



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 02:06 PM UTC

PDB ID : 1QGR / pdb_00001qgr
Title : STRUCTURE OF IMPORTIN BETA BOUND TO THE IBB DOMAIN OF IMPORTIN ALPHA (II CRYSTAL FORM, GROWN AT LOW PH)
Authors : Cingolani, G.; Petosa, C.; Weis, K.; Muller, C.W.
Deposited on : 1999-05-04
Resolution : 2.30 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

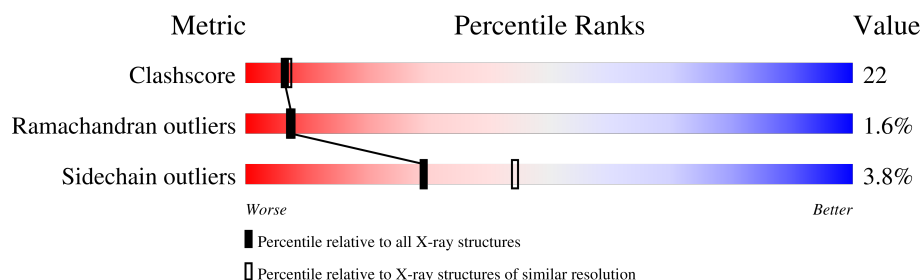
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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	6919 (2.30-2.30)
Ramachandran outliers	187476	6854 (2.30-2.30)
Sidechain outliers	187428	6854 (2.30-2.30)

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	876	
2	B	27	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 7181 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 PROTEIN (IMPORTIN BETA SUBUNIT).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	872	Total	C	N	O	S	55	0	1
			6780	4271	1140	1322	47			

- Molecule 2 is a protein called PROTEIN (IMPORTIN ALPHA-2 SUBUNIT).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	24	Total	C	N	O	S	0	0	0
			215	129	51	34	1			

- Molecule 3 is water.

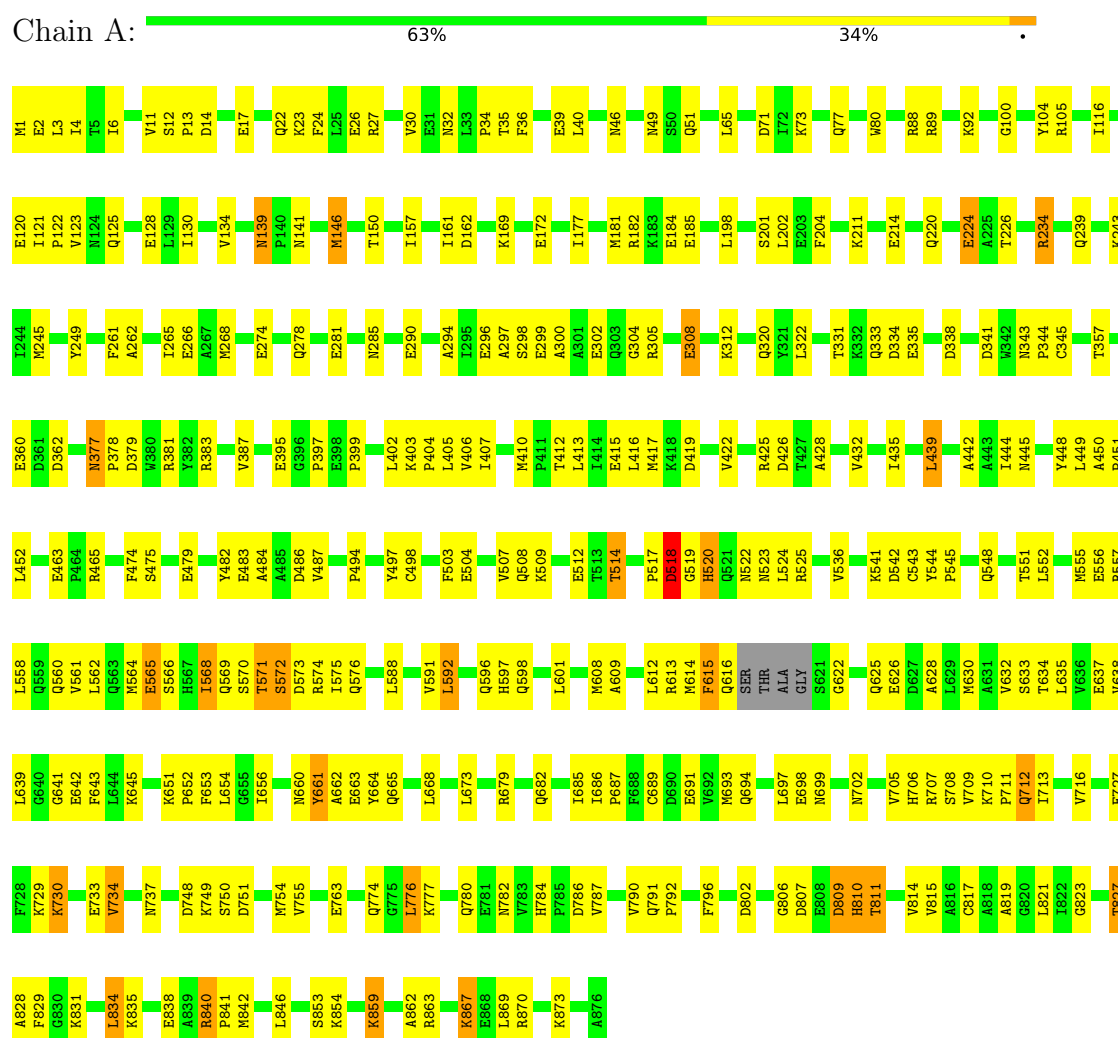
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	183	Total	O	0	0
			183	183		
3	B	3	Total	O	0	0
			3	3		

