A:249:TRP:CD1	1:A:260:PRO:HD2	2.54	0.42
1:A:429:LYS:O	1:A:432:TYR:HB3	2.20	0.42
1:B:375:MET:HE3	1:B:434:TRP:CZ3	2.54	0.42
1:C:405:GLU:HB3	1:C:408:GLU:HB2	2.01	0.42
1:D:304:ASN:HA	1:D:305:PRO:HD2	1.89	0.42
1:A:77:ARG:HH12	1:A:165:ASN:ND2	2.18	0.42
1:D:293:ILE:HD13	1:D:293:ILE:HA	1.81	0.42
1:B:144:VAL:O	1:B:148:GLU:HG3	2.20	0.42
1:B:77:ARG:HH21	1:B:352:GLU:HG3	1.84	0.42
1:B:331:ARG:NH2	2:B:576:HOH:O	2.52	0.42
1:C:422:ARG:NH1	1:D:430:GLU:OE1	2.53	0.42
1:D:172:PHE:CZ	1:D:245:LEU:HD11	2.55	0.42
1:D:249:TRP:CH2	2:D:627:HOH:O	2.70	0.42
1:C:249:TRP:CD1	1:C:260:PRO:HD2	2.55	0.42
1:D:140:ILE:O	1:D:144:VAL:HG23	2.19	0.42
1:B:422:ARG:HD3	1:C:433:TYR:CE2	2.54	0.42
1:D:144:VAL:O	1:D:148:GLU:HG3	2.20	0.42
1:C:144:VAL:O	1:C:148:GLU:HG3	2.20	0.42
1:B:13:GLY:HA2	1:B:73:ILE:CG1	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:47:ASN:HD22	1:C:447:ARG:HH12	1.67	0.41
1:B:429:LYS:O	1:B:432:TYR:HB3	2.20	0.41
1:C:304:ASN:HA	1:C:305:PRO:HD2	1.88	0.41
1:D:107:LEU:HD12	1:D:107:LEU:HA	1.89	0.41
1:D:379:LEU:HD23	1:D:379:LEU:HA	1.90	0.41
1:A:249:TRP:HZ3	2:A:656:HOH:O	2.00	0.41
1:B:155:HIS:CD2	1:B:214:SER:H	2.37	0.41
1:D:197:LEU:CD1	2:D:761:HOH:O	2.59	0.41
1:A:155:HIS:CD2	1:A:214:SER:H	2.38	0.41
1:B:31:GLY:O	1:B:83:PRO:HB2	2.20	0.41
1:B:175:ASN:ND2	1:B:193:VAL:HG21	2.35	0.41
1:A:430:GLU:OE1	1:D:422:ARG:NH1	2.53	0.41
1:C:259:TYR:CE2	1:C:274:VAL:HG11	2.55	0.41
1:A:31:GLY:O	1:A:83:PRO:HB2	2.20	0.41
1:A:160:HIS:CD2	2:A:483:HOH:O	2.71	0.41
1:B:77:ARG:HH12	1:B:165:ASN:ND2	2.18	0.41
1:C:154:PHE:O	1:C:155:HIS:C	2.64	0.41
1:D:250:PHE:HD1	2:D:761:HOH:O	1.99	0.41
1:B:127:ALA:O	1:B:130:ASP:HB2	2.21	0.41
1:C:65:ILE:HA	1:C:68:MET:HG2	2.02	0.41
1:C:77:ARG:HH12	1:C:165:ASN:ND2	2.19	0.41
1:A:65:ILE:HA	1:A:68:MET:HG2	2.02	0.41
