



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 09:57 PM GMT

PDB ID : 1RFB
Title : CRYSTAL STRUCTURE OF RECOMBINANT BOVINE INTERFERON-
GAMMA AT 3.0 ANGSTROMS RESOLUTION
Authors : Samudzi, C.T.; Rubin, J.R.
Deposited on : 1993-06-30
Resolution : 3.00 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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

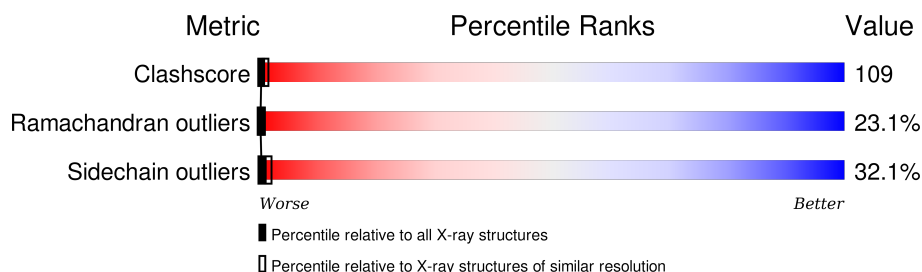
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 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	102246	1912 (3.00-3.00)
Ramachandran outliers	100387	1853 (3.00-3.00)
Sidechain outliers	100360	1856 (3.00-3.00)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	119	
1	B	119	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 2023 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 INTERFERON-GAMMA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	119	Total	C	N	O	S	0	0	0
			990	636	163	188	3			
1	B	119	Total	C	N	O	S	0	0	0
			990	636	163	188	3			

- Molecule 2 is water.

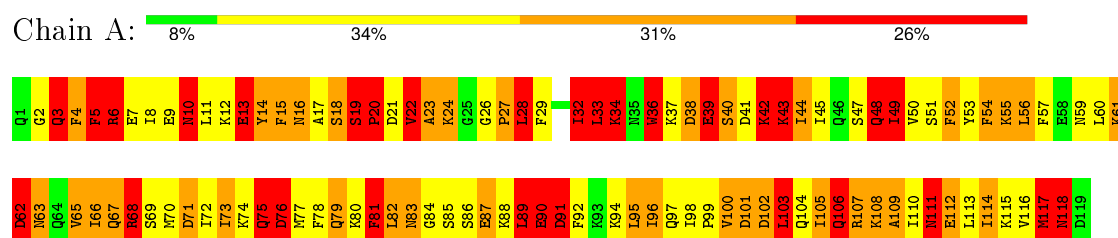
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	20	Total	O	0	0
			20	20		
2	B	23	Total	O	0	0
			23	23		

3 Residue-property plots

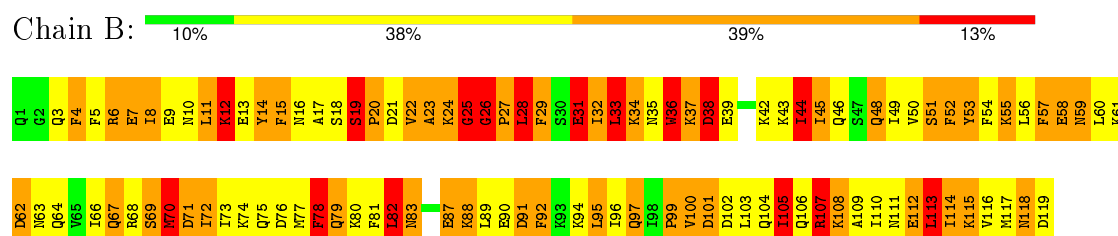
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according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

Note EDS was not executed.

• Molecule 1: INTERFERON-GAMMA



• Molecule 1: INTERFERON-GAMMA



4 Data and refinement statistics

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

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	42.80 Å 79.90 Å 85.40 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	(Not available) – 3.00	Depositor
% Data completeness (in resolution range)	(Not available) ((Not available)-3.00)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR	Depositor
R, R_{free}	0.192 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	2023	wwPDB-VP
Average B, all atoms (Å ²)	37.0	wwPDB-VP

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	1.03	1/1006 (0.1%)	2.27	51/1343 (3.8%)
1	B	1.02	3/1006 (0.3%)	2.27	46/1343 (3.4%)
All	All	1.03	4/2012 (0.2%)	2.27	97/2686 (3.6%)

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	B	0	4

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	26	GLY	C-O	8.45	1.37	1.23
1	B	20	PRO	N-CD	7.59	1.58	1.47
1	B	26	GLY	CA-C	-6.59	1.41	1.51
1	A	20	PRO	CA-CB	5.31	1.64	1.53