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: PROTEIN (IMPORTIN BETA SUBUNIT)



• Molecule 2: PROTEIN (IMPORTIN ALPHA-2 SUBUNIT)



R28	R29	R30	R31	I32	V36	R39	K42	M47	L48	R49	R50	R51	ASN	VAL	SER
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4 Data and refinement statistics

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

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	57.90Å 101.17Å 83.83Å 90.00° 87.86° 90.00°	Depositor
Resolution (Å)	40.00 – 2.30	Depositor
% Data completeness (in resolution range)	98.5 (40.00-2.30)	Depositor
R_{merge}	0.09	Depositor
R_{sym}	0.09	Depositor
Refinement program	CNS 0.4	Depositor
R, R_{free}	0.235 , 0.285	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	7181	wwPDB-VP
Average B, all atoms (Å ²)	51.0	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	0.47	1/6891 (0.0%)	0.89	17/9354 (0.2%)
2	B	0.25	0/214	0.84	0/278
All	All	0.46	1/7105 (0.0%)	0.89	17/9632 (0.2%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	615	PHE	C-N	-5.72	1.25	1.33

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	120	GLU	N-CA-C	8.08	123.68	112.45
1	A	689	CYS	N-CA-C	7.40	120.40	111.82
1	A	840	ARG	CA-C-N	7.30	128.97	119.84
1	A	840	ARG	C-N-CA	7.30	128.97	119.84
1	A	185	GLU	CA-C-N	7.08	126.33	118.97
1	A	185	GLU	C-N-CA	7.08	126.33	118.97
1	A	810	HIS	CB-CA-C	-6.21	107.69	115.89
1	A	519	GLY	N-CA-C	-6.09	107.55	115.59
1	A	312	LYS	N-CA-C	-5.97	105.73	114.39
1	A	360	GLU	CB-CA-C	-5.53	109.21	115.79
1	A	568	ILE	N-CA-C	5.37	111.96	106.21
1	A	439	LEU	CA-C-N	5.33	124.79	119.24
1	A	439	LEU	C-N-CA	5.33	124.79	119.24
1	A	463	GLU	CA-C-N	5.26	124.72	119.24
1	A	463	GLU	C-N-CA	5.26	124.72	119.24
1	A	486	ASP	CB-CA-C	-5.19	109.59	117.07
1	A	486	ASP	CA-C-O	5.01	120.84	117.94

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	6780	0	6776	290	0
2	B	215	0	241	21	0
3	A	183	0	0	34	0
3	B	3	0	0	4	0
All	All	7181	0	7017	304	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 22.

