



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 05:52 PM UTC

PDB ID : 2P8Q / pdb_00002p8q
Title : Crystal Structure of human Importin beta bound to the Snurportin1 IBB-domain
Authors : Mitrousis, G.; Cingolani, G.
Deposited on : 2007-03-22
Resolution : 2.35 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

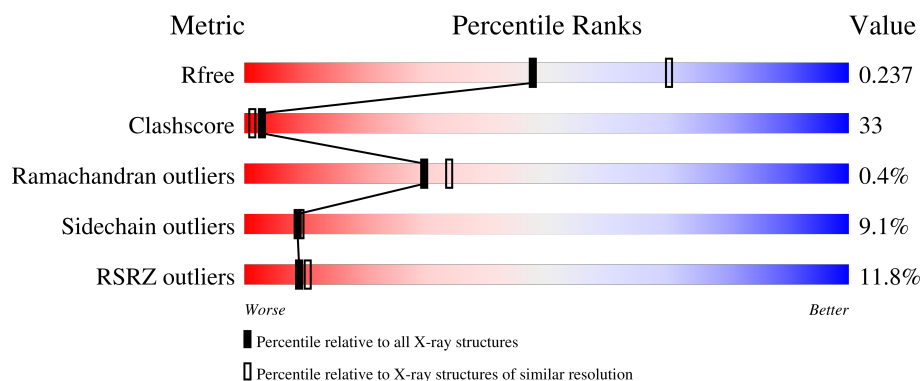
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.35 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	1596 (2.36-2.36)
Clashscore	190562	1663 (2.36-2.36)
Ramachandran outliers	187476	1646 (2.36-2.36)
Sidechain outliers	187428	1646 (2.36-2.36)
RSRZ outliers	180081	1598 (2.36-2.36)

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	876	11% 60% 34% 5%
2	B	40	30% 32% 50% 10% 5%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 7471 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 Importin beta-1 subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	873	Total	C	N	O	S	0	0	0
			6782	4273	1136	1326	47			

- Molecule 2 is a protein called Snurportin-1.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	B	39	Total	C	N	O	0	0	0
			344	210	73	61			

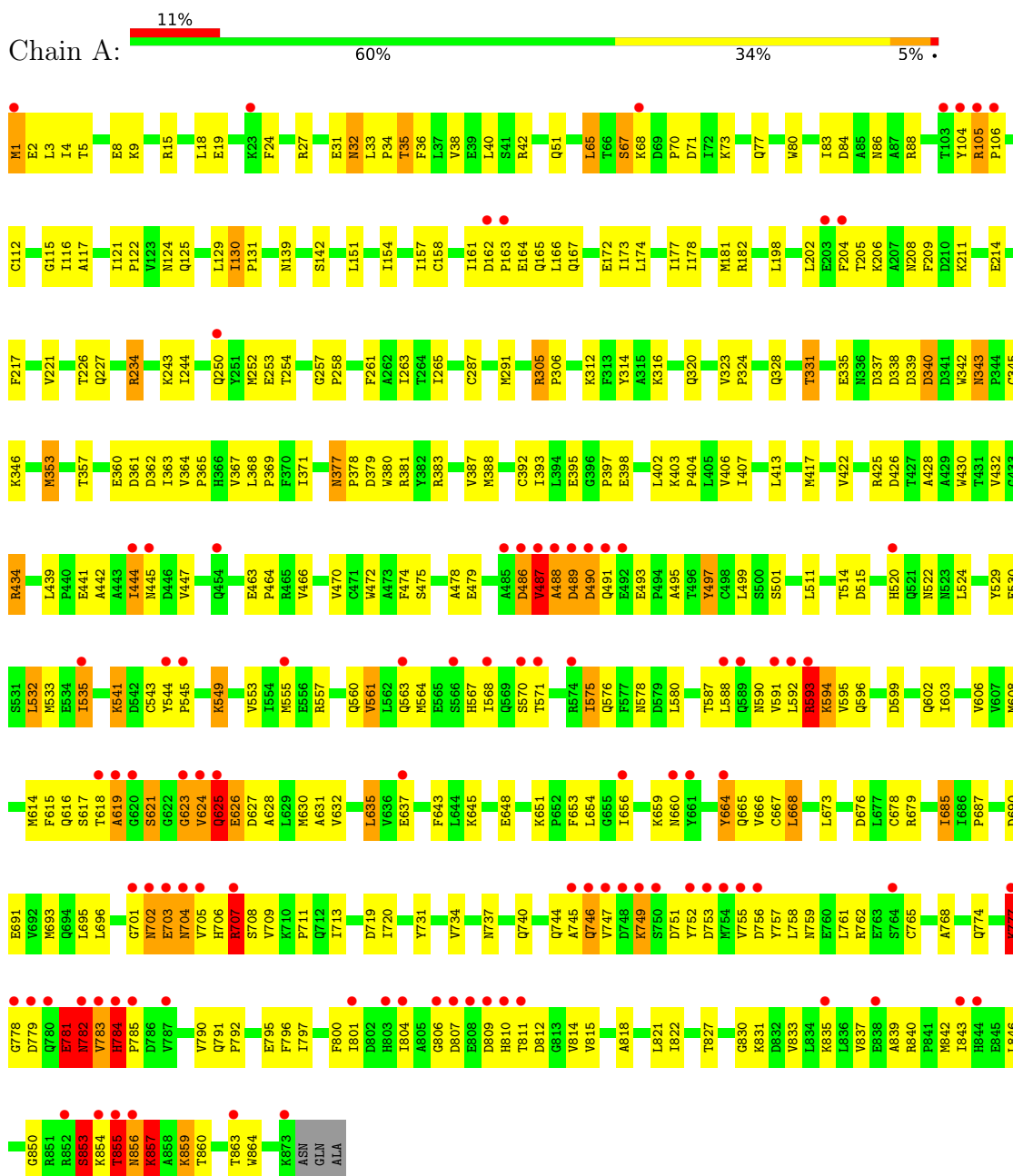
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	332	Total	O	0	0
			332	332		
3	B	13	Total	O	0	0
			13	13		

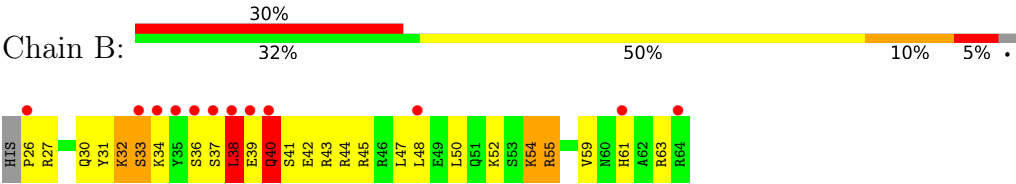
3 Residue-property plots [i](#)

