



Full wwPDB X-ray Structure Validation Report ⓘ

Jun 16, 2024 – 01:56 AM EDT

PDB ID : 2PJQ
Title : Crystal structure of Q88U62_LACPL from Lactobacillus plantarum. Northeast Structural Genomics target LpR71
Authors : Benach, J.; Su, M.; Seetharaman, J.; Forouhar, F.; Chen, C.X.; Cunningham, K.; Ma, L.-C.; Owens, L.; Baran, M.; Acton, T.B.; Montelione, G.T.; Tong, L.; Hunt, J.F.; Northeast Structural Genomics Consortium (NESG)
Deposited on : 2007-04-16
Resolution : 2.80 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	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.20.1
EDS	:	2.37.1
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)	:	2.37.1

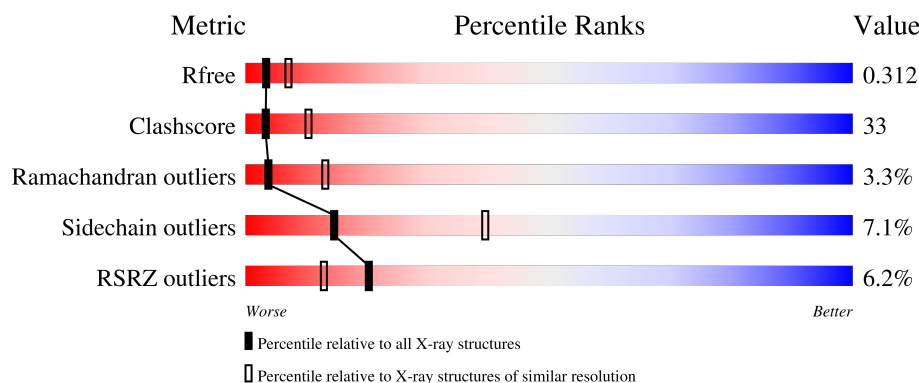
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION


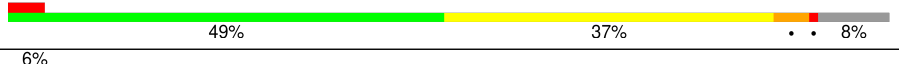
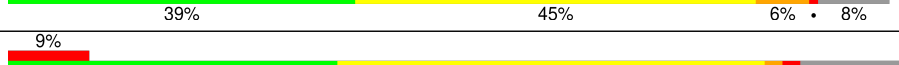

The reported resolution of this entry is 2.80 Å.

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	3140 (2.80-2.80)
Clashscore	141614	3569 (2.80-2.80)
Ramachandran outliers	138981	3498 (2.80-2.80)
Sidechain outliers	138945	3500 (2.80-2.80)
RSRZ outliers	127900	3078 (2.80-2.80)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	231	
1	B	231	
1	C	231	
1	D	231	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 6575 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 Uncharacterized protein lp_2664.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	206	Total	C	N	O	Se	0	0	0
			1625	1019	298	303	5			
1	B	212	Total	C	N	O	Se	0	0	0
			1667	1047	306	308	6			
1	C	212	Total	C	N	O	Se	0	0	0
			1667	1045	306	310	6			
1	D	203	Total	C	N	O	Se	0	0	0
			1604	1008	295	296	5			

There are 76 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-4	MSE	-	CLONING ARTIFACT	UNP Q88U62
A	-3	ALA	-	CLONING ARTIFACT	UNP Q88U62
A	-2	GLY	-	CLONING ARTIFACT	UNP Q88U62
A	-1	ASP	-	CLONING ARTIFACT	UNP Q88U62
A	0	PRO	-	CLONING ARTIFACT	UNP Q88U62
A	1	MSE	MET	MODIFIED RESIDUE	UNP Q88U62
A	66	MSE	MET	MODIFIED RESIDUE	UNP Q88U62
A	100	MSE	MET	MODIFIED RESIDUE	UNP Q88U62
A	158	MSE	MET	MODIFIED RESIDUE	UNP Q88U62
A	185	MSE	MET	MODIFIED RESIDUE	UNP Q88U62
A	201	MSE	MET	MODIFIED RESIDUE	UNP Q88U62
A	219	LEU	-	CLONING ARTIFACT	UNP Q88U62
A	220	GLU	-	CLONING ARTIFACT	UNP Q88U62
A	221	HIS	-	CLONING ARTIFACT	UNP Q88U62
A	222	HIS	-	CLONING ARTIFACT	UNP Q88U62
A	223	HIS	-	CLONING ARTIFACT	UNP Q88U62
A	224	HIS	-	CLONING ARTIFACT	UNP Q88U62
A	225	HIS	-	CLONING ARTIFACT	UNP Q88U62
A	226	HIS	-	CLONING ARTIFACT	UNP Q88U62
B	-4	MSE	-	CLONING ARTIFACT	UNP Q88U62
B	-3	ALA	-	CLONING ARTIFACT	UNP Q88U62

