



# Full wwPDB X-ray Structure Validation Report ⓘ

Aug 21, 2023 – 01:45 PM EDT

PDB ID : 2P8Q  
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](mailto: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>.

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

MolProbity : 4.02b-467  
Xtriage (Phenix) : 1.13  
EDS : 2.35  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.35

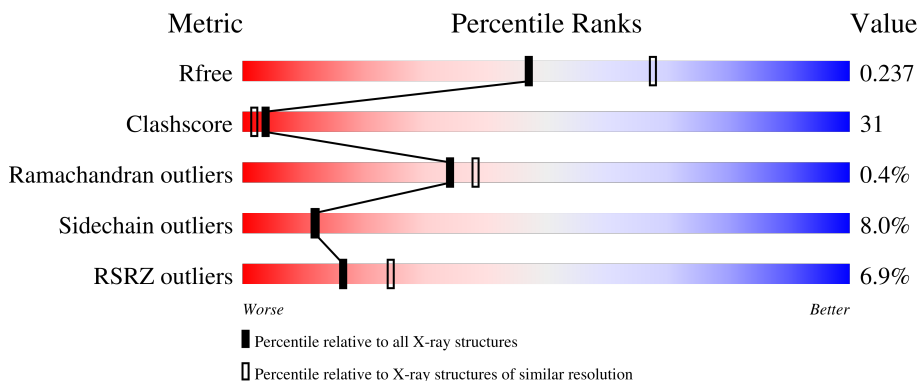
# 1 Overall quality at a glance

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))
$R_{free}$	130704	1164 (2.36-2.36)
Clashscore	141614	1232 (2.36-2.36)
Ramachandran outliers	138981	1211 (2.36-2.36)
Sidechain outliers	138945	1212 (2.36-2.36)
RSRZ outliers	127900	1150 (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  $\geq 3$ , 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	 7% 60% 33% 5% •
2	B	40	 15% 38% 50% 5% 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
			Total	C	N	O	S			
1	A	873	6782	4273	1136	1326	47	0	0	0

- Molecule 2 is a protein called Snurportin-1.