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: Importin beta-1 subunit



● Molecule 2: Snurportin-1



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	64.75Å 97.89Å 84.29Å 90.00° 90.86° 90.00°	Depositor
Resolution (Å)	40.00 – 2.35 40.00 – 2.35	Depositor EDS
% Data completeness (in resolution range)	98.7 (40.00-2.35) 97.3 (40.00-2.35)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	0.08	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.42 (at 2.31Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.227 , 0.250 0.236 , 0.237	Depositor DCC
R_{free} test set	4338 reflections (9.44%)	wwPDB-VP
Wilson B-factor (Å ²)	33.4	Xtriage
Anisotropy	0.390	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 45.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.027 for h,-k,-l	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	7471	wwPDB-VP
Average B, all atoms (Å ²)	47.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.22% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	0.41	0/6893	0.83	5/9360 (0.1%)
2	B	0.29	0/348	0.79	0/458
All	All	0.41	0/7241	0.83	5/9818 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	24
2	B	0	2
All	All	0	26

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	575	ILE	N-CA-C	6.32	116.48	110.42
1	A	753	ASP	N-CA-C	-5.53	106.48	113.18
1	A	784	HIS	CA-C-N	5.36	127.53	121.04
1	A	784	HIS	C-N-CA	5.36	127.53	121.04
1	A	561	VAL	CB-CA-C	-5.02	105.54	111.97

There are no chirality outliers.

All (26) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	487	VAL	Peptide
1	A	488	ALA	Peptide
1	A	489	ASP	Peptide
1	A	490	ASP	Peptide

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Mol	Chain	Res	Type	Group
1	A	593	ARG	Peptide
1	A	619	ALA	Peptide
1	A	623	GLY	Peptide
1	A	625	GLN	Peptide
1	A	701	GLY	Peptide
1	A	702	ASN	Peptide
1	A	703	GLU	Peptide
1	A	704	ASN	Peptide
1	A	707	ARG	Peptide
1	A	749	LYS	Peptide
1	A	756	ASP	Peptide
1	A	777	LYS	Peptide
1	A	781	GLU	Peptide
1	A	782	ASN	Peptide
1	A	783	VAL	Peptide
1	A	784	HIS	Peptide
1	A	830	GLY	Peptide
1	A	853	SER	Peptide
1	A	855	THR	Peptide
1	A	857	LYS	Peptide
2	B	38	LEU	Peptide
2	B	40	GLN	Peptide

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	6782	0	6781	439	0
2	B	344	0	359	46	0
3	A	332	0	0	56	0
3	B	13	0	0	4	0
All	All	7471	0	7140	464	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 33.

All (464) 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:702:ASN:CB	1:A:703:GLU:HG3	1.47	1.41
1:A:702:ASN:HB3	1:A:703:GLU:CG	1.48	1.40
2:B:37:SER:C	2:B:38:LEU:HD13	1.48	1.36
1:A:316:LYS:HD2	3:A:1193:HOH:O	1.40	1.21
1:A:702:ASN:O	1:A:705:VAL:HG23	1.37	1.19
1:A:707:ARG:HD2	1:A:757:TYR:CD1	1.78	1.18
1:A:397:PRO:HB2	1:A:402:LEU:HD11	1.29	1.14
1:A:593:ARG:HG3	1:A:593:ARG:HH11	1.11	1.13
1:A:777:LYS:HG2	1:A:778:GLY:H	1.06	1.12
1:A:68:LYS:H	1:A:68:LYS:HD2	1.16	1.10
1:A:105:ARG:HB3	1:A:106:PRO:CD	1.80	1.10
1:A:860:THR:O	1:A:863:THR:HG22	1.51	1.10
1:A:856:ASN:O	1:A:857:LYS:HG2	1.53	1.07
1:A:783:VAL:C	1:A:785:PRO:HD3	1.79	1.07
1:A:514:THR:HG21	1:A:557:ARG:HH12	1.19	1.05
1:A:777:LYS:HG2	1:A:778:GLY:N	1.55	1.05
2:B:38:LEU:HD13	2:B:38:LEU:N	1.66	1.05
1:A:105:ARG:HB3	1:A:106:PRO:HD3	1.36	1.04
1:A:708:SER:HB2	3:A:1203:HOH:O	1.56	1.03
1:A:320:GLN:HG3	3:A:879:HOH:O	1.57	1.03
2:B:37:SER:C	2:B:38:LEU:CD1	2.30	1.03
1:A:856:ASN:C	1:A:857:LYS:HG2	1.79	1.02
1:A:619:ALA:HB2	1:A:623:GLY:HA3	1.42	1.02
1:A:488:ALA:HB1	1:A:489:ASP:HA	1.38	1.02
1:A:783:VAL:O	1:A:785:PRO:HD3	1.59	1.01
1:A:855:THR:CG2	1:A:856:ASN:H	1.73	1.01
1:A:342:TRP:NE1	2:B:26:PRO:HD2	1.76	1.00
1:A:608:MET:HE2	1:A:635:LEU:HD23	1.37	1.00
1:A:619:ALA:HA	1:A:621:SER:H	1.27	0.99
1:A:511:LEU:O	1:A:514:THR:HG22	1.61	0.99
1:A:855:THR:HG22	1:A:856:ASN:N	1.57	0.99
1:A:855:THR:HG22	1:A:856:ASN:H	0.86	0.99
1:A:702:ASN:HD22	1:A:703:GLU:HG2	1.24	0.99
1:A:478:ALA:HB1	1:A:535:ILE:HD13	1.42	0.99
1:A:342:TRP:CD1	2:B:26:PRO:HD2	1.96	0.99
1:A:593:ARG:HH11	1:A:593:ARG:CG	1.75	0.99
1:A:778:GLY:HA3	1:A:781:GLU:OE2	1.62	0.98
1:A:707:ARG:CD	1:A:757:TYR:CD1	2.47	0.97
1:A:702:ASN:ND2	1:A:703:GLU:HG2	1.80	0.97
1:A:784:HIS:N	1:A:785:PRO:HD3	1.79	0.97
1:A:154:ILE:HG21	1:A:177:ILE:HD11	1.44	0.96
1:A:162:ASP:OD2	1:A:163:PRO:HD2	1.67	0.95