All (97) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	26	GLY	CA-C-O	-21.34	82.19	120.60
1	B	26	GLY	CA-C-N	16.15	162.33	117.10
1	B	20	PRO	CA-N-CD	-14.35	91.41	111.50
1	B	19	SER	CA-C-O	-13.45	91.86	120.10
1	B	20	PRO	N-CA-CB	12.46	118.25	103.30
1	A	36	TRP	CA-CB-CG	-11.73	91.42	113.70
1	A	2	GLY	C-N-CA	11.63	150.78	121.70
1	B	91	ASP	CB-CG-OD1	11.54	128.69	118.30
1	A	20	PRO	N-CA-CB	-10.61	90.57	103.30
1	A	20	PRO	N-CA-C	9.89	137.82	112.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	21	ASP	CB-CG-OD1	8.88	126.29	118.30
1	A	15	PHE	CA-CB-CG	8.78	134.97	113.90
1	A	107	ARG	NE-CZ-NH1	8.54	124.57	120.30
1	B	26	GLY	O-C-N	-8.53	104.89	121.10
1	B	19	SER	C-N-CD	-8.31	102.32	120.60
1	A	10	ASN	CA-CB-CG	8.13	131.28	113.40
1	A	78	PHE	CA-CB-CG	7.88	132.81	113.90
1	A	117	MET	CB-CA-C	7.82	126.05	110.40
1	A	22	VAL	N-CA-C	-7.68	90.26	111.00
1	B	107	ARG	NE-CZ-NH1	7.66	124.13	120.30
1	A	81	PHE	CA-CB-CG	7.47	131.82	113.90
1	A	49	ILE	C-N-CA	7.47	140.37	121.70
1	A	83	ASN	N-CA-CB	7.10	123.38	110.60
1	A	62	ASP	C-N-CA	6.98	139.14	121.70
1	A	89	LEU	CA-CB-CG	6.83	131.01	115.30
1	A	22	VAL	CA-C-O	-6.76	105.91	120.10
1	A	118	ASN	C-N-CA	6.72	138.49	121.70
1	A	82	LEU	C-N-CA	6.69	138.43	121.70
1	B	78	PHE	N-CA-CB	6.62	122.52	110.60
1	A	105	ILE	C-N-CA	6.58	138.14	121.70
1	A	36	TRP	N-CA-C	6.57	128.72	111.00
1	B	71	ASP	CB-CG-OD1	6.52	124.17	118.30
1	A	3	GLN	N-CA-C	6.51	128.57	111.00
1	A	28	LEU	N-CA-C	6.48	128.50	111.00
1	B	21	ASP	CB-CG-OD2	-6.45	112.50	118.30
1	B	58	GLU	CB-CG-CD	6.36	131.37	114.20
1	A	103	LEU	C-N-CA	6.31	137.48	121.70
1	B	69	SER	CA-CB-OG	6.29	128.19	111.20
1	B	62	ASP	CB-CG-OD1	6.28	123.95	118.30
1	B	102	ASP	CB-CG-OD1	6.24	123.91	118.30
1	B	107	ARG	NE-CZ-NH2	-6.23	117.19	120.30
1	A	89	LEU	N-CA-CB	-6.21	97.98	110.40
1	A	117	MET	N-CA-CB	-6.15	99.52	110.60
1	A	71	ASP	CB-CG-OD2	-6.11	112.81	118.30
1	A	83	ASN	CA-CB-CG	-6.03	100.13	113.40
1	B	57	PHE	CB-CA-C	5.99	122.39	110.40
1	B	91	ASP	CB-CG-OD2	-5.97	112.93	118.30
1	B	71	ASP	CB-CG-OD2	-5.96	112.94	118.30
1	A	91	ASP	CB-CG-OD2	-5.93	112.96	118.30
1	A	75	GLN	CB-CG-CD	5.93	127.01	111.60
1	A	38	ASP	CB-CG-OD2	5.88	123.59	118.30
1	A	90	GLU	CB-CA-C	-5.84	98.72	110.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	19	SER	O-C-N	5.83	132.17	121.10
1	B	31	GLU	CA-CB-CG	5.82	126.20	113.40
1	A	13	GLU	CB-CG-CD	5.79	129.85	114.20
1	A	20	PRO	CB-CA-C	-5.77	97.58	112.00
1	B	22	VAL	CB-CA-C	5.76	122.35	111.40
1	A	90	GLU	CA-CB-CG	5.75	126.06	113.40
1	A	112	GLU	CG-CD-OE2	5.74	129.78	118.30
1	A	27	PRO	C-N-CA	5.71	135.99	121.70
1	B	53	TYR	CB-CA-C	5.70	121.80	110.40
1	B	27	PRO	N-CA-CB	5.68	110.12	103.30
1	B	19	SER	C-N-CA	5.68	145.84	122.00
1	B	26	GLY	N-CA-C	5.65	127.22	113.10
1	A	68	ARG	NE-CZ-NH2	5.64	123.12	120.30
1	A	66	ILE	N-CA-CB	5.63	123.75	110.80
1	B	69	SER	N-CA-CB	5.59	118.88	110.50
1	B	38	ASP	CB-CG-OD1	5.59	123.33	118.30
1	B	58	GLU	N-CA-CB	5.57	120.63	110.60
1	A	52	PHE	N-CA-CB	5.57	120.62	110.60
1	A	6	ARG	N-CA-C	5.54	125.97	111.00
1	B	70	MET	CA-CB-CG	5.46	122.58	113.30
1	B	102	ASP	CA-CB-CG	5.44	125.37	113.40
1	A	39	GLU	C-N-CA	5.41	135.23	121.70
1	B	12	LYS	CA-CB-CG	5.41	125.29	113.40
1	A	48	GLN	CB-CG-CD	5.40	125.65	111.60
1	A	5	PHE	CA-CB-CG	5.40	126.86	113.90
1	B	27	PRO	N-CD-CG	5.39	111.29	103.20
1	B	62	ASP	CA-CB-CG	5.36	125.20	113.40
1	A	42	LYS	C-N-CA	5.36	135.10	121.70
1	B	113	LEU	CB-CA-C	5.23	120.13	110.20
1	B	82	LEU	N-CA-C	5.22	125.11	111.00
1	A	107	ARG	CD-NE-CZ	5.22	130.90	123.60
1	B	78	PHE	CA-CB-CG	5.21	126.39	113.90
1	A	23	ALA	CB-CA-C	5.20	117.90	110.10
1	A	117	MET	N-CA-C	-5.20	96.97	111.00
1	B	15	PHE	CA-CB-CG	5.18	126.34	113.90
1	B	92	PHE	N-CA-CB	5.17	119.90	110.60
1	A	79	GLN	CB-CG-CD	5.14	124.98	111.60
1	A	10	ASN	CB-CA-C	5.14	120.69	110.40
1	B	99	PRO	C-N-CA	5.11	134.47	121.70
1	B	55	LYS	N-CA-CB	5.10	119.77	110.60
1	B	90	GLU	C-N-CA	5.09	134.44	121.70
1	B	70	MET	CB-CA-C	5.08	120.55	110.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	76	ASP	CB-CG-OD1	-5.06	113.75	118.30
1	B	25	GLY	N-CA-C	-5.06	100.46	113.10
1	A	109	ALA	N-CA-CB	-5.00	103.09	110.10

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	19	SER	Mainchain,Peptide
1	B	26	GLY	Mainchain,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	990	0	999	241	1
1	B	990	0	1002	237	1
2	A	20	0	0	12	0
2	B	23	0	0	15	0
All	All	2023	0	2001	433	1

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 109.

All (433) 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:8:ILE:HA	2:A:443:HOH:O	1.42	1.17
1:A:19:SER:HB3	1:A:20:PRO:CD	1.74	1.16
1:A:19:SER:CB	1:A:20:PRO:HD3	1.75	1.16
1:A:8:ILE:HD13	1:A:69:SER:HB3	1.25	1.10
1:A:105:ILE:HD12	1:B:28:LEU:HG	1.28	1.09
1:A:44:ILE:HG23	1:B:82:LEU:HD13	1.30	1.06
1:B:8:ILE:HD12	1:B:72:ILE:CG2	1.87	1.04
1:B:79:GLN:HA	1:B:83:ASN:HB2	1.39	1.03