All (304) 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:774:GLN:HG3	2:B:47:MET:HE1	1.29	1.14
1:A:565:GLU:HB3	3:A:945:HOH:O	1.60	1.01
1:A:645:LYS:HG3	3:A:963:HOH:O	1.62	0.98
1:A:608:MET:HE3	1:A:635:LEU:HD23	1.48	0.92
1:A:405:LEU:HB2	3:A:1055:HOH:O	1.69	0.91
1:A:663:GLU:HG2	3:A:928:HOH:O	1.69	0.90
1:A:377:ASN:ND2	1:A:379:ASP:H	1.71	0.89
1:A:834:LEU:HD11	1:A:873:LYS:HG2	1.55	0.87
1:A:377:ASN:HD22	1:A:379:ASP:H	1.21	0.86
1:A:796:PHE:HE2	3:A:938:HOH:O	1.58	0.86
1:A:665:GLN:HB2	3:A:928:HOH:O	1.74	0.85
1:A:139:ASN:HD22	1:A:141:ASN:H	1.24	0.84
1:A:811:THR:HG23	1:A:814:VAL:H	1.43	0.84
1:A:23:LYS:HE3	1:A:27:ARG:HH12	1.42	0.84
1:A:652:PRO:O	1:A:656:ILE:HG13	1.79	0.82
2:B:28:ARG:HA	2:B:31:ARG:HD3	1.59	0.82
1:A:508:GLN:HB3	3:A:1037:HOH:O	1.79	0.82
1:A:1:MET:HB3	1:A:6:ILE:HD11	1.60	0.81
1:A:23:LYS:HE3	1:A:27:ARG:NH1	1.96	0.80
1:A:654:LEU:HD13	1:A:673:LEU:HD22	1.64	0.79
1:A:32:ASN:HD22	1:A:34:PRO:HD2	1.48	0.79
1:A:139:ASN:ND2	1:A:141:ASN:H	1.81	0.78
1:A:320:GLN:HG2	3:A:991:HOH:O	1.84	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:734:VAL:HG23	3:A:920:HOH:O	1.85	0.76
1:A:633:SER:O	1:A:637:GLU:HG3	1.85	0.75
1:A:128:GLU:HB3	3:A:1011:HOH:O	1.86	0.75
1:A:419:ASP:O	1:A:425:ARG:HD3	1.89	0.73
1:A:713:ILE:O	1:A:716:VAL:HG12	1.88	0.73
1:A:403:LYS:O	1:A:407:ILE:HG12	1.88	0.72
1:A:181:MET:HE1	1:A:198:LEU:HD22	1.72	0.72
1:A:608:MET:O	1:A:612:LEU:HB2	1.90	0.71
1:A:105:ARG:HG2	3:A:908:HOH:O	1.88	0.71
1:A:626:GLU:CD	2:B:31:ARG:HH21	1.99	0.70
1:A:377:ASN:HD22	1:A:377:ASN:C	2.00	0.70
1:A:130:ILE:HG13	1:A:169:LYS:HD2	1.72	0.69
1:A:262:ALA:O	1:A:266:GLU:HG3	1.93	0.68
1:A:608:MET:CE	1:A:635:LEU:HD23	2.20	0.68
2:B:28:ARG:HG3	2:B:31:ARG:CZ	2.24	0.68
1:A:406:VAL:HG12	1:A:410:MET:HE2	1.76	0.68
1:A:123:VAL:HG23	1:A:125:GLN:HG3	1.75	0.68
1:A:815:VAL:HG22	1:A:846:LEU:HD11	1.76	0.67
1:A:630:MET:HE1	2:B:31:ARG:HG3	1.77	0.67
1:A:475:SER:O	1:A:479:GLU:HG3	1.94	0.67
1:A:32:ASN:ND2	1:A:34:PRO:HD2	2.10	0.67
1:A:626:GLU:OE1	1:A:665:GLN:HB3	1.95	0.66
1:A:13:PRO:HD2	3:A:992:HOH:O	1.95	0.65
1:A:211:LYS:HD2	1:A:214:GLU:CD	2.21	0.65
1:A:518:ASP:C	1:A:520:HIS:H	2.04	0.65
2:B:28:ARG:HG3	2:B:31:ARG:NH1	2.12	0.64
1:A:608:MET:HE1	1:A:632:VAL:HG13	1.78	0.64
1:A:614:MET:HE3	3:A:1027:HOH:O	1.97	0.64
1:A:6:ILE:HG21	1:A:24:PHE:HD2	1.63	0.64
1:A:498:CYS:SG	3:A:937:HOH:O	2.55	0.64
1:A:383:ARG:O	1:A:387:VAL:HG23	1.98	0.64
1:A:381:ARG:HD2	3:A:927:HOH:O	1.98	0.63
1:A:139:ASN:HD22	1:A:139:ASN:C	2.06	0.63
1:A:428:ALA:O	1:A:432:VAL:HG23	1.98	0.62
1:A:445:ASN:HD21	1:A:448:TYR:HB2	1.65	0.62
1:A:448:TYR:O	1:A:452:LEU:HB2	1.99	0.61
1:A:482:TYR:CE1	1:A:494:PRO:HG3	2.35	0.61
1:A:80:TRP:O	1:A:88:ARG:HD3	2.00	0.61