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:544:TYR:N	1:A:545:PRO:HD2	1.82	0.94
1:A:857:LYS:HB3	1:A:860:THR:OG1	1.66	0.94
1:A:560:GLN:HG2	1:A:564:MET:HE2	1.47	0.93
1:A:124:ASN:HB3	3:A:1185:HOH:O	1.68	0.93
1:A:342:TRP:CD1	2:B:26:PRO:CD	2.53	0.92
1:A:707:ARG:HD3	1:A:757:TYR:CD2	2.06	0.90
1:A:807:ASP:HB3	1:A:809:ASP:OD1	1.72	0.90
1:A:377:ASN:ND2	1:A:379:ASP:H	1.69	0.88
1:A:785:PRO:HD2	3:A:1189:HOH:O	1.75	0.86
1:A:614:MET:O	1:A:618:THR:HG22	1.77	0.85
1:A:206:LYS:HB2	3:A:1170:HOH:O	1.77	0.84
1:A:514:THR:CG2	1:A:557:ARG:HH12	1.91	0.83
1:A:707:ARG:HD3	1:A:757:TYR:CG	2.13	0.83
1:A:234:ARG:HD3	3:A:1171:HOH:O	1.78	0.83
1:A:369:PRO:HG2	3:A:980:HOH:O	1.79	0.82
1:A:323:VAL:N	1:A:324:PRO:HD2	1.94	0.82
1:A:777:LYS:CG	1:A:778:GLY:N	2.42	0.81
1:A:88:ARG:HH12	1:A:125:GLN:HG2	1.42	0.81
1:A:678:CYS:SG	1:A:720:ILE:HD13	2.20	0.81
1:A:685:ILE:HD13	1:A:685:ILE:O	1.79	0.81
1:A:707:ARG:CD	1:A:757:TYR:CG	2.64	0.81
1:A:115:GLY:HA3	3:A:1196:HOH:O	1.78	0.81
1:A:331:THR:CG2	3:A:1174:HOH:O	2.29	0.80
1:A:618:THR:HG23	1:A:619:ALA:N	1.97	0.80
1:A:35:THR:HG23	3:A:1187:HOH:O	1.80	0.80
1:A:707:ARG:HD2	1:A:757:TYR:CE1	2.16	0.80
1:A:857:LYS:CB	1:A:860:THR:OG1	2.30	0.80
1:A:478:ALA:CB	1:A:535:ILE:HD13	2.11	0.80
1:A:707:ARG:CD	1:A:757:TYR:CE1	2.66	0.79
1:A:15:ARG:O	1:A:19:GLU:HG2	1.81	0.79
1:A:860:THR:C	1:A:863:THR:HG22	2.06	0.79
1:A:702:ASN:HD22	1:A:703:GLU:CG	1.97	0.78
1:A:377:ASN:HD22	1:A:379:ASP:H	1.28	0.78
1:A:162:ASP:OD2	1:A:163:PRO:CD	2.31	0.78
1:A:594:LYS:HG3	1:A:594:LYS:O	1.84	0.78
1:A:744:GLN:O	1:A:746:GLN:HG3	1.84	0.78
1:A:35:THR:CG2	3:A:1187:HOH:O	2.30	0.78
1:A:835:LYS:HG3	3:A:1204:HOH:O	1.83	0.78
1:A:488:ALA:HB3	1:A:489:ASP:OD1	1.83	0.78
1:A:530:GLU:OE1	2:B:38:LEU:CD2	2.32	0.77
1:A:734:VAL:HG23	3:A:941:HOH:O	1.83	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:488:ALA:CB	1:A:489:ASP:HA	2.15	0.77
1:A:543:CYS:C	1:A:545:PRO:HD2	2.10	0.77
1:A:783:VAL:O	1:A:785:PRO:CD	2.33	0.77
1:A:599:ASP:O	1:A:603:ILE:HD13	1.85	0.76
1:A:530:GLU:OE1	2:B:38:LEU:HD22	1.85	0.76
1:A:860:THR:O	1:A:863:THR:CG2	2.32	0.76
1:A:112:CYS:O	1:A:116:ILE:HD13	1.86	0.76
1:A:377:ASN:HD22	1:A:378:PRO:N	1.84	0.76
1:A:174:LEU:O	1:A:178:ILE:HD13	1.85	0.75
1:A:593:ARG:HG3	1:A:593:ARG:NH1	1.94	0.75
1:A:619:ALA:CB	1:A:623:GLY:HA3	2.15	0.75
1:A:173:ILE:O	1:A:177:ILE:HD13	1.85	0.75
1:A:855:THR:CG2	1:A:856:ASN:N	2.30	0.75
1:A:441:GLU:HG3	3:A:962:HOH:O	1.87	0.74
1:A:778:GLY:CA	1:A:781:GLU:OE2	2.35	0.74
1:A:71:ASP:OD2	1:A:704:ASN:HB2	1.87	0.74
1:A:104:TYR:HB2	3:A:975:HOH:O	1.87	0.74
1:A:486:ASP:CG	1:A:486:ASP:O	2.30	0.74
1:A:857:LYS:HA	1:A:860:THR:H	1.53	0.74
1:A:487:VAL:HG23	1:A:488:ALA:O	1.87	0.74
1:A:511:LEU:O	1:A:514:THR:CG2	2.36	0.74
1:A:719:ASP:OD1	2:B:55:ARG:HD3	1.88	0.73
2:B:37:SER:O	2:B:38:LEU:CD1	2.35	0.73
1:A:27:ARG:NH2	3:A:950:HOH:O	2.22	0.73
1:A:177:ILE:HG22	1:A:181:MET:HE2	1.71	0.72
1:A:407:ILE:HD11	1:A:442:ALA:HA	1.71	0.72
1:A:664:TYR:CZ	1:A:706:HIS:CE1	2.77	0.72
1:A:444:ILE:HG22	1:A:444:ILE:O	1.88	0.72
1:A:593:ARG:CG	1:A:593:ARG:NH1	2.45	0.72
1:A:343:ASN:C	1:A:343:ASN:HD22	1.98	0.72
1:A:368:LEU:N	1:A:369:PRO:HD2	2.05	0.72
3:A:1207:HOH:O	2:B:31:TYR:CD1	2.42	0.71
1:A:342:TRP:CE2	2:B:26:PRO:HD2	2.24	0.71
1:A:71:ASP:HB2	1:A:704:ASN:HD22	1.54	0.71
1:A:130:ILE:N	1:A:131:PRO:HD2	2.06	0.71
1:A:342:TRP:CD1	2:B:26:PRO:HD3	2.25	0.71
1:A:544:TYR:N	1:A:545:PRO:CD	2.52	0.70
1:A:105:ARG:HB3	1:A:106:PRO:HD2	1.74	0.70
1:A:618:THR:HG23	1:A:619:ALA:H	1.57	0.70
1:A:707:ARG:HD3	1:A:757:TYR:CE2	2.25	0.70
1:A:800:PHE:O	1:A:804:ILE:HG12	1.92	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:328:GLN:O	1:A:331:THR:HB	1.92	0.70
1:A:422:VAL:CG2	3:A:1180:HOH:O	2.40	0.69
1:A:514:THR:HG21	1:A:557:ARG:NH1	2.02	0.69
1:A:608:MET:HE3	1:A:643:PHE:HE1	1.58	0.68
1:A:535:ILE:HD12	1:A:535:ILE:O	1.93	0.68
1:A:364:VAL:N	1:A:365:PRO:HD2	2.09	0.67
1:A:676:ASP:HA	1:A:679:ARG:NH1	2.10	0.67
1:A:428:ALA:O	1:A:432:VAL:HG23	1.95	0.67
1:A:181:MET:HE1	1:A:198:LEU:HD22	1.78	0.66
1:A:702:ASN:ND2	1:A:703:GLU:CG	2.56	0.66
2:B:37:SER:O	2:B:38:LEU:HD12	1.96	0.66
1:A:702:ASN:CB	1:A:703:GLU:CG	2.33	0.66
1:A:68:LYS:HD2	1:A:68:LYS:N	2.00	0.66
1:A:693:MET:CE	1:A:720:ILE:HG21	2.26	0.66
1:A:121:ILE:N	1:A:122:PRO:HD2	2.11	0.66
1:A:1:MET:HG2	1:A:2:GLU:H	1.60	0.66
1:A:696:LEU:HD22	1:A:713:ILE:HD12	1.78	0.65
1:A:745:ALA:C	1:A:746:GLN:HG3	2.21	0.65
1:A:167:GLN:HG3	1:A:204:PHE:HB2	1.79	0.65
1:A:252:MET:HE2	1:A:252:MET:HA	1.76	0.65
1:A:784:HIS:N	1:A:785:PRO:CD	2.52	0.65
1:A:204:PHE:CD2	3:A:1172:HOH:O	2.49	0.65
1:A:702:ASN:O	1:A:705:VAL:CG2	2.31	0.65
1:A:67:SER:HB2	3:A:1161:HOH:O	1.97	0.64