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:19:SER:HB3	1:A:20:PRO:HD3	1.02	1.02
1:A:22:VAL:O	1:A:24:LYS:N	1.92	1.01
1:A:3:GLN:HG3	1:A:4:PHE:H	1.23	0.99
1:B:3:GLN:HB3	1:B:6:ARG:NH1	1.76	0.99
1:A:28:LEU:O	1:A:32:ILE:HD13	1.64	0.98
1:A:114:ILE:HG23	2:A:407:HOH:O	1.64	0.97
1:B:118:ASN:O	1:B:119:ASP:HB2	1.59	0.97
1:B:28:LEU:O	1:B:32:ILE:HG12	1.65	0.97
1:A:69:SER:HA	1:A:72:ILE:HG22	1.46	0.96
1:B:37:LYS:H	1:B:37:LYS:HD3	1.27	0.96
1:A:61:LYS:HA	1:A:67:GLN:NE2	1.80	0.95
1:A:82:LEU:HD13	1:A:84:GLY:H	1.31	0.94
1:A:81:PHE:HB3	1:A:88:LYS:HZ1	1.33	0.93
1:A:92:PHE:HA	1:A:95:LEU:HB2	1.51	0.92
1:A:117:MET:O	1:A:118:ASN:HB2	1.67	0.92
1:B:62:ASP:HB3	1:B:66:ILE:HB	1.50	0.89
1:B:108:LYS:HZ1	1:B:111:ASN:HB2	1.38	0.89
1:A:18:SER:O	1:A:19:SER:HB2	1.70	0.89
1:A:36:TRP:HE1	1:A:45:ILE:HD13	1.34	0.89
1:A:47:SER:HB3	1:B:44:ILE:HD13	1.55	0.88
1:A:105:ILE:HG12	1:B:29:PHE:CD2	2.08	0.88
1:A:86:SER:HB3	2:A:416:HOH:O	1.74	0.86
1:A:44:ILE:HD12	1:A:45:ILE:HG13	1.59	0.85
1:B:88:LYS:HD2	1:B:91:ASP:HB2	1.57	0.84
1:A:8:ILE:HG22	2:A:401:HOH:O	1.77	0.84
1:B:7:GLU:HA	1:B:10:ASN:ND2	1.93	0.84
1:B:52:PHE:HE1	1:B:56:LEU:HD13	1.43	0.84
1:A:44:ILE:HG13	1:A:45:ILE:H	1.43	0.83
1:B:3:GLN:O	1:B:5:PHE:N	2.10	0.83
1:B:55:LYS:O	2:B:438:HOH:O	1.95	0.83
1:A:55:LYS:HB2	1:A:55:LYS:NZ	1.92	0.83
1:B:32:ILE:HG22	1:B:33:LEU:HD12	1.60	0.82
1:B:113:LEU:O	1:B:116:VAL:HG23	1.79	0.82
1:B:18:SER:O	1:B:19:SER:HB3	1.79	0.81
1:B:12:LYS:N	1:B:12:LYS:HZ3	1.77	0.81
1:A:105:ILE:HD11	1:B:29:PHE:HB2	1.62	0.81
1:B:89:LEU:HD23	2:B:420:HOH:O	1.80	0.81
1:B:108:LYS:HZ1	1:B:111:ASN:CB	1.94	0.80
1:A:82:LEU:HD13	1:A:84:GLY:N	1.96	0.80
1:B:36:TRP:HE3	1:B:36:TRP:N	1.80	0.80
1:A:82:LEU:CD1	1:A:84:GLY:H	1.94	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:44:ILE:CG1	1:A:45:ILE:H	1.91	0.80
1:B:67:GLN:HG3	1:B:68:ARG:N	1.98	0.78
1:B:81:PHE:HB3	2:B:425:HOH:O	1.83	0.78
1:B:56:LEU:HD12	1:B:59:ASN:ND2	2.00	0.77
1:B:26:GLY:HA3	1:B:28:LEU:HD22	1.65	0.77
1:A:70:MET:HA	1:A:73:ILE:CD1	2.15	0.77
1:B:24:LYS:O	1:B:26:GLY:N	2.17	0.76
1:A:82:LEU:HB3	1:A:88:LYS:HD3	1.67	0.76
1:A:11:LEU:O	1:A:14:TYR:N	2.17	0.76
1:B:116:VAL:HG12	1:B:117:MET:HG3	1.66	0.76
1:A:11:LEU:HD13	1:A:14:TYR:HD2	1.50	0.76
1:B:107:ARG:NH2	1:B:108:LYS:HA	2.01	0.76
1:A:108:LYS:NZ	1:A:110:ILE:HG23	2.00	0.76
1:B:64:GLN:HE21	1:B:68:ARG:NE	1.83	0.76
1:A:3:GLN:CG	1:A:4:PHE:H	1.99	0.75
1:A:96:ILE:HG23	1:A:97:GLN:H	1.49	0.75
1:B:15:PHE:HZ	1:B:73:ILE:HD13	1.50	0.75
1:B:8:ILE:HD12	1:B:72:ILE:HG23	1.66	0.75
1:B:43:LYS:O	1:B:46:GLN:HG2	1.87	0.75
1:A:54:PHE:CE1	1:A:74:LYS:HG2	2.22	0.74
1:A:105:ILE:CD1	1:B:28:LEU:HG	2.12	0.74
1:A:110:ILE:O	1:A:112:GLU:HG2	1.87	0.74
1:B:62:ASP:OD2	1:B:66:ILE:HD12	1.88	0.74
1:A:53:TYR:CE1	1:B:109:ALA:HA	2.23	0.73
1:B:28:LEU:HA	1:B:31:GLU:HG3	1.70	0.73
1:B:37:LYS:HD3	1:B:37:LYS:N	2.02	0.73
1:B:52:PHE:CZ	1:B:56:LEU:HD22	2.24	0.73
1:A:48:GLN:HE22	1:B:48:GLN:HE22	1.37	0.73
1:B:37:LYS:H	1:B:37:LYS:CD	1.95	0.73
1:A:62:ASP:OD1	1:A:65:VAL:HB	1.89	0.72
1:B:81:PHE:O	1:B:82:LEU:HD12	1.88	0.72
1:A:53:TYR:CZ	1:B:109:ALA:HA	2.24	0.72
1:B:12:LYS:HA	1:B:15:PHE:CD2	2.24	0.72
1:B:61:LYS:HB2	2:B:424:HOH:O	1.89	0.72
1:A:57:PHE:HB3	1:A:70:MET:HG3	1.71	0.72
1:B:35:ASN:O	1:B:38:ASP:OD1	2.07	0.72
1:B:8:ILE:HD12	1:B:72:ILE:HG22	1.72	0.71
1:A:43:LYS:HG3	1:A:44:ILE:H	1.55	0.71
1:A:105:ILE:HG12	1:B:29:PHE:HD2	1.56	0.70
1:A:112:GLU:HG3	1:B:80:LYS:HE2	1.71	0.70
1:B:26:GLY:CA	1:B:28:LEU:HD22	2.21	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:50:VAL:O	1:B:54:PHE:HD1	1.73	0.70
1:A:7:GLU:O	1:A:10:ASN:OD1	2.08	0.70
2:A:426:HOH:O	1:B:50:VAL:HG22	1.91	0.69
1:B:32:ILE:O	1:B:36:TRP:CH2	2.45	0.69
1:B:8:ILE:HD13	2:B:409:HOH:O	1.92	0.69
1:B:36:TRP:CE3	1:B:36:TRP:N	2.61	0.69
1:A:81:PHE:HB3	1:A:88:LYS:NZ	2.07	0.69
1:A:57:PHE:HD2	1:A:74:LYS:HB2	1.56	0.69
1:A:91:ASP:C	1:A:95:LEU:HD12	2.14	0.68
1:A:11:LEU:HD23	2:A:402:HOH:O	1.94	0.68
1:A:44:ILE:HD12	1:A:45:ILE:CG1	2.23	0.68
1:A:69:SER:CA	1:A:72:ILE:HG22	2.24	0.67
1:B:108:LYS:O	1:B:108:LYS:NZ	2.26	0.67
1:B:10:ASN:O	1:B:13:GLU:OE1	2.11	0.67
1:B:36:TRP:HB3	2:B:403:HOH:O	1.95	0.67
1:B:61:LYS:O	1:B:61:LYS:HG2	1.95	0.67
1:A:44:ILE:HG23	1:B:82:LEU:CD1	2.18	0.67
1:B:46:GLN:HA	1:B:49:ILE:CD1	2.25	0.67
1:B:12:LYS:HG3	1:B:15:PHE:HE2	1.59	0.67
1:A:8:ILE:HD12	1:A:8:ILE:O	1.95	0.66
1:A:8:ILE:HD13	1:A:69:SER:CB	2.14	0.66
1:A:36:TRP:H	1:A:36:TRP:HE3	1.40	0.66
1:B:27:PRO:HG2	1:B:31:GLU:HG2	1.76	0.66
1:A:3:GLN:HG3	1:A:4:PHE:N	2.05	0.66