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-2	GLY	-	CLONING ARTIFACT	UNP Q88U62
B	-1	ASP	-	CLONING ARTIFACT	UNP Q88U62
B	0	PRO	-	CLONING ARTIFACT	UNP Q88U62
B	1	MSE	MET	MODIFIED RESIDUE	UNP Q88U62
B	66	MSE	MET	MODIFIED RESIDUE	UNP Q88U62
B	100	MSE	MET	MODIFIED RESIDUE	UNP Q88U62
B	158	MSE	MET	MODIFIED RESIDUE	UNP Q88U62
B	185	MSE	MET	MODIFIED RESIDUE	UNP Q88U62
B	201	MSE	MET	MODIFIED RESIDUE	UNP Q88U62
B	219	LEU	-	CLONING ARTIFACT	UNP Q88U62
B	220	GLU	-	CLONING ARTIFACT	UNP Q88U62
B	221	HIS	-	CLONING ARTIFACT	UNP Q88U62
B	222	HIS	-	CLONING ARTIFACT	UNP Q88U62
B	223	HIS	-	CLONING ARTIFACT	UNP Q88U62
B	224	HIS	-	CLONING ARTIFACT	UNP Q88U62
B	225	HIS	-	CLONING ARTIFACT	UNP Q88U62
B	226	HIS	-	CLONING ARTIFACT	UNP Q88U62
C	-4	MSE	-	CLONING ARTIFACT	UNP Q88U62
C	-3	ALA	-	CLONING ARTIFACT	UNP Q88U62
C	-2	GLY	-	CLONING ARTIFACT	UNP Q88U62
C	-1	ASP	-	CLONING ARTIFACT	UNP Q88U62
C	0	PRO	-	CLONING ARTIFACT	UNP Q88U62
C	1	MSE	MET	MODIFIED RESIDUE	UNP Q88U62
C	66	MSE	MET	MODIFIED RESIDUE	UNP Q88U62
C	100	MSE	MET	MODIFIED RESIDUE	UNP Q88U62
C	158	MSE	MET	MODIFIED RESIDUE	UNP Q88U62
C	185	MSE	MET	MODIFIED RESIDUE	UNP Q88U62
C	201	MSE	MET	MODIFIED RESIDUE	UNP Q88U62
C	219	LEU	-	CLONING ARTIFACT	UNP Q88U62
C	220	GLU	-	CLONING ARTIFACT	UNP Q88U62
C	221	HIS	-	CLONING ARTIFACT	UNP Q88U62
C	222	HIS	-	CLONING ARTIFACT	UNP Q88U62
C	223	HIS	-	CLONING ARTIFACT	UNP Q88U62
C	224	HIS	-	CLONING ARTIFACT	UNP Q88U62
C	225	HIS	-	CLONING ARTIFACT	UNP Q88U62
C	226	HIS	-	CLONING ARTIFACT	UNP Q88U62
D	-4	MSE	-	CLONING ARTIFACT	UNP Q88U62
D	-3	ALA	-	CLONING ARTIFACT	UNP Q88U62
D	-2	GLY	-	CLONING ARTIFACT	UNP Q88U62
D	-1	ASP	-	CLONING ARTIFACT	UNP Q88U62
D	0	PRO	-	CLONING ARTIFACT	UNP Q88U62
D	1	MSE	MET	MODIFIED RESIDUE	UNP Q88U62