1:A:748:ASP:OD2	1:A:750:SER:HB3	2.00	0.60
1:A:413:LEU:HA	1:A:416:LEU:HD12	1.84	0.60
1:A:377:ASN:HD22	1:A:378:PRO:N	2.00	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:541:LYS:C	1:A:543:CYS:H	2.10	0.60
1:A:71:ASP:OD2	1:A:707:ARG:NH1	2.34	0.60
1:A:867:LYS:HB2	1:A:867:LYS:NZ	2.17	0.59
2:B:39:ARG:HA	2:B:42:LYS:HE3	1.84	0.59
1:A:777:LYS:HA	1:A:787:VAL:CG2	2.32	0.59
1:A:660:ASN:C	1:A:662:ALA:H	2.09	0.59
1:A:13:PRO:CD	3:A:992:HOH:O	2.50	0.59
1:A:177:ILE:HG22	1:A:181:MET:HE2	1.83	0.59
1:A:854:LYS:HD3	1:A:854:LYS:C	2.28	0.59
1:A:574:ARG:HB3	3:A:968:HOH:O	2.01	0.59
1:A:558:LEU:HD21	1:A:614:MET:SD	2.42	0.58
1:A:575:ILE:N	3:A:968:HOH:O	2.35	0.58
1:A:426:ASP:OD2	1:A:465:ARG:HG2	2.03	0.58
1:A:298:SER:O	1:A:302:GLU:HG2	2.03	0.58
2:B:39:ARG:HA	2:B:42:LYS:CE	2.33	0.58
1:A:834:LEU:HD11	1:A:873:LYS:CG	2.31	0.58
1:A:763:GLU:HG3	1:A:817:CYS:SG	2.44	0.58
1:A:35:THR:O	1:A:39:GLU:HG2	2.04	0.57
1:A:308:GLU:CD	1:A:308:GLU:H	2.12	0.57
1:A:748:ASP:C	1:A:750:SER:H	2.12	0.57
1:A:796:PHE:CE2	3:A:938:HOH:O	2.41	0.57
1:A:65:LEU:CD1	1:A:116:ILE:HG13	2.33	0.57
1:A:562:LEU:CD1	1:A:613:ARG:HH11	2.17	0.57
1:A:146:MET:HE2	1:A:150:THR:OG1	2.04	0.57
1:A:402:LEU:HD23	1:A:405:LEU:HD12	1.86	0.57
1:A:508:GLN:O	1:A:512:GLU:HG3	2.05	0.57
1:A:575:ILE:HG13	3:A:968:HOH:O	2.04	0.57
1:A:668:LEU:HD21	1:A:709:VAL:HA	1.85	0.57
1:A:338:ASP:HB3	1:A:341:ASP:HB2	1.86	0.56
1:A:561:VAL:O	1:A:564:MET:HB3	2.06	0.56
1:A:634:THR:O	1:A:638:VAL:HG23	2.05	0.56
1:A:410:MET:HE1	1:A:435:ILE:HG21	1.87	0.56
1:A:504:GLU:HG2	1:A:508:GLN:HE21	1.71	0.56
1:A:569:GLN:O	1:A:570:SER:HB3	2.06	0.56
1:A:729:LYS:HB2	1:A:729:LYS:NZ	2.21	0.56
1:A:588:LEU:O	1:A:592:LEU:HB2	2.06	0.55
1:A:412:THR:O	1:A:416:LEU:HG	2.05	0.55
1:A:6:ILE:HG12	1:A:24:PHE:CD2	2.42	0.55
1:A:626:GLU:O	1:A:630:MET:HG3	2.07	0.55
1:A:790:VAL:HG12	1:A:790:VAL:O	2.06	0.55
1:A:51:GLN:HG3	1:A:104:TYR:CD1	2.42	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:564:MET:C	1:A:566:SER:H	2.15	0.54
1:A:558:LEU:O	1:A:558:LEU:HD23	2.08	0.54
1:A:14:ASP:HB3	1:A:17:GLU:HB3	1.90	0.54
1:A:36:PHE:CZ	1:A:40:LEU:HD11	2.42	0.54
1:A:571:THR:N	3:A:1054:HOH:O	2.38	0.53
1:A:626:GLU:HG2	1:A:630:MET:HE2	1.89	0.53
1:A:162:ASP:OD2	1:A:750:SER:HB2	2.08	0.53
1:A:518:ASP:HB3	1:A:525:ARG:HH21	1.74	0.53
1:A:377:ASN:HD22	1:A:379:ASP:N	2.00	0.53
1:A:265:ILE:HD13	1:A:268:MET:CE	2.38	0.53
1:A:665:GLN:CD	2:B:28:ARG:HH21	2.17	0.53
1:A:397:PRO:HB2	1:A:402:LEU:HD11	1.91	0.53
1:A:668:LEU:HD22	1:A:712:GLN:HG3	1.91	0.53
1:A:518:ASP:C	1:A:520:HIS:N	2.67	0.52
1:A:562:LEU:HD13	1:A:613:ARG:HD2	1.90	0.52
1:A:869:LEU:O	1:A:873:LYS:HG3	2.10	0.52
2:B:28:ARG:CZ	2:B:31:ARG:NH2	2.73	0.52