1:B:75:GLN:O	1:B:79:GLN:NE2	2.28	0.66
1:A:24:LYS:O	1:A:24:LYS:HE2	1.96	0.66
1:A:18:SER:O	1:A:19:SER:CB	2.43	0.65
1:B:16:ASN:OD1	1:B:17:ALA:N	2.29	0.65
1:A:82:LEU:H	1:A:88:LYS:NZ	1.93	0.65
1:A:104:GLN:HG3	1:B:56:LEU:HD11	1.78	0.65
1:A:82:LEU:HD12	1:A:88:LYS:CG	2.27	0.65
1:A:111:ASN:HD22	1:A:112:GLU:H	1.43	0.64
1:A:33:LEU:HD23	1:A:49:ILE:HD13	1.78	0.64
1:A:44:ILE:HG13	1:A:45:ILE:N	2.12	0.64
1:A:47:SER:HB3	1:B:44:ILE:CD1	2.26	0.64
1:A:82:LEU:HB3	1:A:88:LYS:NZ	2.13	0.64
1:A:57:PHE:CG	1:A:70:MET:HB2	2.32	0.64
1:A:76:ASP:O	1:A:79:GLN:HG2	1.98	0.64
1:A:108:LYS:HZ1	1:A:110:ILE:HG23	1.62	0.64
1:A:14:TYR:HB3	1:A:66:ILE:HD11	1.80	0.63
1:B:97:GLN:O	1:B:99:PRO:HD3	1.96	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:99:PRO:O	1:A:100:VAL:O	2.17	0.63
1:B:13:GLU:HA	1:B:16:ASN:ND2	2.14	0.63
1:A:8:ILE:HG13	1:A:12:LYS:HZ1	1.64	0.63
1:B:28:LEU:HD23	1:B:29:PHE:H	1.63	0.63
1:A:11:LEU:HD13	1:A:14:TYR:CD2	2.32	0.62
1:A:36:TRP:NE1	1:A:45:ILE:HD13	2.12	0.62
1:B:89:LEU:HD12	2:B:433:HOH:O	1.99	0.62
1:A:82:LEU:N	1:A:88:LYS:HZ1	1.98	0.62
1:B:24:LYS:HD2	1:B:25:GLY:H	1.64	0.62
1:A:108:LYS:HB3	1:B:29:PHE:CE1	2.35	0.61
1:B:52:PHE:CE1	1:B:56:LEU:HD13	2.30	0.61
1:A:51:SER:O	1:A:55:LYS:NZ	2.34	0.61
1:A:69:SER:O	1:A:73:ILE:CD1	2.49	0.61
1:B:111:ASN:O	1:B:114:ILE:HG22	2.00	0.61
1:B:92:PHE:CD2	1:B:92:PHE:C	2.74	0.61
1:A:67:GLN:NE2	1:A:70:MET:SD	2.74	0.61
1:A:14:TYR:HB3	1:A:66:ILE:CD1	2.31	0.60
1:B:88:LYS:HD2	1:B:88:LYS:O	2.01	0.60
1:B:3:GLN:HB3	1:B:6:ARG:HH12	1.64	0.60
1:A:36:TRP:N	1:A:36:TRP:CE3	2.68	0.60
1:B:12:LYS:H	1:B:12:LYS:HZ3	1.49	0.60
1:B:45:ILE:HG13	1:B:46:GLN:OE1	2.01	0.60
1:A:44:ILE:CG2	1:B:82:LEU:HD22	2.32	0.60
1:A:70:MET:HA	1:A:73:ILE:HD11	1.83	0.60
1:A:82:LEU:N	1:A:88:LYS:NZ	2.49	0.60
1:B:12:LYS:HG3	1:B:15:PHE:CE2	2.37	0.60
1:B:76:ASP:HA	1:B:79:GLN:NE2	2.17	0.60
1:A:105:ILE:HB	2:A:429:HOH:O	2.02	0.60
1:A:3:GLN:C	1:A:5:PHE:H	2.04	0.59
1:B:46:GLN:O	1:B:49:ILE:HG12	2.02	0.59
1:B:11:LEU:HD22	1:B:69:SER:OG	2.02	0.59
1:B:36:TRP:CB	1:B:37:LYS:HD3	2.31	0.59
1:A:48:GLN:OE1	1:B:95:LEU:HD22	2.02	0.59
1:B:58:GLU:N	2:B:413:HOH:O	2.35	0.59
1:A:53:TYR:O	1:A:56:LEU:HB3	2.02	0.59
1:A:55:LYS:HB2	1:A:55:LYS:HZ3	1.66	0.59
1:A:44:ILE:HG12	1:B:82:LEU:HD22	1.85	0.59
1:B:23:ALA:O	1:B:24:LYS:HB2	2.02	0.59
1:A:57:PHE:HB3	1:A:70:MET:CG	2.32	0.59
1:B:83:ASN:O	1:B:83:ASN:ND2	2.33	0.59
1:A:36:TRP:HE1	1:A:45:ILE:CD1	2.11	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:82:LEU:HB3	1:A:88:LYS:CD	2.33	0.58
1:B:36:TRP:HB2	1:B:37:LYS:HD3	1.85	0.58
1:A:5:PHE:HA	1:A:9:GLU:OE2	2.03	0.58
1:A:7:GLU:C	1:A:10:ASN:HB3	2.24	0.58
1:A:36:TRP:CD1	1:A:45:ILE:HG21	2.38	0.58
1:B:107:ARG:HH21	1:B:108:LYS:HA	1.68	0.58
1:A:82:LEU:HD13	1:A:83:ASN:N	2.20	0.57
1:A:105:ILE:HD11	1:B:29:PHE:CB	2.33	0.57
1:B:70:MET:O	1:B:74:LYS:HB2	2.03	0.57
1:A:42:LYS:O	1:A:44:ILE:HG12	2.04	0.57
1:A:101:ASP:C	1:A:103:LEU:H	2.07	0.57
1:A:82:LEU:HB3	1:A:88:LYS:HZ2	1.69	0.57
1:A:7:GLU:HA	1:A:10:ASN:OD1	2.05	0.57
1:B:107:ARG:NH2	1:B:108:LYS:HE2	2.20	0.57
1:A:82:LEU:HD12	1:A:88:LYS:HD3	1.87	0.56
1:A:44:ILE:HG12	1:B:82:LEU:CD2	2.35	0.56
1:B:15:PHE:CZ	1:B:73:ILE:HD13	2.36	0.56
1:A:92:PHE:N	1:A:95:LEU:HD12	2.20	0.56
1:B:92:PHE:HB3	2:B:433:HOH:O	2.05	0.56
1:A:107:ARG:C	1:A:109:ALA:H	2.08	0.56
1:A:52:PHE:CD1	1:A:52:PHE:O	2.59	0.56
1:B:67:GLN:O	1:B:70:MET:HG2	2.06	0.56
1:B:26:GLY:C	1:B:28:LEU:HD22	2.27	0.55
1:A:28:LEU:C	1:A:32:ILE:HD13	2.26	0.55
1:A:42:LYS:HZ3	1:A:42:LYS:H	1.52	0.55
1:A:61:LYS:O	1:A:63:ASN:N	2.39	0.55
1:A:40:SER:C	1:A:42:LYS:HZ3	2.09	0.55
1:A:22:VAL:HG13	1:A:24:LYS:HB2	1.87	0.55
1:B:62:ASP:CB	1:B:66:ILE:HB	2.32	0.55
1:A:57:PHE:CE2	1:A:73:ILE:HD13	2.41	0.55
1:B:111:ASN:O	1:B:113:LEU:N	2.40	0.55
1:A:87:GLU:OE1	1:A:87:GLU:HA	2.08	0.54
1:A:42:LYS:NZ	1:A:42:LYS:H	2.05	0.54
1:A:43:LYS:CG	1:A:44:ILE:H	2.20	0.54
1:B:116:VAL:HG12	1:B:117:MET:N	2.21	0.54
1:B:3:GLN:C	1:B:5:PHE:H	2.09	0.54
1:B:45:ILE:HD12	1:B:49:ILE:HG23	1.90	0.54
1:B:24:LYS:C	1:B:26:GLY:N	2.57	0.54
1:B:100:VAL:O	1:B:100:VAL:HG12	2.07	0.54
1:A:91:ASP:O	1:A:94:LYS:HB3	2.07	0.54
1:B:5:PHE:O	1:B:9:GLU:HG2	2.08	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:28:LEU:O	1:B:32:ILE:N	2.30	0.54
1:A:48:GLN:NE2	1:B:48:GLN:HE22	2.04	0.54
1:A:44:ILE:CG2	1:B:82:LEU:HD13	2.22	0.54
1:A:44:ILE:CG1	1:B:82:LEU:HD22	2.37	0.54
1:B:89:LEU:HA	2:B:433:HOH:O	2.07	0.54
1:A:60:LEU:O	1:A:70:MET:HE1	2.08	0.53
1:B:24:LYS:CD	1:B:25:GLY:H	2.21	0.53
1:B:94:LYS:HE2	1:B:95:LEU:HD23	1.90	0.53