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

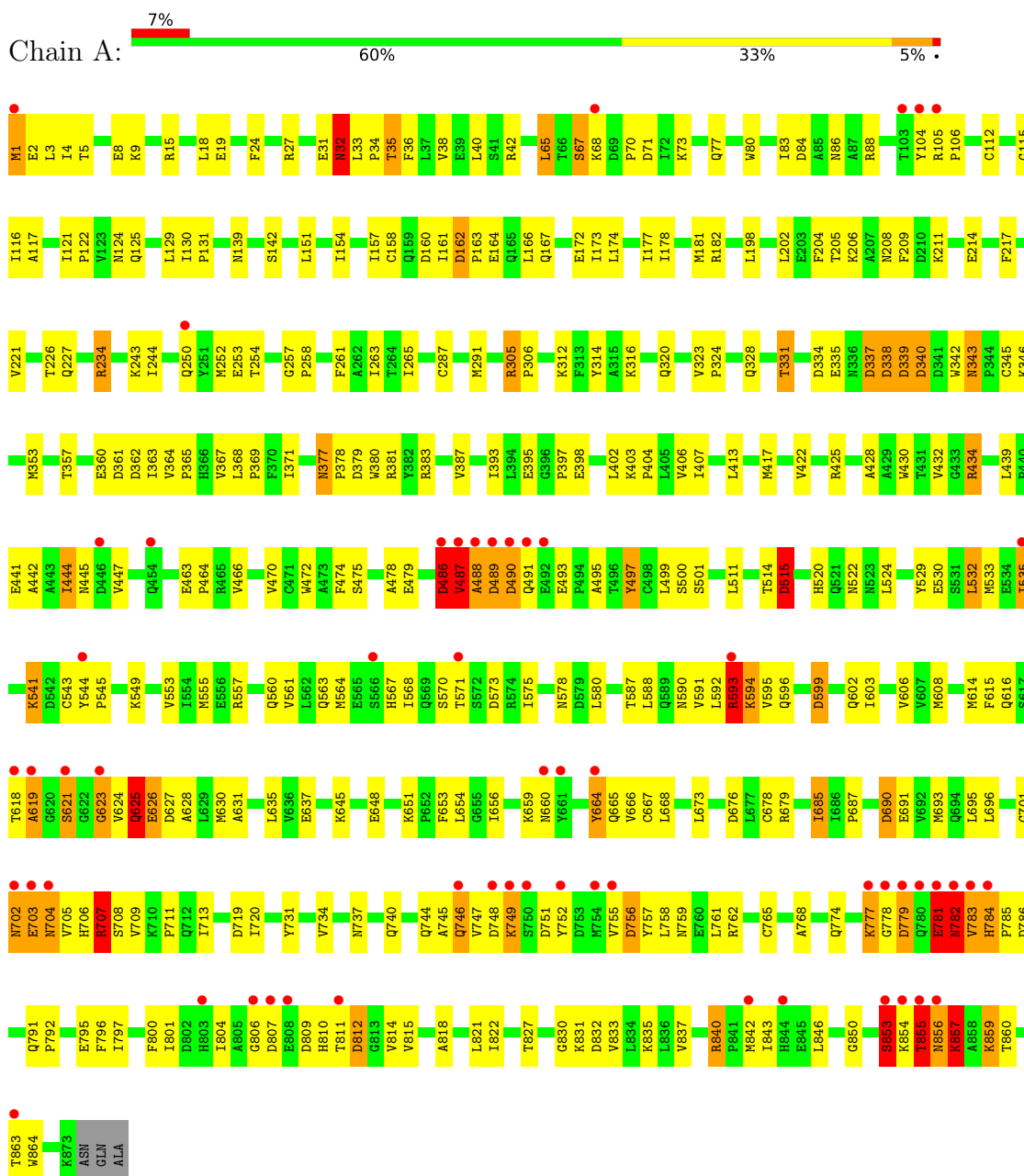
- Molecule 3 is water.

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

### 3 Residue-property plots [i](#)

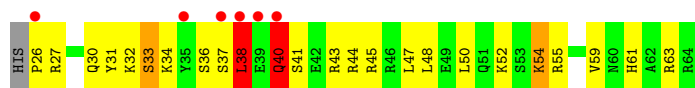
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density.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

Chain B: 



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	64.75Å 97.89Å 84.29Å 90.00° 90.86° 90.00°	Depositor
Resolution (Å)	40.00 – 2.35 39.04 – 2.31	Depositor EDS
% Data completeness (in resolution range)	98.7 (40.00-2.35) 94.2 (39.04-2.31)	Depositor EDS
$R_{merge}$	0.08	Depositor
$R_{sym}$	0.08	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.42 (at 2.31Å)	Xtrriage
Refinement program	CNS	Depositor
R, $R_{free}$	0.227 , 0.250 0.236 , 0.237	Depositor DCC
$R_{free}$ test set	4338 reflections (10.02%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	33.4	Xtrriage
Anisotropy	0.390	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.30 , 45.8	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	0.027 for h,-k,-l	Xtrriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	7471	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	47.0	wwPDB-VP

Xtrriage'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.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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	0.32	0/6893	0.56	18/9360 (0.2%)
2	B	0.25	0/348	0.42	0/458
All	All	0.32	0/7241	0.56	18/9818 (0.2%)