1:A:81:SER:O	1:A:84:ARG:HB2	2.21	0.41
1:A:422:ARG:HD3	1:B:433:TYR:CE2	2.55	0.41
1:B:437:ASN:ND2	2:B:788:HOH:O	2.52	0.41
1:C:88:ASN:ND2	1:C:91:GLY:N	2.67	0.41
1:A:155:HIS:HD2	1:A:213:THR:HA	1.86	0.41
1:A:175:ASN:ND2	1:A:193:VAL:HG21	2.36	0.41
1:C:88:ASN:HA	2:C:672:HOH:O	2.21	0.41
1:C:175:ASN:ND2	1:C:193:VAL:HG21	2.36	0.41
1:C:299:SER:HB2	1:C:314:GLU:CG	2.49	0.41
1:D:299:SER:HB2	1:D:314:GLU:CG	2.48	0.41
1:D:316:ASN:HD22	1:D:318:GLY:H	1.69	0.41
1:D:429:LYS:O	1:D:432:TYR:HB3	2.21	0.41
1:A:121:HIS:CD2	2:A:499:HOH:O	2.62	0.41
1:C:189:THR:O	1:C:193:VAL:HG23	2.21	0.41
1:A:290:MET:HG3	1:A:349:TYR:CE1	2.56	0.40
1:A:442:ASN:HD22	1:A:442:ASN:HA	1.74	0.40
1:B:155:HIS:HD2	1:B:213:THR:HA	1.87	0.40
1:D:77:ARG:HH21	1:D:352:GLU:HG3	1.86	0.40
1:A:47:ASN:ND2	1:B:447:ARG:HH22	2.19	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:316:ASN:ND2	1:A:318:GLY:H	2.18	0.40
1:B:442:ASN:HD22	1:B:442:ASN:HA	1.74	0.40
1:D:24:ALA:HB1	1:D:27:GLU:CB	2.52	0.40
1:D:102:HIS:CD2	1:D:157:LYS:HZ2	2.39	0.40
1:C:24:ALA:HB1	1:C:27:GLU:CB	2.51	0.40
1:D:154:PHE:O	1:D:155:HIS:C	2.64	0.40
1:C:140:ILE:O	1:C:144:VAL:HG23	2.21	0.40
1:C:144:VAL:CG2	2:C:809:HOH:O	2.69	0.40
1:C:310:LEU:HD12	1:C:310:LEU:HA	1.95	0.40
1:C:316:ASN:ND2	1:C:318:GLY:H	2.18	0.40
1:D:77:ARG:HH12	1:D:165:ASN:ND2	2.20	0.40
1:D:79:SER:HA	1:D:118:THR:O	2.21	0.40
1:D:81:SER:O	1:D:84:ARG:HB2	2.22	0.40
1:D:175:ASN:ND2	1:D:193:VAL:HG21	2.37	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	445/447 (100%)	424 (95%)	19 (4%)	2 (0%)	30	43
1	B	445/447 (100%)	426 (96%)	17 (4%)	2 (0%)	30	43
1	C	445/447 (100%)	426 (96%)	17 (4%)	2 (0%)	30	43
1	D	445/447 (100%)	426 (96%)	17 (4%)	2 (0%)	30	43
All	All	1780/1788 (100%)	1702 (96%)	70 (4%)	8 (0%)	30	43