1:A:105:ILE:O	1:A:107:ARG:N	2.31	0.53
1:B:24:LYS:C	1:B:26:GLY:H	2.09	0.53
1:B:107:ARG:HH21	1:B:110:ILE:HG22	1.73	0.53
1:A:105:ILE:HD11	1:B:29:PHE:H	1.71	0.53
1:A:95:LEU:CD2	1:B:48:GLN:HB3	2.38	0.53
1:A:82:LEU:HB3	1:A:88:LYS:CE	2.39	0.53
1:B:64:GLN:HE21	1:B:68:ARG:CZ	2.21	0.53
1:A:108:LYS:HZ3	1:A:110:ILE:HG23	1.74	0.53
1:A:41:ASP:N	1:A:42:LYS:HZ3	2.07	0.53
1:B:91:ASP:O	1:B:95:LEU:HG	2.09	0.52
1:B:96:ILE:O	1:B:97:GLN:CB	2.57	0.52
1:A:80:LYS:NZ	1:B:113:LEU:O	2.32	0.52
1:B:108:LYS:NZ	1:B:111:ASN:HB2	2.19	0.52
1:B:99:PRO:O	1:B:104:GLN:NE2	2.42	0.52
1:A:66:ILE:O	1:A:68:ARG:N	2.43	0.52
1:B:100:VAL:O	1:B:101:ASP:O	2.28	0.52
1:A:21:ASP:OD1	1:A:24:LYS:HB2	2.10	0.52
1:A:87:GLU:OE1	1:A:87:GLU:CA	2.57	0.52
1:B:5:PHE:N	1:B:5:PHE:CD1	2.76	0.52
1:B:5:PHE:HB3	1:B:9:GLU:CG	2.39	0.52
1:B:64:GLN:NE2	1:B:68:ARG:NE	2.55	0.52
1:B:107:ARG:HE	1:B:107:ARG:C	2.13	0.51
1:A:33:LEU:CD2	1:A:49:ILE:HD13	2.40	0.51
1:B:96:ILE:O	1:B:97:GLN:HB3	2.10	0.51
1:B:79:GLN:HG3	1:B:83:ASN:OD1	2.11	0.51
1:A:9:GLU:O	1:A:12:LYS:HG2	2.10	0.51
1:A:61:LYS:CA	1:A:67:GLN:NE2	2.64	0.51
1:B:114:ILE:C	1:B:116:VAL:H	2.14	0.51
1:A:95:LEU:HD11	1:B:45:ILE:CG2	2.41	0.51
1:B:42:LYS:HZ2	1:B:45:ILE:HG23	1.75	0.51
1:B:101:ASP:N	1:B:104:GLN:OE1	2.43	0.51
1:A:110:ILE:HD11	1:A:113:LEU:HD11	1.91	0.51
1:B:29:PHE:HZ	1:B:53:TYR:OH	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:6:ARG:O	1:A:10:ASN:HB2	2.11	0.51
1:B:76:ASP:O	1:B:79:GLN:HB2	2.10	0.51
1:A:92:PHE:HA	1:A:95:LEU:HD12	1.93	0.51
1:A:86:SER:O	1:A:89:LEU:HB3	2.10	0.51
1:B:12:LYS:HE3	1:B:15:PHE:CE2	2.46	0.51
1:A:16:ASN:O	1:A:17:ALA:HB3	2.11	0.51
1:A:54:PHE:CD1	1:A:74:LYS:HG2	2.45	0.51
1:A:111:ASN:ND2	1:A:112:GLU:H	2.08	0.51
1:A:43:LYS:CG	1:A:44:ILE:N	2.74	0.50
1:A:43:LYS:HE3	1:B:43:LYS:HB3	1.94	0.50
1:B:4:PHE:CE1	1:B:8:ILE:HG21	2.47	0.50
1:B:12:LYS:HA	1:B:15:PHE:CE2	2.46	0.50
1:A:54:PHE:HA	1:A:74:LYS:HD2	1.94	0.50
1:B:44:ILE:HG13	1:B:45:ILE:N	2.27	0.50
1:B:79:GLN:CG	1:B:83:ASN:OD1	2.59	0.50
1:B:56:LEU:HA	1:B:59:ASN:HD22	1.77	0.50
2:A:437:HOH:O	1:B:15:PHE:HB2	2.10	0.50
1:A:11:LEU:HD22	1:A:14:TYR:CD2	2.46	0.50
1:A:70:MET:HA	1:A:73:ILE:HD12	1.92	0.50
1:B:37:LYS:O	1:B:39:GLU:N	2.45	0.50
1:B:59:ASN:OD1	1:B:60:LEU:HD23	2.12	0.50
1:A:112:GLU:CG	1:B:80:LYS:HE2	2.41	0.49
1:B:57:PHE:HB3	1:B:70:MET:HB2	1.94	0.49
1:A:70:MET:CA	1:A:73:ILE:HD12	2.42	0.49
1:A:77:MET:HA	1:A:80:LYS:HG2	1.92	0.49
1:A:105:ILE:CG1	1:B:29:PHE:CD2	2.89	0.49
1:A:105:ILE:CD1	1:B:29:PHE:HB2	2.39	0.49
1:A:19:SER:CB	1:A:20:PRO:CD	2.52	0.49
1:A:82:LEU:HD12	1:A:88:LYS:HG3	1.93	0.49
1:A:52:PHE:O	1:A:56:LEU:HB2	2.13	0.49
1:A:34:LYS:HA	1:A:34:LYS:HE3	1.94	0.49
1:A:106:GLN:O	1:A:109:ALA:HB2	2.12	0.49
1:B:32:ILE:HG22	1:B:33:LEU:N	2.28	0.49
1:B:50:VAL:HA	1:B:53:TYR:HB2	1.94	0.49
1:B:18:SER:O	1:B:19:SER:CB	2.54	0.49
1:A:63:ASN:O	1:A:63:ASN:ND2	2.46	0.49
1:A:110:ILE:HG13	2:A:435:HOH:O	2.13	0.49
1:A:56:LEU:HD12	1:A:57:PHE:CE1	2.48	0.49
1:A:61:LYS:HA	1:A:67:GLN:HE21	1.70	0.49
1:B:107:ARG:NH2	1:B:108:LYS:HZ3	2.10	0.49
1:A:83:ASN:H	1:A:88:LYS:HZ2	1.61	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:101:ASP:C	1:B:103:LEU:H	2.16	0.48
1:A:117:MET:O	1:A:118:ASN:CB	2.46	0.48
1:B:28:LEU:CA	1:B:31:GLU:HG3	2.42	0.48
1:A:91:ASP:O	1:A:95:LEU:HG	2.14	0.48
1:A:8:ILE:HG13	1:A:12:LYS:NZ	2.29	0.48
1:B:5:PHE:HB3	1:B:9:GLU:CD	2.33	0.48
1:A:88:LYS:O	1:A:91:ASP:OD1	2.31	0.48
1:A:94:LYS:C	1:A:96:ILE:H	2.17	0.48
2:A:410:HOH:O	1:B:56:LEU:HD21	2.13	0.48
1:A:14:TYR:HB3	1:A:66:ILE:CG1	2.42	0.48
1:A:14:TYR:HB3	1:A:66:ILE:HG12	1.94	0.48
1:A:40:SER:C	1:A:42:LYS:NZ	2.67	0.48
1:A:29:PHE:HA	1:A:32:ILE:HB	1.96	0.48
1:A:95:LEU:HD22	1:B:48:GLN:HB3	1.96	0.48
1:B:92:PHE:O	1:B:92:PHE:CG	2.64	0.48
1:B:112:GLU:CD	1:B:112:GLU:O	2.51	0.48
1:A:74:LYS:HA	1:A:77:MET:HG2	1.94	0.47
1:B:5:PHE:N	1:B:5:PHE:HD1	2.11	0.47
1:A:108:LYS:NZ	1:A:111:ASN:H	2.12	0.47
1:A:70:MET:HG2	1:A:71:ASP:N	2.30	0.47
1:A:48:GLN:HE22	1:B:48:GLN:NE2	2.09	0.47
1:B:46:GLN:O	1:B:49:ILE:CG1	2.62	0.47
1:B:56:LEU:HD12	1:B:59:ASN:HD22	1.78	0.47
1:A:55:LYS:HZ2	1:A:55:LYS:HB2	1.74	0.47
1:A:67:GLN:O	1:A:70:MET:HG2	2.14	0.47
1:A:11:LEU:C	1:A:13:GLU:N	2.65	0.47
1:B:62:ASP:O	1:B:67:GLN:N	2.43	0.47
1:A:42:LYS:HB3	2:A:422:HOH:O	2.13	0.47
1:B:6:ARG:H	1:B:6:ARG:HD3	1.79	0.47
1:A:43:LYS:NZ	1:A:115:LYS:NZ	2.63	0.47
1:A:37:LYS:HG2	1:A:37:LYS:O	2.15	0.47
1:A:57:PHE:CD1	1:A:70:MET:HB2	2.50	0.47
1:A:82:LEU:CB	1:A:88:LYS:HD3	2.42	0.47
1:B:11:LEU:CD1	2:B:411:HOH:O	2.63	0.47