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 (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
1	A	515	ASP	CB-CG-OD2	5.28	123.05	118.30
1	A	338	ASP	CB-CG-OD2	5.28	123.05	118.30
1	A	361	ASP	CB-CG-OD2	5.27	123.04	118.30
1	A	334	ASP	CB-CG-OD2	5.27	123.04	118.30
1	A	690	ASP	CB-CG-OD2	5.25	123.03	118.30
1	A	160	ASP	CB-CG-OD2	5.25	123.03	118.30
1	A	362	ASP	CB-CG-OD2	5.25	123.02	118.30
1	A	339	ASP	CB-CG-OD2	5.24	123.02	118.30
1	A	337	ASP	CB-CG-OD2	5.24	123.01	118.30
1	A	786	ASP	CB-CG-OD2	5.23	123.01	118.30
1	A	486	ASP	CB-CG-OD2	5.22	123.00	118.30
1	A	832	ASP	CB-CG-OD2	5.20	122.98	118.30
1	A	573	ASP	CB-CG-OD2	5.20	122.98	118.30
1	A	162	ASP	CB-CG-OD2	5.19	122.97	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	779	ASP	CB-CG-OD2	5.18	122.96	118.30
1	A	748	ASP	CB-CG-OD2	5.18	122.96	118.30
1	A	812	ASP	CB-CG-OD2	5.17	122.95	118.30
1	A	756	ASP	CB-CG-OD2	5.16	122.94	118.30

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
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 [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	6782	0	6781	417	0
2	B	344	0	359	41	0
3	A	332	0	0	56	0
3	B	13	0	0	4	0
All	All	7471	0	7140	441	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 31.