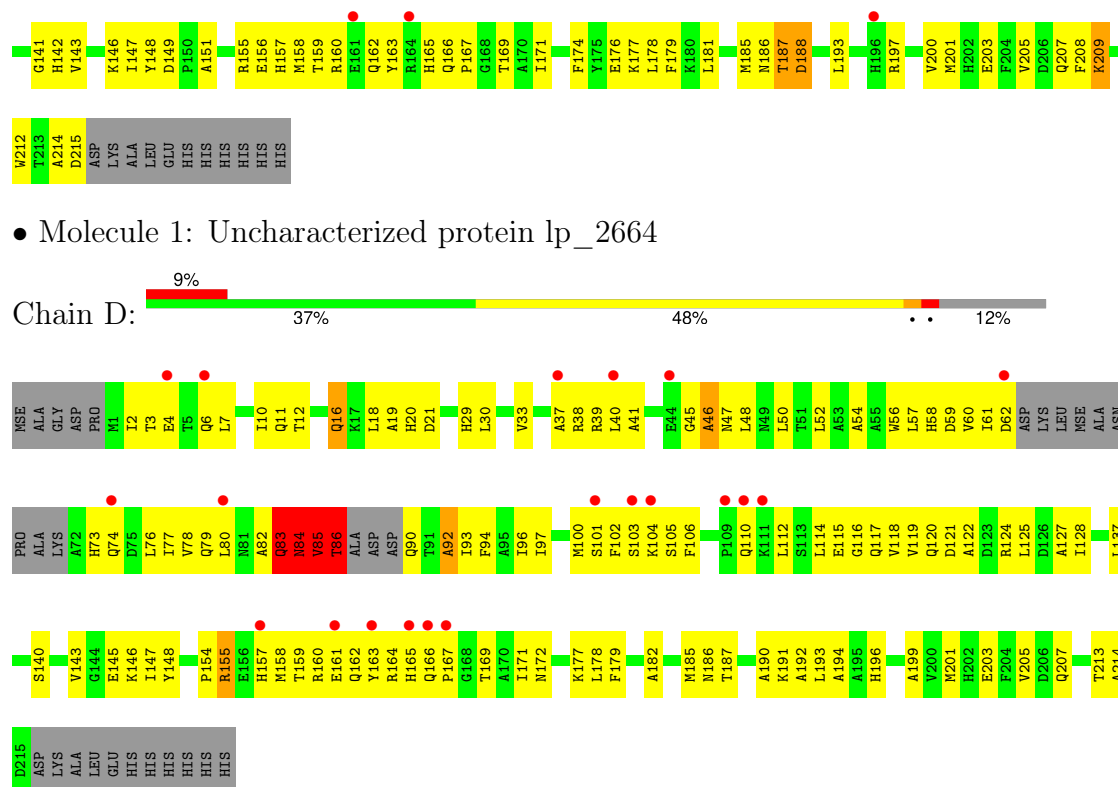
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Chain	Residue	Modelled	Actual	Comment	Reference
D	66	MSE	MET	MODIFIED RESIDUE	UNP Q88U62
D	100	MSE	MET	MODIFIED RESIDUE	UNP Q88U62
D	158	MSE	MET	MODIFIED RESIDUE	UNP Q88U62
D	185	MSE	MET	MODIFIED RESIDUE	UNP Q88U62
D	201	MSE	MET	MODIFIED RESIDUE	UNP Q88U62
D	219	LEU	-	CLONING ARTIFACT	UNP Q88U62
D	220	GLU	-	CLONING ARTIFACT	UNP Q88U62
D	221	HIS	-	CLONING ARTIFACT	UNP Q88U62
D	222	HIS	-	CLONING ARTIFACT	UNP Q88U62
D	223	HIS	-	CLONING ARTIFACT	UNP Q88U62
D	224	HIS	-	CLONING ARTIFACT	UNP Q88U62
D	225	HIS	-	CLONING ARTIFACT	UNP Q88U62
D	226	HIS	-	CLONING ARTIFACT	UNP Q88U62

- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	2	Total O 2 2	0	0
2	B	6	Total O 6 6	0	0
2	C	3	Total O 3 3	0	0
2	D	1	Total O 1 1	0	0



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	79.93Å 167.44Å 63.77Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.80 47.78 – 2.80	Depositor EDS
% Data completeness (in resolution range)	87.1 (20.00-2.80) 96.4 (47.78-2.80)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.85 (at 2.81Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.236 , 0.307 0.242 , 0.312	Depositor DCC
R_{free} test set	3984 reflections (9.83%)	wwPDB-VP
Wilson B-factor (Å ²)	32.7	Xtriage
Anisotropy	0.176	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 40.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.86	EDS
Total number of atoms	6575	wwPDB-VP
Average B, all atoms (Å ²)	32.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.09% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality i