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	155	HIS

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Mol	Chain	Res	Type
1	B	155	HIS
1	C	155	HIS
1	D	155	HIS
1	A	91	GLY
1	B	91	GLY
1	C	91	GLY
1	D	91	GLY

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	383/383 (100%)	363 (95%)	20 (5%)	21	36
1	B	383/383 (100%)	364 (95%)	19 (5%)	22	38
1	C	383/383 (100%)	362 (94%)	21 (6%)	19	34
1	D	383/383 (100%)	363 (95%)	20 (5%)	21	36
All	All	1532/1532 (100%)	1452 (95%)	80 (5%)	21	36

All (80) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	THR
1	A	73	ILE
1	A	90	ASP
1	A	93	VAL
1	A	96	GLU
1	A	187	LEU
1	A	197	LEU
1	A	206	ARG
1	A	223	VAL
1	A	227	VAL
1	A	249	TRP
1	A	293	ILE
1	A	310	LEU
1	A	316	ASN

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Mol	Chain	Res	Type
1	A	328	VAL
1	A	333	LEU
1	A	365	LYS
1	A	399	SER
1	A	437	ASN
1	A	448	ARG
1	B	2	THR
1	B	73	ILE
1	B	90	ASP
1	B	93	VAL
1	B	96	GLU
1	B	187	LEU
1	B	197	LEU
1	B	206	ARG
1	B	223	VAL
1	B	227	VAL
1	B	249	TRP
1	B	293	ILE
1	B	310	LEU
1	B	328	VAL
1	B	333	LEU
1	B	365	LYS
1	B	399	SER
1	B	437	ASN
1	B	448	ARG
1	C	2	THR
1	C	73	ILE
1	C	90	ASP
1	C	93	VAL
1	C	96	GLU
1	C	187	LEU
1	C	197	LEU
1	C	206	ARG
1	C	223	VAL
1	C	227	VAL
1	C	249	TRP
1	C	293	ILE
1	C	310	LEU
1	C	316	ASN
1	C	328	VAL
1	C	333	LEU
1	C	365	LYS

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Mol	Chain	Res	Type
1	C	399	SER
1	C	405	GLU
1	C	437	ASN
1	C	448	ARG
1	D	2	THR
1	D	73	ILE
1	D	90	ASP
1	D	93	VAL
1	D	96	GLU
1	D	187	LEU
1	D	197	LEU
1	D	206	ARG
1	D	223	VAL
1	D	227	VAL
1	D	249	TRP
1	D	293	ILE
1	D	310	LEU
1	D	316	ASN
1	D	328	VAL
1	D	333	LEU
1	D	365	LYS
1	D	399	SER
1	D	437	ASN
1	D	448	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (94) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	20	GLN
1	A	40	HIS
1	A	47	ASN
1	A	88	ASN
1	A	95	GLN
1	A	102	HIS
1	A	121	HIS
1	A	126	GLN
1	A	129	GLN
1	A	155	HIS
1	A	201	HIS
1	A	216	GLN
1	A	252	GLN
1	A	261	GLN

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Mol	Chain	Res	Type
1	A	294	ASN
1	A	311	GLN
1	A	316	ASN
1	A	338	HIS
1	A	353	ASN
1	A	381	GLN
1	A	387	HIS
1	A	391	HIS
1	A	442	ASN
1	B	8	GLN
1	B	20	GLN
1	B	40	HIS
1	B	47	ASN
1	B	52	ASN
1	B	88	ASN
1	B	95	GLN
1	B	102	HIS
1	B	111	ASN
1	B	121	HIS
1	B	126	GLN
1	B	129	GLN
1	B	155	HIS
1	B	175	ASN
1	B	201	HIS
1	B	216	GLN
1	B	252	GLN
1	B	261	GLN
1	B	294	ASN
1	B	311	GLN
1	B	316	ASN
1	B	338	HIS
1	B	353	ASN
1	B	377	GLN
1	B	381	GLN
1	B	387	HIS
1	B	403	ASN
1	B	437	ASN
1	B	442	ASN
1	C	20	GLN
1	C	40	HIS
1	C	47	ASN
1	C	88	ASN

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Mol	Chain	Res	Type
1	C	95	GLN
1	C	102	HIS
1	C	111	ASN
1	C	126	GLN
1	C	129	GLN
1	C	155	HIS
1	C	201	HIS
1	C	216	GLN
1	C	246	HIS
1	C	252	GLN
1	C	261	GLN
1	C	311	GLN
1	C	316	ASN
1	C	338	HIS
1	C	381	GLN
1	C	387	HIS
1	C	442	ASN
1	D	20	GLN
1	D	40	HIS
1	D	47	ASN
1	D	88	ASN
1	D	95	GLN
1	D	102	HIS
1	D	111	ASN
1	D	126	GLN
1	D	129	GLN
1	D	155	HIS
1	D	201	HIS
1	D	216	GLN
1	D	252	GLN
1	D	261	GLN
1	D	311	GLN
1	D	316	ASN
1	D	338	HIS
1	D	353	ASN
1	D	381	GLN
1	D	387	HIS
1	D	442	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 oligosaccharides 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

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.