1:B:105:ILE:O	1:B:107:ARG:N	2.43	0.47
1:A:53:TYR:O	1:A:56:LEU:CB	2.63	0.47
1:A:105:ILE:CD1	1:B:29:PHE:CB	2.92	0.47
1:A:44:ILE:HG21	1:B:82:LEU:HD22	1.97	0.46
1:B:114:ILE:C	1:B:116:VAL:N	2.68	0.46
1:B:117:MET:C	1:B:119:ASP:H	2.18	0.46
1:B:24:LYS:CG	1:B:25:GLY:N	2.79	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:95:LEU:HD11	1:B:45:ILE:HG21	1.97	0.46
1:A:89:LEU:HD23	1:A:90:GLU:N	2.30	0.46
1:B:107:ARG:HH21	1:B:110:ILE:CG2	2.28	0.46
1:A:92:PHE:CA	1:A:95:LEU:HD12	2.46	0.46
1:A:8:ILE:HG12	1:A:73:ILE:HG13	1.98	0.46
1:B:52:PHE:HA	1:B:55:LYS:HD2	1.96	0.46
1:A:6:ARG:NH2	2:A:401:HOH:O	2.48	0.46
1:A:104:GLN:O	1:A:104:GLN:HG2	2.15	0.46
1:B:32:ILE:HG22	1:B:33:LEU:CD1	2.39	0.46
1:B:48:GLN:HA	1:B:51:SER:HB2	1.97	0.46
1:A:80:LYS:NZ	1:B:113:LEU:HA	2.31	0.45
1:A:5:PHE:CG	1:A:6:ARG:N	2.84	0.45
1:B:26:GLY:HA3	1:B:28:LEU:CD2	2.40	0.45
1:B:77:MET:HG3	2:B:412:HOH:O	2.15	0.45
1:A:82:LEU:HD12	1:A:88:LYS:CD	2.46	0.45
1:B:56:LEU:HD12	1:B:59:ASN:HD21	1.75	0.45
1:A:26:GLY:HA2	1:A:27:PRO:HD3	1.59	0.45
1:A:70:MET:CG	1:A:71:ASP:N	2.79	0.45
1:B:101:ASP:C	1:B:103:LEU:N	2.69	0.45
1:B:107:ARG:HH22	1:B:108:LYS:HE2	1.81	0.45
1:B:110:ILE:HG13	1:B:110:ILE:O	2.17	0.45
1:B:115:LYS:HD2	1:B:115:LYS:O	2.16	0.45
1:B:36:TRP:HB2	1:B:37:LYS:CE	2.47	0.45
1:B:12:LYS:HZ1	1:B:73:ILE:HD11	1.82	0.45
1:A:102:ASP:O	1:A:103:LEU:HB2	2.16	0.45
1:B:56:LEU:HA	1:B:59:ASN:ND2	2.32	0.45
1:B:94:LYS:C	1:B:96:ILE:H	2.20	0.44
1:A:52:PHE:O	1:A:52:PHE:CG	2.71	0.44
1:A:106:GLN:CA	1:B:29:PHE:HE2	2.30	0.44
1:A:108:LYS:HZ2	1:A:111:ASN:H	1.64	0.44
1:A:32:ILE:C	1:A:34:LYS:H	2.21	0.44
1:A:22:VAL:C	1:A:24:LYS:N	2.69	0.44
1:A:66:ILE:O	1:A:67:GLN:C	2.56	0.44
1:A:91:ASP:O	1:A:94:LYS:CB	2.66	0.44
1:A:99:PRO:O	1:A:103:LEU:HB3	2.17	0.44
1:B:46:GLN:HA	1:B:49:ILE:HD11	1.97	0.44
1:A:52:PHE:CE1	1:A:55:LYS:HB3	2.53	0.43
1:A:79:GLN:HG3	1:A:80:LYS:HD2	2.00	0.43
1:A:50:VAL:HG12	1:A:81:PHE:CE1	2.53	0.43
1:B:75:GLN:C	1:B:79:GLN:HE22	2.19	0.43
1:B:59:ASN:ND2	2:B:438:HOH:O	2.48	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:70:MET:CA	1:A:73:ILE:CD1	2.92	0.43
1:A:106:GLN:C	1:B:29:PHE:HE2	2.21	0.43
1:B:70:MET:HE3	1:B:70:MET:HB3	1.72	0.43
1:B:68:ARG:O	1:B:71:ASP:HB3	2.18	0.43
1:A:48:GLN:HG2	1:B:95:LEU:CD2	2.48	0.43
1:B:28:LEU:C	1:B:32:ILE:HG12	2.35	0.43
1:B:78:PHE:CE1	1:B:89:LEU:HD13	2.53	0.43
1:A:105:ILE:HD11	1:B:29:PHE:N	2.34	0.43
1:B:34:LYS:CG	1:B:35:ASN:H	2.32	0.43
1:A:8:ILE:O	1:A:12:LYS:NZ	2.49	0.43
1:B:12:LYS:HE3	1:B:15:PHE:CZ	2.54	0.42
1:B:11:LEU:HD12	2:B:411:HOH:O	2.19	0.42
1:B:11:LEU:O	1:B:14:TYR:HB2	2.19	0.42
1:A:108:LYS:HB3	1:B:29:PHE:CD1	2.55	0.42
1:A:33:LEU:HD23	1:A:49:ILE:CD1	2.48	0.42
1:A:113:LEU:HD11	1:B:5:PHE:HE2	1.84	0.42
1:B:76:ASP:HB3	2:B:412:HOH:O	2.19	0.42
1:A:11:LEU:O	1:A:14:TYR:HB2	2.20	0.42
1:B:110:ILE:O	1:B:110:ILE:CG1	2.67	0.42
1:B:101:ASP:H	1:B:104:GLN:HE22	1.66	0.42
1:A:87:GLU:OE1	1:A:87:GLU:N	2.52	0.42
1:A:43:LYS:HZ1	1:A:115:LYS:NZ	2.16	0.42
1:B:46:GLN:NE2	1:B:49:ILE:HD13	2.35	0.42
1:B:87:GLU:O	1:B:89:LEU:N	2.52	0.42
1:B:12:LYS:N	1:B:12:LYS:NZ	2.57	0.42
1:A:91:ASP:O	1:A:95:LEU:CG	2.68	0.41
1:B:56:LEU:HD12	1:B:56:LEU:HA	1.84	0.41
1:A:70:MET:HB3	1:A:70:MET:HE3	1.85	0.41
1:B:76:ASP:CA	1:B:79:GLN:NE2	2.83	0.41
1:A:37:LYS:O	1:A:39:GLU:N	2.53	0.41
1:B:67:GLN:CG	1:B:68:ARG:N	2.71	0.41
1:B:10:ASN:C	1:B:10:ASN:OD1	2.59	0.41
1:A:101:ASP:O	1:A:103:LEU:N	2.50	0.41
1:B:42:LYS:HG3	1:B:44:ILE:HG23	2.02	0.41
1:B:52:PHE:CE1	1:B:56:LEU:HD22	2.55	0.41
1:A:56:LEU:HA	1:A:56:LEU:HD22	1.93	0.41
1:B:24:LYS:CD	1:B:25:GLY:N	2.84	0.41
1:A:42:LYS:HB2	1:A:43:LYS:H	1.33	0.41
1:A:7:GLU:CA	1:A:10:ASN:OD1	2.68	0.41
1:B:107:ARG:NH2	1:B:110:ILE:CG2	2.84	0.41
1:B:108:LYS:O	1:B:109:ALA:C	2.58	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:105:ILE:CD1	1:B:29:PHE:N	2.84	0.41
1:A:32:ILE:HG22	1:A:33:LEU:N	2.36	0.41
1:B:67:GLN:HG3	1:B:68:ARG:H	1.80	0.41
1:B:14:TYR:HA	1:B:14:TYR:HD1	1.76	0.41
1:A:80:LYS:HZ2	1:B:113:LEU:HA	1.86	0.41
1:A:44:ILE:HD12	1:A:45:ILE:CD1	2.50	0.41
1:A:62:ASP:OD1	1:A:66:ILE:N	2.48	0.40
1:A:71:ASP:O	1:A:75:GLN:HB2	2.20	0.40
1:B:37:LYS:O	1:B:38:ASP:C	2.59	0.40
1:A:6:ARG:H	1:A:6:ARG:HG3	1.48	0.40
1:A:28:LEU:HD22	1:A:29:PHE:CE1	2.55	0.40
1:B:42:LYS:NZ	1:B:45:ILE:HG23	2.35	0.40
1:B:118:ASN:O	1:B:118:ASN:ND2	2.36	0.40
1:B:5:PHE:HB3	1:B:9:GLU:HG2	2.03	0.40
1:A:32:ILE:O	1:A:36:TRP:CZ3	2.73	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:59:ASN:O	1:B:68:ARG:NH1[3_655]	2.11	0.09