5.1 Standard geometry i

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.43	0/1653	0.69	0/2232
1	B	0.50	0/1695	0.74	6/2287 (0.3%)
1	C	0.70	5/1696 (0.3%)	0.78	5/2290 (0.2%)
1	D	0.62	5/1631 (0.3%)	0.86	11/2200 (0.5%)
All	All	0.57	10/6675 (0.1%)	0.77	22/9009 (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	D	0	4

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	60	VAL	CA-CB	-12.41	1.28	1.54
1	C	60	VAL	CB-CG1	-10.32	1.31	1.52
1	D	84	ASN	CA-C	-9.27	1.28	1.52
1	C	60	VAL	CB-CG2	-8.10	1.35	1.52
1	D	82	ALA	CA-CB	-7.50	1.36	1.52
1	D	92	ALA	CA-CB	-7.26	1.37	1.52
1	C	61	ILE	CB-CG2	-5.71	1.35	1.52
1	D	84	ASN	CB-CG	5.20	1.63	1.51
1	D	84	ASN	CA-CB	5.18	1.66	1.53
1	C	60	VAL	C-O	5.02	1.32	1.23

All (22) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	83	GLN	CA-C-N	-9.64	95.99	117.20
1	C	61	ILE	CA-C-N	8.79	136.54	117.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	66	MSE	CG-SE-CE	-8.73	79.68	98.90
1	D	84	ASN	CA-C-N	-8.42	98.67	117.20
1	D	85	VAL	CA-CB-CG1	-8.40	98.31	110.90
1	D	85	VAL	CB-CA-C	-8.28	95.66	111.40
1	C	61	ILE	CA-C-O	-7.74	103.84	120.10
1	D	83	GLN	O-C-N	7.71	135.04	122.70
1	D	85	VAL	CA-C-N	-7.30	101.15	117.20
1	B	61	ILE	CB-CA-C	-6.55	98.50	111.60
1	C	61	ILE	C-N-CA	-6.45	105.56	121.70
1	B	61	ILE	CB-CG1-CD1	6.38	131.76	113.90
1	D	86	THR	CA-CB-CG2	-6.16	103.78	112.40
1	D	85	VAL	CG1-CB-CG2	-5.99	101.31	110.90
1	C	59	ASP	N-CA-CB	-5.87	100.04	110.60
1	B	65	LEU	CB-CA-C	-5.59	99.58	110.20
1	D	86	THR	N-CA-CB	-5.50	99.86	110.30
1	B	61	ILE	CA-CB-CG1	5.46	121.38	111.00
1	D	83	GLN	N-CA-CB	-5.19	101.26	110.60
1	B	61	ILE	CA-CB-CG2	5.07	121.03	110.90
1	D	83	GLN	CB-CA-C	5.07	120.53	110.40
1	B	66	MSE	CB-CG-SE	5.06	127.87	112.70

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	D	83	GLN	Peptide,Mainchain
1	D	84	ASN	Mainchain
1	D	85	VAL	Mainchain

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	1625	0	1590	90	0
1	B	1667	0	1642	98	0
1	C	1667	0	1635	136	0
1	D	1604	0	1576	121	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	2	0	0	1	0
2	B	6	0	0	1	0
2	C	3	0	0	0	0
2	D	1	0	0	0	0
All	All	6575	0	6443	427	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 33.