2:B:41:SER:O	2:B:45:ARG:HG3	1.97	0.64
1:A:744:GLN:O	1:A:746:GLN:CG	2.46	0.64
1:A:18:LEU:C	1:A:18:LEU:HD23	2.23	0.64
1:A:388:MET:HE3	1:A:392:CYS:SG	2.37	0.64
1:A:856:ASN:C	1:A:857:LYS:CG	2.62	0.64
1:A:811:THR:CG2	1:A:814:VAL:HG23	2.27	0.64
1:A:105:ARG:CB	1:A:106:PRO:CD	2.62	0.63
1:A:812:ASP:OD2	1:A:854:LYS:HB3	1.98	0.63
1:A:857:LYS:H	1:A:859:LYS:HD3	1.64	0.63
1:A:626:GLU:C	1:A:626:GLU:OE1	2.42	0.63
1:A:619:ALA:HA	1:A:621:SER:N	2.08	0.63
3:A:1073:HOH:O	2:B:26:PRO:HG2	1.98	0.62
1:A:618:THR:O	1:A:621:SER:HB2	2.00	0.62
1:A:377:ASN:HD22	1:A:377:ASN:C	2.07	0.62
1:A:501:SER:HB3	3:A:1121:HOH:O	2.00	0.62
1:A:664:TYR:CE1	1:A:706:HIS:ND1	2.68	0.61
1:A:204:PHE:HD2	3:A:1172:HOH:O	1.83	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:533:MET:HE1	2:B:38:LEU:HG	1.80	0.61
1:A:856:ASN:O	1:A:857:LYS:CG	2.42	0.61
1:A:227:GLN:NE2	1:A:263:ILE:HD12	2.14	0.61
1:A:859:LYS:HG2	1:A:860:THR:N	2.15	0.61
3:A:1207:HOH:O	2:B:31:TYR:HD1	1.81	0.61
1:A:588:LEU:HA	1:A:591:VAL:HG22	1.82	0.61
1:A:850:GLY:O	1:A:859:LYS:HA	2.00	0.60
1:A:323:VAL:N	1:A:324:PRO:CD	2.64	0.60
1:A:594:LYS:O	1:A:594:LYS:CG	2.49	0.60
1:A:511:LEU:C	1:A:514:THR:HG22	2.25	0.60
1:A:257:GLY:N	1:A:258:PRO:HD2	2.16	0.60
1:A:853:SER:HA	1:A:854:LYS:C	2.27	0.60
1:A:744:GLN:O	1:A:746:GLN:NE2	2.32	0.60
1:A:204:PHE:HA	3:A:1170:HOH:O	2.01	0.59
1:A:261:PHE:O	1:A:265:ILE:HD13	2.02	0.59
1:A:464:PRO:HB2	1:A:522:ASN:HD22	1.68	0.59
1:A:71:ASP:HB2	1:A:704:ASN:ND2	2.16	0.59
1:A:343:ASN:ND2	1:A:346:LYS:H	2.00	0.59
1:A:608:MET:HE3	1:A:643:PHE:CE1	2.37	0.59
1:A:702:ASN:HB3	1:A:703:GLU:CB	2.28	0.59
1:A:178:ILE:HG21	1:A:217:PHE:CE2	2.37	0.59
1:A:533:MET:HG2	1:A:590:ASN:HD22	1.68	0.59
1:A:533:MET:HE1	2:B:38:LEU:CG	2.32	0.59
1:A:668:LEU:HD13	1:A:709:VAL:HG22	1.84	0.59
2:B:31:TYR:CE2	2:B:32:LYS:HD2	2.38	0.59
1:A:693:MET:HE1	1:A:720:ILE:HG21	1.85	0.58
1:A:762:ARG:CZ	1:A:804:ILE:HD12	2.33	0.58
1:A:664:TYR:CE1	1:A:706:HIS:CE1	2.92	0.58
1:A:205:THR:HA	1:A:208:ASN:HD22	1.67	0.58
1:A:441:GLU:CG	3:A:962:HOH:O	2.48	0.58
1:A:618:THR:CG2	3:A:1168:HOH:O	2.50	0.58
1:A:665:GLN:OE1	1:A:665:GLN:HA	2.03	0.58
1:A:815:VAL:HG13	1:A:846:LEU:HD11	1.84	0.58
1:A:422:VAL:HG23	3:A:897:HOH:O	2.04	0.58
1:A:860:THR:HA	1:A:863:THR:HG22	1.86	0.57
1:A:174:LEU:HD22	1:A:178:ILE:HD11	1.86	0.57
1:A:676:ASP:HA	1:A:679:ARG:HH12	1.69	0.57
1:A:618:THR:HG21	3:A:1168:HOH:O	2.03	0.57
1:A:571:THR:O	1:A:575:ILE:HG12	2.04	0.57
1:A:664:TYR:O	1:A:668:LEU:HB2	2.05	0.57
1:A:751:ASP:OD1	1:A:752:TYR:N	2.38	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:164:GLU:C	3:A:1175:HOH:O	2.48	0.57
1:A:860:THR:CA	1:A:863:THR:HG22	2.34	0.57
1:A:397:PRO:CB	1:A:402:LEU:HD11	2.18	0.57
1:A:364:VAL:N	1:A:365:PRO:CD	2.67	0.56
1:A:618:THR:CG2	1:A:619:ALA:N	2.67	0.56
1:A:653:PHE:HA	1:A:656:ILE:HG22	1.86	0.56
1:A:18:LEU:HD23	1:A:18:LEU:O	2.05	0.56
2:B:48:LEU:CD2	3:B:66:HOH:O	2.53	0.56
1:A:840:ARG:HB2	1:A:843:ILE:HD12	1.88	0.56
1:A:544:TYR:OH	1:A:596:GLN:HG3	2.05	0.56
1:A:783:VAL:HG22	1:A:784:HIS:H	1.71	0.56
1:A:533:MET:CG	1:A:587:THR:HA	2.36	0.56
1:A:182:ARG:HB3	3:A:1117:HOH:O	2.04	0.55
1:A:863:THR:HG23	1:A:864:TRP:N	2.20	0.55
1:A:32:ASN:HD22	1:A:34:PRO:HD2	1.71	0.55
1:A:305:ARG:CB	1:A:305:ARG:HH11	2.20	0.55
1:A:234:ARG:CD	3:A:1171:HOH:O	2.44	0.55
1:A:762:ARG:NH1	1:A:804:ILE:HD12	2.21	0.55
1:A:80:TRP:O	1:A:88:ARG:HD3	2.07	0.55
1:A:162:ASP:OD2	1:A:163:PRO:N	2.40	0.55
1:A:161:ILE:HG21	1:A:166:LEU:CD1	2.37	0.55
1:A:157:ILE:O	1:A:161:ILE:HG22	2.07	0.54
1:A:614:MET:O	1:A:618:THR:CG2	2.52	0.54
1:A:130:ILE:N	1:A:131:PRO:CD	2.70	0.54
1:A:818:ALA:O	1:A:822:ILE:HG12	2.06	0.54
1:A:88:ARG:HH12	1:A:125:GLN:CG	2.15	0.54
1:A:615:PHE:HB3	1:A:653:PHE:CE1	2.42	0.54
1:A:488:ALA:CB	1:A:489:ASP:OD1	2.56	0.54
1:A:105:ARG:CB	1:A:106:PRO:HD3	2.24	0.54
1:A:226:THR:O	1:A:234:ARG:HG2	2.07	0.54
1:A:560:GLN:O	1:A:564:MET:HG3	2.07	0.54
1:A:590:ASN:O	1:A:593:ARG:HB2	2.07	0.54
1:A:161:ILE:HD13	1:A:166:LEU:HG	1.90	0.54
1:A:860:THR:HA	1:A:863:THR:CG2	2.38	0.54
1:A:257:GLY:N	1:A:258:PRO:CD	2.71	0.53
1:A:514:THR:OG1	1:A:529:TYR:CE2	2.60	0.53
1:A:853:SER:HA	1:A:854:LYS:O	2.08	0.53
1:A:65:LEU:HD13	1:A:116:ILE:CD1	2.39	0.53
1:A:335:GLU:HB2	3:A:985:HOH:O	2.08	0.53
1:A:368:LEU:N	1:A:369:PRO:CD	2.72	0.53
1:A:497:TYR:CZ	1:A:499:LEU:HB2	2.44	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:530:GLU:OE1	2:B:38:LEU:HD21	2.05	0.53
1:A:795:GLU:HB3	3:A:907:HOH:O	2.09	0.53
1:A:422:VAL:HG23	3:A:1180:HOH:O	2.07	0.53
1:A:791:GLN:N	1:A:792:PRO:HD2	2.24	0.52
1:A:702:ASN:HB3	1:A:703:GLU:HG3	0.62	0.52
1:A:520:HIS:HB3	3:A:901:HOH:O	2.09	0.52
1:A:762:ARG:HD3	1:A:804:ILE:HD12	1.90	0.52