All (441) 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	1.31
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:777:LYS:HG2	1:A:778:GLY:N	1.55	1.15
1:A:397:PRO:HB2	1:A:402:LEU:HD11	1.29	1.14
1:A:855:THR:HG22	1:A:856:ASN:N	1.57	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:514:THR:HG21	1:A:557:ARG:HH12	1.19	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
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:783:VAL:C	1:A:785:PRO:HD3	1.79	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: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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
2:B:37:SER:C	2:B:38:LEU:CD1	2.30	0.98
1:A:856:ASN:C	1:A:857:LYS:HG2	1.79	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
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: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:533:MET:HE3	2:B:38:LEU:HD21	1.56	0.87
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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: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
1:A:488:ALA:CB	1:A:489:ASP:HA	2.15	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:860:THR:C	1:A:863:THR:HG22	2.06	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: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:543:CYS:C	1:A:545:PRO:HD2	2.10	0.72
1:A:593:ARG:CG	1:A:593:ARG:NH1	2.45	0.72
1:A:368:LEU:N	1:A:369:PRO:HD2	2.05	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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:486:ASP:CG	1:A:486:ASP:O	2.30	0.69
1:A:514:THR:HG21	1:A:557:ARG:NH1	2.02	0.69
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:343:ASN:C	1:A:343:ASN:HD22	1.98	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: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:167:GLN:HG3	1:A:204:PHE:HB2	1.79	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
1:A:693:MET:HE1	1:A:720:ILE:HG21	1.79	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: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: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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:618:THR:O	1:A:621:SER:HB2	2.00	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
1:A:856:ASN:O	1:A:857:LYS:CG	2.42	0.61
1:A:856:ASN:C	1:A:857:LYS:CG	2.62	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:608:MET:CE	1:A:635:LEU:HD23	2.30	0.60
1:A:594:LYS:O	1:A:594:LYS:CG	2.49	0.60
1:A:745:ALA:C	1:A:746:GLN:HG3	2.21	0.60
1:A:257:GLY:N	1:A:258:PRO:HD2	2.16	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:702:ASN:HB3	1:A:703:GLU:CB	2.28	0.59
1:A:18:LEU:C	1:A:18:LEU:HD23	2.23	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: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:762:ARG:CZ	1:A:804:ILE:HD12	2.33	0.58
1:A:626:GLU:C	1:A:626:GLU:OE1	2.42	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:608:MET:HE1	1:A:635:LEU:HD23	1.85	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:377:ASN:HD22	1:A:377:ASN:C	2.07	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
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:511:LEU:C	1:A:514:THR:HG22	2.25	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:853:SER:HA	1:A:854:LYS:C	2.27	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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:560:GLN:HG2	1:A:564:MET:CE	2.38	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:497:TYR:HD1	1:A:500:SER:HG	1.55	0.52
1:A:164:GLU:C	3:A:1175:HOH:O	2.48	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: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
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:252:MET:CE	1:A:252:MET:HA	2.41	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:560:GLN:HG2	1:A:564:MET:HE2	1.94	0.50
1:A:619:ALA:CB	1:A:623:GLY:CA	2.88	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:615:PHE:HA	1:A:618:THR:HG22	1.94	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: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: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
1:A:782:ASN:N	1:A:782:ASN:ND2	2.61	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: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: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:337:ASP:HA	3:A:1208:HOH:O	2.16	0.46
1:A:121:ILE:N	1:A:122:PRO:CD	2.78	0.46
1:A:338:ASP:C	1:A:340:ASP:H	2.18	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:403:LYS:N	1:A:404:PRO:HD2	2.30	0.46
2:B:32:LYS:O	2:B:33:SER:C	2.53	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:702:ASN:CG	1:A:703:GLU:CG	2.82	0.46
1:A:831:LYS:O	1:A:831:LYS:HG2	2.14	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: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: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:343:ASN:C	1:A:343:ASN:ND2	2.69	0.45
1:A:181:MET:HE1	1:A:198:LEU:HD22	1.99	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:360:GLU:O	1:A:363:ILE:HG22	2.16	0.45
1:A:533:MET:HE3	2:B:38:LEU:CD2	2.38	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: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:778:GLY:HA3	1:A:781:GLU:CD	2.34	0.44
1:A:840:ARG:HB2	1:A:843:ILE:CD1	2.46	0.44
1:A:591:VAL:HG23	1:A:592:LEU:N	2.33	0.44
1:A:497:TYR:CD1	1:A:497:TYR:C	2.90	0.44
1:A:693:MET:HG2	1:A:731:TYR:CD1	2.52	0.44
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:158:CYS:SG	1:A:204:PHE:HZ	2.41	0.44
1:A:162:ASP:CG	1:A:163:PRO:HD2	2.36	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:618:THR:O	1:A:621:SER:CB	2.63	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:162:ASP:OD2	1:A:162:ASP:C	2.56	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
1:A:445:ASN:ND2	3:A:960:HOH:O	2.51	0.42
1:A:73:LYS:O	1:A:77:GLN:HG3	2.20	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:24:PHE:C	1:A:24:PHE:CD1	2.92	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: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:702:ASN:CG	1:A:703:GLU:HG2	2.39	0.41
1:A:83:ILE:O	1:A:84:ASP:C	2.59	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:560:GLN:HG2	1:A:564:MET:HE1	2.03	0.41
1:A:161:ILE:HG21	1:A:166:LEU:HD12	2.02	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:806:GLY:HA2	1:A:842:MET:HE3	2.02	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
2:B:36:SER:C	2:B:38:LEU:N	2.74	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:129:LEU:C	1:A:131:PRO:HD2	2.41	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
1:A:466:VAL:O	1:A:470:VAL:HG23	2.21	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:444:ILE:O	1:A:444:ILE:CG2	2.60	0.40
1:A:809:ASP:OD1	1:A:809:ASP:N	2.50	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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%)	29	32
2	B	37/40 (92%)	31 (84%)	6 (16%)	0	100	100
All	All	908/916 (99%)	840 (92%)	64 (7%)	4 (0%)	34	38

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 [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	749/751 (100%)	691 (92%)	58 (8%)	13	12
2	B	38/39 (97%)	33 (87%)	5 (13%)	4	4
All	All	787/790 (100%)	724 (92%)	63 (8%)	12	12

All (63) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	MET
1	A	3	LEU
1	A	32	ASN
1	A	35	THR
1	A	65	LEU
1	A	67	SER
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	515	ASP
1	A	524	LEU
1	A	532	LEU
1	A	535	ILE
1	A	541	LYS
1	A	561	VAL
1	A	563	GLN
1	A	580	LEU
1	A	593	ARG
1	A	594	LYS
1	A	595	VAL