All (427) 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:C:60:VAL:O	1:C:61:ILE:HG22	1.45	1.12
1:B:18:LEU:HD12	1:B:30:LEU:HD11	1.42	0.99
1:D:38:ARG:HH12	1:D:48:LEU:HD21	1.27	0.99
1:C:187:THR:HG22	1:C:188:ASP:H	1.26	0.98
1:C:174:PHE:HA	1:C:178:LEU:HB2	1.44	0.96
1:C:60:VAL:O	1:C:60:VAL:HG12	1.65	0.95
1:B:71:LYS:HE3	1:B:74:GLN:HE21	1.28	0.95
1:A:50:LEU:HD13	1:A:115:GLU:HG3	1.51	0.93
1:C:60:VAL:C	1:C:61:ILE:HG22	1.82	0.90
1:D:18:LEU:HD12	1:D:30:LEU:HD11	1.52	0.89
1:C:59:ASP:C	1:C:61:ILE:H	1.70	0.89
1:A:85:VAL:HG13	1:A:86:THR:N	1.88	0.86
1:B:178:LEU:HB3	1:B:201:MSE:HE1	1.57	0.86
1:B:50:LEU:HD13	1:B:115:GLU:HG3	1.58	0.86
1:A:47:ASN:HD22	1:A:50:LEU:HB2	1.39	0.86
1:D:105:SER:HA	1:D:110:GLN:HE22	1.40	0.85
1:C:60:VAL:C	1:C:61:ILE:CG2	2.44	0.85
1:C:10:ILE:HG23	1:C:57:LEU:HD21	1.59	0.84
1:A:40:LEU:HB3	1:A:118:VAL:HG13	1.60	0.84
1:B:47:ASN:ND2	1:B:50:LEU:HB2	1.94	0.83
1:C:47:ASN:HD22	1:C:50:LEU:HB2	1.44	0.82
1:B:15:LEU:HD22	1:B:27:ARG:HG2	1.59	0.82
1:B:35:ARG:HD2	1:C:215:ASP:C	2.01	0.81
1:C:124:ARG:HD3	1:C:181:LEU:HD22	1.60	0.81
1:C:59:ASP:C	1:C:61:ILE:N	2.25	0.81
1:D:120:GLN:NE2	1:D:186:ASN:HD21	1.80	0.80
1:D:61:ILE:HG13	1:D:62:ASP:N	1.96	0.79
1:D:2:ILE:HD12	1:D:50:LEU:HA	1.65	0.79
1:C:94:PHE:O	1:C:98:ASP:HB2	1.83	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:61:ILE:O	1:C:62:ASP:CB	2.26	0.79
1:D:125:LEU:HD22	1:D:193:LEU:HD23	1.65	0.79
1:B:115:GLU:O	1:B:119:VAL:HG23	1.84	0.77
1:B:18:LEU:CD1	1:B:30:LEU:HD11	2.14	0.77
1:B:155:ARG:CZ	1:B:158:MSE:HE3	2.15	0.76
1:D:159:THR:OG1	1:D:162:GLN:HG3	1.85	0.76
1:B:47:ASN:HD22	1:B:50:LEU:HB2	1.50	0.76
1:D:73:HIS:O	1:D:77:ILE:HD12	1.85	0.76
1:C:54:ALA:HA	1:C:97:ILE:HD11	1.68	0.75
1:A:12:THR:HG23	1:A:16:GLN:HE22	1.51	0.75
1:A:47:ASN:ND2	1:A:50:LEU:HB2	2.01	0.75
1:B:35:ARG:HD2	1:C:215:ASP:O	1.87	0.75
1:A:85:VAL:HG13	1:A:86:THR:H	1.50	0.75
1:C:71:LYS:HE2	1:C:75:ASP:OD2	1.87	0.75
1:A:94:PHE:O	1:A:98:ASP:HB2	1.87	0.74
1:C:40:LEU:HB3	1:C:118:VAL:HG13	1.69	0.74
1:C:61:ILE:O	1:C:62:ASP:HB2	1.85	0.74
1:B:47:ASN:HD22	1:B:50:LEU:CB	2.01	0.74
1:A:182:ALA:HA	1:A:185:MSE:HE2	1.71	0.73
1:C:120:GLN:NE2	1:C:186:ASN:HD21	1.86	0.73
1:C:12:THR:HG23	1:C:16:GLN:HE22	1.51	0.72
1:D:18:LEU:O	1:D:21:ASP:HB2	1.89	0.72
1:C:60:VAL:O	1:C:61:ILE:CG2	2.32	0.72