1:A:807:ASP:O	1:A:810:HIS:CD2	2.62	0.52
1:A:702:ASN:CG	1:A:703:GLU:CG	2.82	0.52
1:A:533:MET:HE1	2:B:38:LEU:CD2	2.40	0.52
1:A:533:MET:HE1	2:B:38:LEU:HD21	1.92	0.52
1:A:707:ARG:HD3	1:A:757:TYR:CD1	2.34	0.52
1:A:758:LEU:O	1:A:762:ARG:HG3	2.10	0.52
1:A:383:ARG:O	1:A:387:VAL:HG23	2.10	0.52
1:A:38:VAL:O	1:A:42:ARG:HG3	2.10	0.51
1:A:811:THR:CG2	1:A:814:VAL:CG2	2.88	0.51
1:A:707:ARG:HD3	1:A:757:TYR:CZ	2.46	0.51
1:A:4:ILE:O	1:A:8:GLU:HG3	2.09	0.51
1:A:445:ASN:OD1	1:A:447:VAL:N	2.41	0.51
1:A:1:MET:HG2	1:A:2:GLU:N	2.24	0.51
1:A:364:VAL:HB	1:A:365:PRO:HD3	1.92	0.51
2:B:32:LYS:O	2:B:33:SER:C	2.53	0.51
1:A:338:ASP:C	1:A:340:ASP:H	2.18	0.51
1:A:398:GLU:O	1:A:402:LEU:HD13	2.11	0.51
1:A:112:CYS:O	1:A:116:ILE:CD1	2.58	0.51
1:A:202:LEU:HD12	1:A:243:LYS:HD3	1.93	0.51
1:A:815:VAL:HG13	1:A:846:LEU:CD1	2.40	0.50
1:A:407:ILE:CD1	1:A:442:ALA:HA	2.40	0.50
1:A:555:MET:CE	1:A:603:ILE:HG13	2.41	0.50
1:A:570:SER:HB2	3:A:1111:HOH:O	2.11	0.50
1:A:84:ASP:OD2	1:A:86:ASN:HB2	2.11	0.50
1:A:618:THR:CG2	1:A:619:ALA:H	2.24	0.50
1:A:65:LEU:HD13	1:A:116:ILE:HD11	1.93	0.50
1:A:88:ARG:NH1	1:A:125:GLN:HG2	2.21	0.50
1:A:117:ALA:O	1:A:121:ILE:HG12	2.12	0.50
1:A:227:GLN:HE21	1:A:263:ILE:HD12	1.75	0.50
1:A:619:ALA:CB	1:A:623:GLY:CA	2.88	0.49
1:A:343:ASN:C	1:A:343:ASN:ND2	2.69	0.49
2:B:37:SER:OG	2:B:38:LEU:CD1	2.60	0.49
1:A:567:HIS:CD2	3:A:957:HOH:O	2.65	0.49
1:A:252:MET:HA	1:A:252:MET:CE	2.41	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:615:PHE:HA	1:A:618:THR:HG22	1.94	0.49
1:A:778:GLY:HA3	1:A:781:GLU:CD	2.34	0.49
1:A:806:GLY:HA2	1:A:842:MET:CE	2.42	0.49
1:A:833:VAL:O	1:A:837:VAL:HG23	2.12	0.49
1:A:339:ASP:HA	3:A:1067:HOH:O	2.11	0.49
1:A:402:LEU:N	1:A:402:LEU:HD12	2.27	0.49
1:A:422:VAL:HG21	3:A:1180:HOH:O	2.09	0.49
1:A:497:TYR:CD1	1:A:497:TYR:C	2.90	0.49
1:A:367:VAL:HG12	1:A:371:ILE:CD1	2.42	0.49
1:A:648:GLU:HB2	3:A:1136:HOH:O	2.11	0.49
1:A:71:ASP:CB	1:A:704:ASN:HD22	2.23	0.49
1:A:162:ASP:CG	1:A:163:PRO:HD2	2.36	0.49
1:A:305:ARG:HH11	1:A:305:ARG:HB3	1.78	0.49
1:A:151:LEU:HD23	1:A:154:ILE:HD12	1.94	0.49
1:A:211:LYS:HD2	1:A:214:GLU:OE1	2.13	0.48
1:A:342:TRP:CG	2:B:26:PRO:CD	2.95	0.48
1:A:783:VAL:HG22	1:A:784:HIS:N	2.28	0.48
2:B:59:VAL:HG12	2:B:63:ARG:HE	1.78	0.48
2:B:38:LEU:HB3	2:B:43:ARG:HH21	1.78	0.48
1:A:1:MET:CG	1:A:2:GLU:H	2.23	0.48
1:A:343:ASN:HD21	1:A:345:CYS:HB3	1.79	0.48
1:A:489:ASP:O	1:A:490:ASP:OD1	2.31	0.48
1:A:782:ASN:N	1:A:782:ASN:ND2	2.61	0.48
1:A:162:ASP:OD2	1:A:162:ASP:C	2.56	0.48
1:A:831:LYS:CG	1:A:831:LYS:O	2.61	0.48
1:A:357:THR:HG22	1:A:395:GLU:HG2	1.95	0.48
1:A:827:THR:HG21	3:B:76:HOH:O	2.14	0.48
1:A:567:HIS:HD2	3:A:957:HOH:O	1.95	0.47
1:A:24:PHE:C	1:A:24:PHE:CD1	2.92	0.47
1:A:227:GLN:NE2	1:A:263:ILE:CD1	2.77	0.47
1:A:306:PRO:HA	3:A:1165:HOH:O	2.14	0.47
1:A:664:TYR:CZ	1:A:706:HIS:ND1	2.82	0.47
1:A:749:LYS:HG3	1:A:749:LYS:O	2.14	0.47
2:B:38:LEU:HB3	2:B:43:ARG:NH2	2.29	0.47
1:A:305:ARG:HB3	1:A:305:ARG:NH1	2.30	0.47
1:A:707:ARG:CD	1:A:757:TYR:CZ	2.97	0.47
1:A:659:LYS:HE3	1:A:659:LYS:HB2	1.73	0.47
1:A:863:THR:CG2	1:A:864:TRP:N	2.77	0.47
1:A:86:ASN:HB3	3:A:1150:HOH:O	2.15	0.47
1:A:533:MET:CE	2:B:38:LEU:HD21	2.45	0.46
1:A:337:ASP:HA	3:A:1208:HOH:O	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:608:MET:HE1	1:A:632:VAL:HG22	1.98	0.46
1:A:83:ILE:O	1:A:84:ASP:C	2.59	0.46
1:A:121:ILE:N	1:A:122:PRO:CD	2.78	0.46
1:A:403:LYS:N	1:A:404:PRO:HD2	2.30	0.46
1:A:702:ASN:CG	1:A:703:GLU:HG2	2.39	0.46
1:A:651:LYS:HD3	1:A:691:GLU:OE2	2.14	0.46
1:A:626:GLU:HG2	1:A:666:VAL:HA	1.98	0.46
1:A:157:ILE:O	1:A:161:ILE:CG2	2.63	0.46
1:A:626:GLU:HG3	3:A:1006:HOH:O	2.15	0.46
1:A:831:LYS:O	1:A:831:LYS:HG2	2.14	0.46
1:A:628:ALA:O	1:A:631:ALA:HB3	2.15	0.46
1:A:840:ARG:HH11	1:A:840:ARG:HG2	1.81	0.46
1:A:367:VAL:HG12	1:A:371:ILE:HD11	1.98	0.46
1:A:615:PHE:HB3	1:A:653:PHE:CZ	2.51	0.46
1:A:568:ILE:HA	3:A:1166:HOH:O	2.15	0.45
1:A:665:GLN:NE2	2:B:44:ARG:NH1	2.63	0.45
1:A:696:LEU:HD22	1:A:713:ILE:CD1	2.45	0.45
1:A:129:LEU:C	1:A:131:PRO:HD2	2.41	0.45
2:B:36:SER:C	2:B:38:LEU:N	2.74	0.45
1:A:73:LYS:HE3	3:A:954:HOH:O	2.16	0.45
1:A:393:ILE:HD12	1:A:393:ILE:O	2.16	0.45
1:A:660:ASN:O	1:A:667:CYS:HB2	2.17	0.45
1:A:130:ILE:HG22	1:A:131:PRO:N	2.31	0.45
1:A:178:ILE:HG21	1:A:217:PHE:CZ	2.51	0.45
1:A:549:LYS:O	1:A:553:VAL:HG23	2.17	0.45
2:B:37:SER:OG	2:B:38:LEU:HD11	2.16	0.45
1:A:488:ALA:HB1	1:A:489:ASP:CA	2.26	0.45
1:A:857:LYS:HB3	1:A:860:THR:HG1	1.78	0.45
1:A:353:MET:HE1	2:B:33:SER:OG	2.17	0.45
1:A:360:GLU:O	1:A:363:ILE:HG22	2.16	0.45
1:A:762:ARG:CZ	1:A:804:ILE:CD1	2.95	0.45
1:A:811:THR:HG23	1:A:814:VAL:HG23	1.99	0.45
1:A:839:ALA:C	1:A:840:ARG:HD2	2.42	0.45