1:A:51:GLN:NE2	1:A:104:TYR:HB3	2.25	0.52
1:A:609:ALA:O	1:A:613:ARG:HG3	2.09	0.52
1:A:774:GLN:HE22	1:A:777:LYS:NZ	2.08	0.52
2:B:48:LEU:C	2:B:50:ARG:H	2.18	0.52
1:A:220:GLN:O	1:A:224:GLU:HB2	2.10	0.52
1:A:807:ASP:OD2	1:A:809:ASP:HB2	2.10	0.52
1:A:268:MET:HE1	1:A:322:LEU:CD2	2.39	0.52
1:A:343:ASN:HB2	1:A:344:PRO:CD	2.40	0.52
1:A:333:GLN:O	1:A:334:ASP:HB2	2.10	0.52
1:A:598:GLN:N	1:A:598:GLN:OE1	2.43	0.51
1:A:211:LYS:HB2	1:A:214:GLU:HG3	1.92	0.51
1:A:706:HIS:CD2	1:A:708:SER:HB2	2.46	0.51
1:A:802:ASP:OD1	1:A:842:MET:HB2	2.10	0.51
1:A:4:ILE:N	1:A:4:ILE:HD12	2.25	0.51
2:B:30:ARG:N	3:B:156:HOH:O	2.43	0.51
1:A:26:GLU:O	1:A:30:VAL:HG23	2.10	0.51
1:A:182:ARG:HB2	1:A:184:GLU:OE1	2.11	0.51
1:A:296:GLU:O	1:A:299:GLU:HB3	2.11	0.51
1:A:541:LYS:O	1:A:543:CYS:N	2.44	0.51
1:A:660:ASN:O	1:A:661:TYR:CG	2.63	0.51
1:A:601:LEU:HD21	1:A:642:GLU:OE1	2.11	0.50
1:A:663:GLU:CG	3:A:928:HOH:O	2.42	0.50
1:A:686:ILE:HD13	1:A:727:GLU:HG3	1.92	0.50
1:A:479:GLU:O	1:A:483:GLU:HG3	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:673:LEU:C	1:A:673:LEU:HD23	2.36	0.50
1:A:23:LYS:HE3	1:A:27:ARG:CZ	2.42	0.50
1:A:202:LEU:HD12	1:A:243:LYS:HD3	1.94	0.50
1:A:552:LEU:HA	1:A:555:MET:CE	2.41	0.50
1:A:520:HIS:CE1	1:A:525:ARG:HB2	2.47	0.49
1:A:637:GLU:CD	2:B:42:LYS:HE2	2.37	0.49
1:A:338:ASP:HB3	1:A:341:ASP:CB	2.42	0.49
1:A:417:MET:O	1:A:425:ARG:HD2	2.12	0.49
1:A:536:VAL:HG11	1:A:591:VAL:HG12	1.95	0.49
1:A:661:TYR:CD1	1:A:661:TYR:C	2.89	0.49
1:A:139:ASN:HD22	1:A:141:ASN:N	2.04	0.49
1:A:706:HIS:HD2	1:A:708:SER:HB2	1.77	0.49
1:A:11:VAL:CG1	1:A:11:VAL:O	2.60	0.49
1:A:727:GLU:O	1:A:730:LYS:HD3	2.12	0.49
1:A:622:GLY:HA2	1:A:625:GLN:HE21	1.78	0.49
1:A:653:PHE:HA	1:A:656:ILE:HD12	1.94	0.49
1:A:693:MET:O	1:A:697:LEU:HG	2.12	0.49
1:A:504:GLU:HG2	1:A:508:GLN:NE2	2.28	0.49
1:A:710:LYS:HB3	1:A:711:PRO:CD	2.43	0.49
1:A:694:GLN:O	1:A:698:GLU:HG3	2.13	0.48
1:A:831:LYS:HE3	1:A:835:LYS:HE3	1.95	0.48
1:A:784:HIS:HD2	1:A:786:ASP:H	1.60	0.48
1:A:819:ALA:HB1	1:A:862:ALA:HA	1.94	0.48
1:A:562:LEU:HD13	1:A:613:ARG:HH11	1.78	0.48
1:A:660:ASN:O	1:A:662:ALA:N	2.41	0.48
2:B:31:ARG:HG2	2:B:32:ILE:HG13	1.96	0.48
1:A:552:LEU:HA	1:A:555:MET:HE2	1.96	0.48
2:B:30:ARG:CA	3:B:156:HOH:O	2.61	0.48
1:A:525:ARG:HG2	1:A:525:ARG:HH11	1.79	0.48
2:B:30:ARG:HA	3:B:156:HOH:O	2.14	0.48
1:A:226:THR:O	1:A:234:ARG:HG2	2.13	0.47
1:A:504:GLU:O	1:A:508:GLN:HG3	2.14	0.47
1:A:335:GLU:CD	1:A:335:GLU:H	2.21	0.47
1:A:562:LEU:HG	3:A:1027:HOH:O	2.14	0.47
1:A:834:LEU:HD22	1:A:838:GLU:OE1	2.14	0.47
1:A:541:LYS:C	1:A:543:CYS:N	2.72	0.47
1:A:653:PHE:O	1:A:656:ILE:HB	2.15	0.47
1:A:121:ILE:N	1:A:122:PRO:HD2	2.30	0.47
1:A:399:PRO:O	1:A:403:LYS:HG3	2.14	0.47