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	117/119 (98%)	65 (56%)	20 (17%)	32 (27%)	0	0
1	B	117/119 (98%)	64 (55%)	31 (26%)	22 (19%)	0	0
All	All	234/238 (98%)	129 (55%)	51 (22%)	54 (23%)	0	0

All (54) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	5	PHE
1	A	18	SER
1	A	19	SER
1	A	20	PRO
1	A	23	ALA
1	A	28	LEU
1	A	34	LYS
1	A	38	ASP
1	A	40	SER
1	A	43	LYS
1	A	44	ILE
1	A	61	LYS
1	A	62	ASP
1	A	63	ASN
1	A	67	GLN
1	A	100	VAL
1	A	102	ASP
1	A	106	GLN
1	A	111	ASN
1	A	118	ASN
1	B	4	PHE
1	B	19	SER
1	B	20	PRO
1	B	28	LEU
1	B	32	ILE
1	B	63	ASN
1	B	100	VAL
1	B	106	GLN
1	B	112	GLU
1	A	3	GLN
1	A	42	LYS
1	A	96	ILE
1	A	103	LEU
1	A	114	ILE
1	B	23	ALA
1	B	33	LEU
1	B	44	ILE
1	B	95	LEU
1	B	97	GLN
1	B	101	ASP
1	A	33	LEU
1	B	24	LYS
1	B	38	ASP