1:A:209:PHE:CZ	1:A:244:ILE:HD12	2.52	0.45
2:B:27:ARG:HB3	2:B:30:GLN:OE1	2.17	0.45
1:A:425:ARG:NH2	1:A:463:GLU:OE1	2.50	0.44
1:A:532:LEU:O	1:A:535:ILE:HG22	2.16	0.44
1:A:840:ARG:HB2	1:A:843:ILE:CD1	2.46	0.44
1:A:541:LYS:C	1:A:543:CYS:H	2.25	0.44
1:A:591:VAL:HG23	1:A:592:LEU:N	2.33	0.44
1:A:693:MET:HG2	1:A:731:TYR:CD1	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:27:ARG:O	1:A:31:GLU:HG3	2.17	0.44
1:A:121:ILE:H	1:A:122:PRO:HD2	1.80	0.44
2:B:36:SER:C	2:B:38:LEU:H	2.26	0.44
1:A:158:CYS:SG	1:A:204:PHE:HZ	2.41	0.44
2:B:38:LEU:N	2:B:38:LEU:CD1	2.42	0.44
1:A:116:ILE:N	1:A:116:ILE:HD12	2.32	0.44
1:A:331:THR:HG23	3:A:1174:HOH:O	2.07	0.44
1:A:406:VAL:HG21	1:A:439:LEU:HD12	1.99	0.44
1:A:623:GLY:CA	3:A:1028:HOH:O	2.66	0.44
1:A:679:ARG:HH21	2:B:55:ARG:HG3	1.81	0.44
1:A:32:ASN:HD22	1:A:32:ASN:C	2.24	0.44
1:A:790:VAL:O	1:A:791:GLN:C	2.61	0.44
1:A:618:THR:O	1:A:621:SER:CB	2.63	0.43
1:A:806:GLY:HA2	1:A:842:MET:HE3	2.00	0.43
1:A:139:ASN:HB3	1:A:142:SER:OG	2.18	0.43
1:A:615:PHE:HA	1:A:618:THR:CG2	2.48	0.43
1:A:36:PHE:CZ	1:A:40:LEU:HD11	2.54	0.43
1:A:495:ALA:HA	1:A:541:LYS:HG3	2.01	0.43
1:A:530:GLU:HA	1:A:533:MET:HE3	1.99	0.43
1:A:178:ILE:HG23	1:A:221:VAL:HG21	2.01	0.43
1:A:380:TRP:CZ2	1:A:381:ARG:NH1	2.87	0.43
1:A:430:TRP:CZ2	1:A:434:ARG:CD	3.01	0.43
1:A:105:ARG:HD2	1:A:105:ARG:HA	1.71	0.43
1:A:515:ASP:OD2	1:A:557:ARG:NH2	2.51	0.43
1:A:533:MET:HG3	1:A:587:THR:HA	2.01	0.43
1:A:33:LEU:HB3	1:A:34:PRO:HD3	2.00	0.43
1:A:157:ILE:HG22	1:A:166:LEU:HD11	2.00	0.43
1:A:782:ASN:N	1:A:782:ASN:HD22	2.16	0.43
1:A:752:TYR:O	1:A:755:VAL:HG12	2.18	0.43
1:A:34:PRO:O	1:A:38:VAL:HG23	2.18	0.43
1:A:588:LEU:HA	1:A:591:VAL:CG2	2.48	0.43
1:A:121:ILE:HD11	1:A:129:LEU:HD23	2.01	0.43
1:A:287:CYS:O	1:A:291:MET:HG3	2.18	0.43
1:A:623:GLY:HA3	3:A:1028:HOH:O	2.18	0.43
1:A:774:GLN:O	1:A:777:LYS:O	2.37	0.43
1:A:797:ILE:O	1:A:801:ILE:HG12	2.18	0.43
1:A:645:LYS:O	1:A:645:LYS:HG2	2.19	0.42
1:A:206:LYS:HE2	3:A:1170:HOH:O	2.19	0.42
1:A:343:ASN:HD21	1:A:346:LYS:H	1.66	0.42
1:A:250:GLN:HG3	3:A:1188:HOH:O	2.18	0.42
2:B:52:LYS:HE2	3:B:71:HOH:O	2.18	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:445:ASN:ND2	3:A:960:HOH:O	2.51	0.42
1:A:660:ASN:OD1	1:A:660:ASN:C	2.61	0.42
1:A:73:LYS:O	1:A:77:GLN:HG3	2.20	0.42
1:A:181:MET:O	1:A:182:ARG:C	2.63	0.42
1:A:711:PRO:HB3	1:A:761:LEU:HA	2.02	0.42
1:A:811:THR:HG23	1:A:814:VAL:H	1.83	0.42
1:A:857:LYS:CA	1:A:860:THR:OG1	2.68	0.42
1:A:426:ASP:OD1	1:A:426:ASP:C	2.63	0.42
1:A:472:TRP:CD2	2:B:34:LYS:HG2	2.55	0.42
1:A:624:VAL:HG21	1:A:656:ILE:HG23	2.02	0.42
1:A:51:GLN:CD	1:A:104:TYR:HD1	2.26	0.42
1:A:393:ILE:HD12	1:A:393:ILE:C	2.45	0.42
1:A:630:MET:HG2	2:B:47:LEU:CD2	2.49	0.42
1:A:691:GLU:O	1:A:695:LEU:HG	2.19	0.42
1:A:765:CYS:O	1:A:768:ALA:HB3	2.20	0.42
1:A:602:GLN:O	1:A:606:VAL:HG23	2.20	0.42
1:A:5:THR:O	1:A:9:LYS:HG2	2.19	0.41
1:A:166:LEU:HD23	1:A:166:LEU:HA	1.83	0.41
1:A:402:LEU:N	1:A:402:LEU:CD1	2.83	0.41
1:A:495:ALA:HA	1:A:541:LYS:CG	2.50	0.41
1:A:252:MET:HE2	1:A:252:MET:CA	2.46	0.41
1:A:740:GLN:NE2	1:A:796:PHE:CZ	2.88	0.41
1:A:812:ASP:OD2	1:A:854:LYS:CB	2.67	0.41
1:A:68:LYS:O	1:A:70:PRO:HD3	2.20	0.41
1:A:377:ASN:HD22	1:A:379:ASP:N	2.06	0.41
2:B:40:GLN:H	2:B:40:GLN:HG2	1.54	0.41
1:A:161:ILE:HG21	1:A:166:LEU:HD12	2.02	0.41
1:A:338:ASP:C	1:A:340:ASP:N	2.78	0.41
1:A:67:SER:CB	3:A:1161:HOH:O	2.63	0.41
1:A:68:LYS:H	1:A:68:LYS:CD	1.98	0.41
1:A:430:TRP:CZ2	1:A:434:ARG:HD3	2.56	0.41
1:A:702:ASN:HD22	1:A:703:GLU:HA	1.85	0.41
1:A:800:PHE:CE1	1:A:804:ILE:HD11	2.55	0.41
1:A:253:GLU:OE1	1:A:312:LYS:HE3	2.20	0.41
1:A:578:ASN:HD22	1:A:578:ASN:HA	1.68	0.41
1:A:853:SER:O	1:A:853:SER:OG	2.35	0.41
1:A:625:GLN:O	1:A:627:ASP:N	2.54	0.41
1:A:665:GLN:HE21	2:B:44:ARG:NH1	2.19	0.41
1:A:853:SER:HB2	1:A:859:LYS:HB3	2.02	0.41
2:B:48:LEU:HD23	3:B:66:HOH:O	2.17	0.41
1:A:151:LEU:HA	1:A:154:ILE:HD12	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:361:ASP:O	1:A:362:ASP:C	2.64	0.40
1:A:466:VAL:O	1:A:470:VAL:HG23	2.21	0.40
1:A:617:SER:O	1:A:618:THR:C	2.64	0.40
1:A:475:SER:O	1:A:479:GLU:HG3	2.21	0.40
1:A:759:ASN:HB3	1:A:811:THR:HG21	2.03	0.40
1:A:791:GLN:C	1:A:791:GLN:CD	2.89	0.40
1:A:444:ILE:O	1:A:444:ILE:CG2	2.60	0.40
1:A:445:ASN:OD1	1:A:445:ASN:C	2.64	0.40
1:A:809:ASP:OD1	1:A:809:ASP:N	2.50	0.40
2:B:50:LEU:HD11	2:B:54:LYS:NZ	2.36	0.40
1:A:253:GLU:HA	1:A:314:TYR:OH	2.22	0.40
1:A:737:ASN:O	1:A:740:GLN:HB3	2.22	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	871/876 (99%)	809 (93%)	58 (7%)	4 (0%)	24	27
2	B	37/40 (92%)	31 (84%)	6 (16%)	0	100	100
All	All	908/916 (99%)	840 (92%)	64 (7%)	4 (0%)	30	34