1:A:867:LYS:HB2	1:A:867:LYS:HZ3	1.79	0.47
1:A:787:VAL:HG12	1:A:829:PHE:CE1	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:261:PHE:O	1:A:265:ILE:HG12	2.14	0.47
1:A:562:LEU:CD2	3:A:1027:HOH:O	2.62	0.46
2:B:32:ILE:O	2:B:36:VAL:HG23	2.15	0.46
1:A:407:ILE:CD1	1:A:442:ALA:HA	2.46	0.46
1:A:686:ILE:N	1:A:687:PRO:HD2	2.30	0.46
1:A:73:LYS:O	1:A:77:GLN:HG3	2.16	0.46
1:A:570:SER:HB3	1:A:573:ASP:OD2	2.16	0.46
1:A:65:LEU:HD13	1:A:116:ILE:HG13	1.97	0.46
1:A:791:GLN:N	1:A:792:PRO:HD2	2.30	0.46
1:A:449:LEU:HD23	1:A:449:LEU:O	2.16	0.46
1:A:482:TYR:C	1:A:484:ALA:H	2.24	0.46
1:A:661:TYR:HB3	1:A:699:ASN:HD21	1.81	0.46
1:A:706:HIS:CD2	1:A:708:SER:H	2.34	0.46
1:A:104:TYR:CD1	1:A:104:TYR:N	2.84	0.46
1:A:558:LEU:HD23	3:A:1027:HOH:O	2.16	0.46
1:A:597:HIS:HE1	1:A:642:GLU:OE1	1.99	0.46
1:A:635:LEU:O	1:A:639:LEU:HD23	2.16	0.46
1:A:6:ILE:N	1:A:6:ILE:HD12	2.31	0.46
1:A:184:GLU:H	1:A:184:GLU:CD	2.24	0.46
1:A:226:THR:O	1:A:234:ARG:HD3	2.16	0.46
1:A:787:VAL:HG11	1:A:828:ALA:HB1	1.98	0.46
1:A:707:ARG:NH1	1:A:707:ARG:HB3	2.31	0.45
1:A:11:VAL:O	1:A:11:VAL:HG12	2.14	0.45
1:A:403:LYS:N	1:A:404:PRO:HD2	2.31	0.45
1:A:503:PHE:O	1:A:507:VAL:HG13	2.17	0.45
1:A:660:ASN:C	1:A:662:ALA:N	2.75	0.45
1:A:245:MET:HE3	1:A:249:TYR:HA	1.98	0.45
1:A:733:GLU:O	1:A:737:ASN:ND2	2.49	0.45
1:A:642:GLU:C	3:A:963:HOH:O	2.60	0.45
1:A:806:GLY:HA2	1:A:842:MET:HE2	1.98	0.45
1:A:601:LEU:HD21	1:A:642:GLU:CD	2.42	0.45
1:A:854:LYS:HD3	1:A:854:LYS:O	2.17	0.45
1:A:780:GLN:C	1:A:782:ASN:H	2.25	0.45
1:A:343:ASN:HB2	1:A:344:PRO:HD2	1.99	0.45
1:A:702:ASN:HB3	1:A:705:VAL:HG23	1.98	0.45
1:A:239:GLN:HG2	1:A:278:GLN:CD	2.41	0.45
1:A:403:LYS:HB2	1:A:404:PRO:CD	2.47	0.45
1:A:450:ALA:N	1:A:451:PRO:HD2	2.32	0.44
1:A:691:GLU:HG3	3:A:1021:HOH:O	2.17	0.44
1:A:14:ASP:HB2	3:A:992:HOH:O	2.17	0.44
1:A:522:ASN:O	1:A:523:ASN:C	2.60	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:840:ARG:HA	1:A:841:PRO:HD2	1.75	0.44
1:A:544:TYR:CZ	1:A:596:GLN:HG3	2.52	0.44
1:A:568:ILE:HG13	1:A:568:ILE:O	2.18	0.44
1:A:748:ASP:C	1:A:750:SER:N	2.71	0.44
1:A:2:GLU:O	1:A:6:ILE:HD13	2.17	0.44
1:A:294:ALA:O	1:A:297:ALA:HB3	2.18	0.44
1:A:448:TYR:C	1:A:451:PRO:HD2	2.42	0.44
1:A:504:GLU:O	1:A:507:VAL:HG22	2.17	0.44
1:A:211:LYS:CB	1:A:214:GLU:HG3	2.47	0.44
1:A:100:GLY:N	3:A:888:HOH:O	2.43	0.44
1:A:12:SER:C	1:A:14:ASP:H	2.25	0.44
1:A:12:SER:OG	1:A:14:ASP:HB3	2.18	0.43
1:A:300:ALA:HB1	1:A:305:ARG:O	2.18	0.43
1:A:412:THR:HA	1:A:415:GLU:OE1	2.18	0.43
1:A:834:LEU:HD22	1:A:838:GLU:CD	2.43	0.43
1:A:482:TYR:C	1:A:484:ALA:N	2.76	0.43
1:A:679:ARG:NH1	3:A:987:HOH:O	2.41	0.43
1:A:548:GLN:O	1:A:551:THR:HB	2.18	0.43