1:B:2:ILE:HD12	1:B:50:LEU:HA	1.72	0.71
1:C:58:HIS:HA	1:C:97:ILE:HG23	1.72	0.71
1:C:12:THR:CG2	1:C:16:GLN:HE22	2.02	0.71
1:B:85:VAL:CG1	1:B:90:GLN:HG3	2.20	0.71
1:B:137:LEU:HD22	1:C:134:ALA:HA	1.71	0.70
1:D:61:ILE:HG13	1:D:62:ASP:H	1.55	0.70
1:A:145:GLU:HG2	1:A:168:GLY:O	1.92	0.70
1:B:152:ILE:HG12	1:D:146:LYS:HE2	1.72	0.69
1:B:79:GLN:HE22	1:B:83:GLN:HE21	1.39	0.69
1:C:155:ARG:CZ	1:C:158:MSE:HE2	2.22	0.69
1:C:155:ARG:HD3	1:C:176:GLU:OE2	1.92	0.69
1:B:80:LEU:HB3	1:B:85:VAL:HG11	1.74	0.69
1:D:6:GLN:O	1:D:10:ILE:HG13	1.93	0.69
1:D:114:LEU:O	1:D:118:VAL:HG23	1.93	0.69
1:A:57:LEU:HB2	1:A:97:ILE:HD11	1.74	0.68
1:D:105:SER:HA	1:D:110:GLN:NE2	2.06	0.68
1:B:106:PHE:CE2	1:B:158:MSE:HB2	2.29	0.68
1:D:38:ARG:NH1	1:D:48:LEU:HD21	2.04	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:128:ILE:HA	1:D:201:MSE:CE	2.24	0.68
1:A:85:VAL:HG11	1:A:90:GLN:OE1	1.94	0.67
1:C:187:THR:HG22	1:C:188:ASP:N	2.05	0.67
1:A:57:LEU:HD13	1:A:76:LEU:HD11	1.75	0.67
1:C:149:ASP:OD1	1:C:151:ALA:HB3	1.93	0.67
1:D:115:GLU:H	1:D:115:GLU:CD	1.98	0.67
1:D:80:LEU:HD13	1:D:90:GLN:HG3	1.77	0.66
1:A:85:VAL:C	1:A:86:THR:HG22	2.16	0.66
1:D:57:LEU:HA	1:D:60:VAL:CG2	2.26	0.66
1:C:61:ILE:HG12	1:C:62:ASP:N	2.10	0.66
1:B:85:VAL:HG13	1:B:90:GLN:HG3	1.78	0.65
1:B:71:LYS:HE3	1:B:74:GLN:NE2	2.08	0.65
1:D:47:ASN:HD22	1:D:50:LEU:HB2	1.60	0.65
1:B:3:THR:OG1	1:B:6:GLN:HG3	1.97	0.65
1:B:61:ILE:CD1	1:B:97:ILE:HG21	2.27	0.65
1:D:102:PHE:HB2	1:D:177:LYS:HE3	1.78	0.65
1:B:27:ARG:O	1:B:31:GLN:HG3	1.95	0.65
1:A:86:THR:HG23	1:A:89:ASP:HB2	1.78	0.65
1:A:148:TYR:HB2	1:A:171:ILE:HG13	1.78	0.64
1:C:103:SER:HB2	1:C:160:ARG:HH11	1.61	0.64
1:D:92:ALA:C	1:D:94:PHE:N	2.49	0.64
1:C:80:LEU:O	1:C:85:VAL:HB	1.98	0.64
1:D:143:VAL:HG12	1:D:143:VAL:O	1.96	0.63
1:A:159:THR:OG1	1:A:162:GLN:HG3	1.98	0.63
1:D:106:PHE:CE1	1:D:158:MSE:HB2	2.34	0.63
1:D:120:GLN:HE21	1:D:186:ASN:HD21	1.44	0.63
1:A:178:LEU:HD13	1:A:201:MSE:HE1	1.81	0.62
1:C:129:GLY:O	1:C:133:ILE:HG13	2.00	0.62
1:B:58:HIS:HA	1:B:97:ILE:HG23	1.81	0.62
1:A:81:ASN:C	1:A:83:GLN:H	2.01	0.62
1:B:165:HIS:O	1:B:167:PRO:HD3	1.99	0.62
1:A:6:GLN:O	1:A:10:ILE:HG13	1.99	0.62
1:C:115:GLU:CD	1:C:115:GLU:H	2.04	0.62
1:D:79:GLN:O	1:D:83:GLN:CG	2.48	0.62
1:C:100:MSE:HG3	1:C:101:SER:N	2.15	0.61
1:D:201:MSE:O	1:D:205:VAL:HG23	2.00	0.61