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	664	TYR
1	A	32	ASN
1	A	444	ILE
1	A	687	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	749/751 (100%)	686 (92%)	63 (8%)	10	11
2	B	38/39 (97%)	29 (76%)	9 (24%)	1	0
All	All	787/790 (100%)	715 (91%)	72 (9%)	9	9

All (72) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	MET
1	A	3	LEU
1	A	35	THR
1	A	65	LEU
1	A	67	SER
1	A	105	ARG
1	A	130	ILE
1	A	165	GLN
1	A	172	GLU
1	A	234	ARG
1	A	254	THR
1	A	305	ARG
1	A	331	THR
1	A	340	ASP
1	A	343	ASN
1	A	353	MET
1	A	377	ASN
1	A	413	LEU
1	A	417	MET
1	A	434	ARG
1	A	474	PHE
1	A	486	ASP
1	A	487	VAL
1	A	491	GLN
1	A	493	GLU
1	A	497	TYR
1	A	524	LEU

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Mol	Chain	Res	Type
1	A	532	LEU
1	A	535	ILE
1	A	541	LYS
1	A	549	LYS
1	A	561	VAL
1	A	563	GLN
1	A	576	GLN
1	A	580	LEU
1	A	593	ARG
1	A	594	LYS
1	A	595	VAL
1	A	616	GLN
1	A	621	SER
1	A	624	VAL
1	A	625	GLN
1	A	626	GLU
1	A	635	LEU
1	A	637	GLU
1	A	654	LEU
1	A	668	LEU
1	A	673	LEU
1	A	685	ILE
1	A	690	ASP
1	A	707	ARG
1	A	746	GLN
1	A	747	VAL
1	A	777	LYS
1	A	779	ASP
1	A	781	GLU
1	A	782	ASN
1	A	821	LEU
1	A	853	SER
1	A	855	THR
1	A	856	ASN
1	A	857	LYS
1	A	859	LYS
2	B	32	LYS
2	B	33	SER
2	B	38	LEU
2	B	39	GLU
2	B	40	GLN
2	B	42	GLU