1:A:399:PRO:HA	1:A:439:LEU:HD21	2.00	0.43
1:A:410:MET:HE3	1:A:442:ALA:O	2.19	0.43
1:A:588:LEU:HG	1:A:592:LEU:HD22	2.00	0.43
1:A:73:LYS:HE2	1:A:77:GLN:NE2	2.34	0.43
1:A:357:THR:HG22	1:A:395:GLU:HG2	2.01	0.43
1:A:449:LEU:HD23	1:A:449:LEU:C	2.44	0.43
1:A:665:GLN:NE2	2:B:28:ARG:HH21	2.16	0.43
1:A:89:ARG:HA	1:A:92:LYS:HE3	1.99	0.42
1:A:751:ASP:HB3	1:A:754:MET:HB2	2.01	0.42
1:A:823:GLY:O	1:A:827:THR:HG22	2.19	0.42
1:A:751:ASP:O	1:A:755:VAL:HG23	2.19	0.42
1:A:139:ASN:HD21	1:A:141:ASN:HB2	1.84	0.42
1:A:46:ASN:HB3	1:A:49:ASN:ND2	2.34	0.42
1:A:331:THR:O	1:A:331:THR:HG22	2.19	0.42
1:A:201:SER:HB2	1:A:204:PHE:CZ	2.54	0.42
1:A:514:THR:HG22	1:A:557:ARG:HH12	1.84	0.42
1:A:234:ARG:NH2	3:A:896:HOH:O	2.39	0.42
1:A:406:VAL:HG21	1:A:439:LEU:HD12	2.01	0.42
1:A:615:PHE:CE1	1:A:625:GLN:HB3	2.55	0.42
1:A:622:GLY:HA2	1:A:625:GLN:NE2	2.35	0.42
1:A:157:ILE:HG23	1:A:161:ILE:HD12	2.02	0.42
1:A:383:ARG:NH1	1:A:419:ASP:OD2	2.47	0.42
1:A:32:ASN:HD22	1:A:32:ASN:C	2.28	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:134:VAL:HG21	1:A:172:GLU:HB3	2.00	0.42
1:A:139:ASN:ND2	1:A:139:ASN:C	2.76	0.42
1:A:651:LYS:N	1:A:652:PRO:HD2	2.34	0.42
2:B:28:ARG:HG2	2:B:28:ARG:O	2.20	0.42
1:A:870:ARG:HA	1:A:873:LYS:HD2	2.02	0.41
1:A:562:LEU:HD23	3:A:1027:HOH:O	2.20	0.41
1:A:572:SER:O	1:A:576:GLN:HG3	2.20	0.41
1:A:410:MET:CE	1:A:442:ALA:HB1	2.50	0.41
1:A:615:PHE:CG	1:A:616:GLN:N	2.88	0.41
1:A:544:TYR:N	1:A:545:PRO:HD2	2.35	0.41
1:A:635:LEU:HG	1:A:639:LEU:HD23	2.03	0.41
1:A:641:GLY:C	1:A:643:PHE:H	2.27	0.41
1:A:509:LYS:HD2	1:A:509:LYS:HA	1.90	0.41
1:A:592:LEU:HD12	1:A:592:LEU:HA	1.92	0.41
1:A:682:GLN:O	1:A:685:ILE:HG22	2.20	0.41
1:A:710:LYS:HB3	1:A:711:PRO:HD3	2.01	0.41
1:A:810:HIS:O	1:A:811:THR:HB	2.21	0.41
2:B:29:ARG:C	3:B:156:HOH:O	2.64	0.41
1:A:426:ASP:OD1	1:A:426:ASP:C	2.63	0.41
1:A:637:GLU:OE2	2:B:42:LYS:NZ	2.49	0.41
1:A:36:PHE:CE2	1:A:40:LEU:HD11	2.56	0.41
1:A:333:GLN:HG3	1:A:345:CYS:SG	2.60	0.41
1:A:831:LYS:HE3	1:A:835:LYS:CE	2.50	0.41
1:A:23:LYS:HE3	1:A:27:ARG:NH2	2.36	0.40
1:A:628:ALA:O	1:A:632:VAL:HG23	2.21	0.40
1:A:651:LYS:NZ	3:A:1034:HOH:O	2.38	0.40
1:A:679:ARG:NH2	3:A:987:HOH:O	2.48	0.40
1:A:787:VAL:HG12	1:A:829:PHE:CZ	2.56	0.40
1:A:4:ILE:HD12	1:A:4:ILE:H	1.85	0.40
1:A:300:ALA:O	1:A:304:GLY:N	2.54	0.40
1:A:444:ILE:O	1:A:444:ILE:HG22	2.20	0.40
1:A:776:LEU:HD12	1:A:776:LEU:HA	1.90	0.40
1:A:556:GLU:O	1:A:560:GLN:HG3	2.22	0.40
1:A:782:ASN:O	1:A:782:ASN:OD1	2.39	0.40
1:A:859:LYS:NZ	1:A:863:ARG:HH11	2.19	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	868/876 (99%)	794 (92%)	60 (7%)	14 (2%)	7	7
2	B	22/27 (82%)	20 (91%)	2 (9%)	0	100	100
All	All	890/903 (99%)	814 (92%)	62 (7%)	14 (2%)	7	7