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Mol	Chain	Res	Type
1	A	599	ASP
1	A	616	GLN
1	A	621	SER
1	A	625	GLN
1	A	626	GLU
1	A	637	GLU
1	A	654	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	779	ASP
1	A	781	GLU
1	A	782	ASN
1	A	821	LEU
1	A	840	ARG
1	A	853	SER
1	A	855	THR
1	A	856	ASN
1	A	857	LYS
1	A	859	LYS
2	B	33	SER
2	B	38	LEU
2	B	40	GLN
2	B	54	LYS
2	B	61	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (26) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	22	GLN
1	A	32	ASN
1	A	49	ASN
1	A	141	ASN
1	A	145	HIS
1	A	179	GLN
1	A	208	ASN
1	A	227	GLN
1	A	240	ASN
1	A	278	GLN

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Mol	Chain	Res	Type
1	A	320	GLN
1	A	343	ASN
1	A	377	ASN
1	A	401	GLN
1	A	408	GLN
1	A	522	ASN
1	A	578	ASN
1	A	581	GLN
1	A	590	ASN
1	A	702	ASN
1	A	704	ASN
1	A	712	GLN
1	A	740	GLN
1	A	741	GLN
1	A	780	GLN
1	A	782	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 monosaccharides 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

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	873/876 (99%)	0.39	57 (6%) 18 27	16, 42, 88, 160	0
2	B	39/40 (97%)	0.90	6 (15%) 2 3	34, 62, 104, 128	0
All	All	912/916 (99%)	0.42	63 (6%) 16 24	16, 42, 91, 160	0

All (63) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	780	GLN	20.8
1	A	783	VAL	11.8
1	A	488	ALA	9.8
1	A	487	VAL	9.4
1	A	490	ASP	9.0
1	A	489	ASP	8.7
1	A	782	ASN	8.6
1	A	779	ASP	8.3
2	B	38	LEU	8.0
1	A	778	GLY	7.0
1	A	748	ASP	6.6
1	A	750	SER	6.4
1	A	704	ASN	6.3
1	A	491	GLN	6.2
1	A	486	ASP	5.6
1	A	749	LYS	5.6
1	A	618	THR	5.4
1	A	854	LYS	5.1
1	A	752	TYR	4.7
1	A	104	TYR	4.6
1	A	746	GLN	4.3
1	A	784	HIS	4.2
2	B	40	GLN	4.1
1	A	703	GLU	4.1

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	A	664	TYR	3.9
1	A	702	ASN	3.8
1	A	492	GLU	3.8
1	A	446	ASP	3.7
1	A	105	ARG	3.6
2	B	37	SER	3.5
1	A	544	TYR	3.5
1	A	855	THR	3.5
2	B	35	TYR	3.5
1	A	777	LYS	3.2
1	A	856	ASN	3.1
1	A	1	MET	3.1
1	A	619	ALA	3.1
1	A	660	ASN	2.9
1	A	863	THR	2.9
1	A	853	SER	2.8
1	A	808	GLU	2.8
1	A	103	THR	2.7
1	A	661	TYR	2.7
1	A	621	SER	2.7
1	A	566	SER	2.6
1	A	811	THR	2.6
1	A	623	GLY	2.6
1	A	454	GLN	2.5
2	B	26	PRO	2.5
1	A	806	GLY	2.5
1	A	571	THR	2.5
1	A	803	HIS	2.5
2	B	39	GLU	2.5
1	A	754	MET	2.4
1	A	593	ARG	2.4
1	A	781	GLU	2.3
1	A	844	HIS	2.3
1	A	842	MET	2.2
1	A	535	ILE	2.2
1	A	755	VAL	2.1
1	A	68	LYS	2.1
1	A	807	ASP	2.0
1	A	250	GLN	2.0

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

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

## 6.3 Carbohydrates [i](#)

There are no monosaccharides 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.