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Mol	Chain	Res	Type
2	B	54	LYS
2	B	55	ARG
2	B	61	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (36) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	22	GLN
1	A	32	ASN
1	A	60	GLN
1	A	86	ASN
1	A	141	ASN
1	A	165	GLN
1	A	179	GLN
1	A	208	ASN
1	A	227	GLN
1	A	240	ASN
1	A	278	GLN
1	A	320	GLN
1	A	343	ASN
1	A	366	HIS
1	A	377	ASN
1	A	401	GLN
1	A	408	GLN
1	A	522	ASN
1	A	548	GLN
1	A	563	GLN
1	A	567	HIS
1	A	578	ASN
1	A	581	GLN
1	A	590	ASN
1	A	597	HIS
1	A	682	GLN
1	A	702	ASN
1	A	704	ASN
1	A	712	GLN
1	A	740	GLN
1	A	741	GLN
1	A	744	GLN
1	A	759	ASN
1	A	780	GLN
1	A	782	ASN

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Mol	Chain	Res	Type
1	A	856	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no 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

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	873/876 (99%)	0.67	96 (10%)	10 12	16, 42, 88, 160	0
2	B	39/40 (97%)	1.45	12 (30%)	1 0	34, 62, 104, 128	0
All	All	912/916 (99%)	0.70	108 (11%)	9 10	16, 42, 91, 160	0

All (108) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	490	ASP	9.7
1	A	489	ASP	9.5
1	A	488	ALA	7.5
1	A	783	VAL	6.6
2	B	38	LEU	5.9
1	A	487	VAL	5.3
1	A	104	TYR	5.2
1	A	491	GLN	4.8
1	A	618	THR	4.7
1	A	778	GLY	4.3
1	A	544	TYR	4.2
1	A	811	THR	4.2
1	A	656	ILE	4.1
1	A	702	ASN	4.0
2	B	39	GLU	4.0
1	A	777	LYS	3.9
1	A	780	GLN	3.9
1	A	704	ASN	3.8
1	A	620	GLY	3.8
2	B	35	TYR	3.7
1	A	619	ALA	3.7
1	A	105	ARG	3.6
1	A	593	ARG	3.6
1	A	747	VAL	3.6

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Mol	Chain	Res	Type	RSRZ
1	A	748	ASP	3.6
1	A	782	ASN	3.5
2	B	37	SER	3.5
1	A	779	ASP	3.5
1	A	844	HIS	3.4
1	A	749	LYS	3.4
2	B	33	SER	3.4
1	A	486	ASP	3.4
1	A	660	ASN	3.4
1	A	106	PRO	3.3
2	B	26	PRO	3.3
1	A	752	TYR	3.3
1	A	1	MET	3.2
1	A	571	THR	3.2
1	A	535	ILE	3.1
1	A	854	LYS	3.1
1	A	804	ILE	3.1
1	A	623	GLY	3.1
1	A	701	GLY	3.1
1	A	784	HIS	3.0
1	A	873	LYS	3.0
1	A	664	TYR	3.0
1	A	250	GLN	2.9
1	A	785	PRO	2.9
1	A	566	SER	2.8
1	A	803	HIS	2.8
2	B	40	GLN	2.8
1	A	444	ILE	2.8
1	A	856	ASN	2.8
2	B	48	LEU	2.8
1	A	555	MET	2.8
1	A	103	THR	2.8
1	A	163	PRO	2.8
1	A	855	THR	2.8
1	A	203	GLU	2.7
1	A	568	ILE	2.7
1	A	745	ALA	2.7
1	A	843	ILE	2.7
1	A	835	LYS	2.7
1	A	492	GLU	2.6
1	A	755	VAL	2.6
2	B	34	LYS	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	445	ASN	2.6
1	A	204	PHE	2.6
1	A	746	GLN	2.6
1	A	625	GLN	2.5
1	A	454	GLN	2.5
1	A	520	HIS	2.5
1	A	703	GLU	2.5
1	A	863	THR	2.4
2	B	64	ARG	2.4
1	A	588	LEU	2.4
1	A	589	GLN	2.4
1	A	801	ILE	2.4
1	A	707	ARG	2.4
1	A	852	ARG	2.4
1	A	806	GLY	2.3
1	A	624	VAL	2.3
1	A	754	MET	2.3
1	A	591	VAL	2.3
1	A	485	ALA	2.3
1	A	23	LYS	2.3
1	A	705	VAL	2.3
1	A	661	TYR	2.2
1	A	68	LYS	2.2
1	A	545	PRO	2.2
1	A	637	GLU	2.2
1	A	570	SER	2.2
1	A	592	LEU	2.2
1	A	810	HIS	2.2
1	A	750	SER	2.2
2	B	36	SER	2.2
1	A	809	ASP	2.1
1	A	808	GLU	2.1
1	A	764	SER	2.1
1	A	787	VAL	2.1
1	A	838	GLU	2.1
1	A	753	ASP	2.1
1	A	807	ASP	2.1
1	A	563	GLN	2.1
1	A	574	ARG	2.1
1	A	162	ASP	2.0
2	B	61	HIS	2.0
1	A	756	ASP	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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.