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Mol	Chain	Res	Type
1	B	88	LYS
1	B	105	ILE
1	B	34	LYS
1	B	36	TRP
1	A	32	ILE
1	A	36	TRP
1	A	95	LEU
1	A	98	ILE
1	B	25	GLY
1	A	108	LYS
1	A	65	VAL

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	112/112 (100%)	74 (66%)	38 (34%)	0	1
1	B	112/112 (100%)	78 (70%)	34 (30%)	0	2
All	All	224/224 (100%)	152 (68%)	72 (32%)	0	1

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

Mol	Chain	Res	Type
1	A	4	PHE
1	A	5	PHE
1	A	6	ARG
1	A	10	ASN
1	A	13	GLU
1	A	14	TYR
1	A	15	PHE
1	A	16	ASN
1	A	19	SER
1	A	20	PRO
1	A	22	VAL
1	A	24	LYS

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Mol	Chain	Res	Type
1	A	32	ILE
1	A	33	LEU
1	A	34	LYS
1	A	39	GLU
1	A	42	LYS
1	A	43	LYS
1	A	48	GLN
1	A	49	ILE
1	A	54	PHE
1	A	55	LYS
1	A	56	LEU
1	A	68	ARG
1	A	73	ILE
1	A	75	GLN
1	A	76	ASP
1	A	81	PHE
1	A	85	SER
1	A	87	GLU
1	A	89	LEU
1	A	90	GLU
1	A	91	ASP
1	A	101	ASP
1	A	106	GLN
1	A	111	ASN
1	A	116	VAL
1	A	117	MET
1	B	6	ARG
1	B	7	GLU
1	B	8	ILE
1	B	11	LEU
1	B	12	LYS
1	B	14	TYR
1	B	22	VAL
1	B	28	LEU
1	B	29	PHE
1	B	31	GLU
1	B	33	LEU
1	B	36	TRP
1	B	37	LYS
1	B	44	ILE
1	B	45	ILE
1	B	48	GLN

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Mol	Chain	Res	Type
1	B	51	SER
1	B	52	PHE
1	B	59	ASN
1	B	67	GLN
1	B	70	MET
1	B	72	ILE
1	B	78	PHE
1	B	79	GLN
1	B	82	LEU
1	B	83	ASN
1	B	87	GLU
1	B	105	ILE
1	B	107	ARG
1	B	108	LYS
1	B	113	LEU
1	B	114	ILE
1	B	115	LYS
1	B	118	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	63	ASN
1	A	67	GLN
1	A	75	GLN
1	A	106	GLN
1	A	111	ASN
1	B	48	GLN
1	B	64	GLN
1	B	79	GLN

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 carbohydrates 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 will therefore be empty.

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

EDS was not executed - this section will therefore be empty.

6.3 Carbohydrates ⓘ

EDS was not executed - this section will therefore be empty.

6.4 Ligands ⓘ

EDS was not executed - this section will therefore be empty.

6.5 Other polymers ⓘ

EDS was not executed - this section will therefore be empty.