All (14) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	572	SER
1	A	811	THR
1	A	362	ASP
1	A	487	VAL
1	A	518	ASP
1	A	542	ASP
1	A	853	SER
1	A	571	THR
1	A	664	TYR
1	A	565	GLU
1	A	749	LYS
1	A	661	TYR
1	A	809	ASP
1	A	517	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	748/751 (100%)	719 (96%)	29 (4%)	28	43
2	B	23/26 (88%)	23 (100%)	0	100	100
All	All	771/777 (99%)	742 (96%)	29 (4%)	29	44

All (29) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3	LEU
1	A	22	GLN
1	A	139	ASN
1	A	146	MET
1	A	224	GLU
1	A	234	ARG
1	A	274	GLU
1	A	281	GLU
1	A	285	ASN
1	A	290	GLU
1	A	308	GLU
1	A	377	ASN
1	A	422	VAL
1	A	474	PHE
1	A	497	TYR
1	A	514	THR
1	A	518	ASP
1	A	520	HIS
1	A	524	LEU
1	A	592	LEU
1	A	712	GLN
1	A	730	LYS
1	A	734	VAL
1	A	776	LEU
1	A	821	LEU
1	A	827	THR
1	A	834	LEU
1	A	859	LYS
1	A	867	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (33) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	32	ASN

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Mol	Chain	Res	Type
1	A	51	GLN
1	A	139	ASN
1	A	141	ASN
1	A	165	GLN
1	A	179	GLN
1	A	208	ASN
1	A	240	ASN
1	A	250	GLN
1	A	328	GLN
1	A	377	ASN
1	A	401	GLN
1	A	454	GLN
1	A	508	GLN
1	A	520	HIS
1	A	521	GLN
1	A	522	ASN
1	A	523	ASN
1	A	567	HIS
1	A	576	GLN
1	A	578	ASN
1	A	590	ASN
1	A	597	HIS
1	A	625	GLN
1	A	682	GLN
1	A	699	ASN
1	A	706	HIS
1	A	741	GLN
1	A	744	GLN
1	A	774	GLN
1	A	782	ASN
1	A	784	HIS
2	B	35	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [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.