1:C:61:ILE:HG12	1:C:62:ASP:H	1.63	0.61
1:B:158:MSE:HE1	1:B:163:TYR:HD1	1.65	0.61
1:D:155:ARG:NE	1:D:158:MSE:HE3	2.16	0.61
1:B:172:ASN:HB3	1:B:176:GLU:OE2	2.00	0.61
1:D:79:GLN:NE2	1:D:83:GLN:HG3	2.15	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:81:ASN:O	1:C:83:GLN:N	2.34	0.61
1:A:155:ARG:NH2	1:A:166:GLN:O	2.34	0.60
1:C:59:ASP:O	1:C:61:ILE:N	2.33	0.60
1:A:57:LEU:HB2	1:A:97:ILE:CD1	2.31	0.60
1:B:47:ASN:ND2	1:B:50:LEU:H	2.00	0.60
1:C:47:ASN:ND2	1:C:50:LEU:HB2	2.14	0.60
1:D:207:GLN:HA	1:D:207:GLN:OE1	2.01	0.60
1:D:3:THR:OG1	1:D:6:GLN:HG3	2.01	0.60
1:C:81:ASN:C	1:C:83:GLN:H	2.05	0.60
1:D:128:ILE:HA	1:D:201:MSE:HE3	1.84	0.60
1:A:11:GLN:HG3	1:A:56:TRP:CZ2	2.37	0.60
1:D:47:ASN:ND2	1:D:50:LEU:HB2	2.17	0.59
1:A:75:ASP:O	1:A:78:VAL:HG23	2.02	0.59
1:B:102:PHE:CD2	1:B:177:LYS:HD2	2.37	0.59
1:B:196:HIS:O	1:B:196:HIS:ND1	2.34	0.59
1:B:65:LEU:N	1:B:65:LEU:HD23	2.17	0.59
1:D:77:ILE:HG23	1:D:90:GLN:HE22	1.67	0.59
1:C:29:HIS:O	1:C:33:VAL:HG23	2.03	0.59
1:D:125:LEU:HD13	1:D:193:LEU:CD2	2.33	0.59
1:A:115:GLU:O	1:A:119:VAL:HG23	2.03	0.59
1:A:131:ILE:O	1:A:135:ARG:HG3	2.03	0.59
1:C:186:ASN:O	1:C:187:THR:O	2.21	0.59
1:A:125:LEU:HD22	1:A:193:LEU:HD23	1.85	0.58
1:C:58:HIS:HA	1:C:97:ILE:CG2	2.31	0.58
1:C:155:ARG:CZ	1:C:158:MSE:CE	2.80	0.58
1:C:125:LEU:CD2	1:C:185:MSE:HE3	2.33	0.58
1:D:92:ALA:C	1:D:94:PHE:H	2.05	0.58
1:D:120:GLN:HE21	1:D:186:ASN:ND2	2.01	0.58
1:D:187:THR:O	1:D:191:LYS:HG3	2.03	0.58
1:A:11:GLN:HE21	1:A:15:LEU:HD11	1.68	0.58
1:D:57:LEU:HD13	1:D:76:LEU:HD21	1.84	0.58
1:C:47:ASN:HD22	1:C:50:LEU:CB	2.15	0.58
1:D:90:GLN:C	1:D:92:ALA:H	2.07	0.58
1:D:48:LEU:O	1:D:52:LEU:HG	2.04	0.58
1:D:104:LYS:HD3	1:D:160:ARG:NH1	2.18	0.58
1:D:125:LEU:CD2	1:D:193:LEU:HD23	2.33	0.57
1:C:18:LEU:HD12	1:C:30:LEU:HD11	1.86	0.57
1:A:148:TYR:HB2	1:A:171:ILE:CG1	2.34	0.57
1:C:60:VAL:O	1:C:60:VAL:CG1	2.43	0.57
1:B:11:GLN:HG3	1:B:56:TRP:CZ2	2.40	0.57
1:B:207:GLN:HG3	1:C:200:VAL:HG21	1.87	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:100:MSE:HG3	1:C:101:SER:H	1.70	0.57
1:C:57:LEU:HB2	1:C:97:ILE:CD1	2.35	0.57
1:D:160:ARG:O	1:D:164:ARG:HB2	2.04	0.57
1:A:80:LEU:O	1:A:85:VAL:HB	2.05	0.57
1:A:81:ASN:O	1:A:83:GLN:N	2.37	0.57
1:C:187:THR:CG2	1:C:188:ASP:H	2.03	0.57
1:B:104:LYS:HB3	1:B:110:GLN:HE22	1.70	0.56
1:B:192:ALA:O	1:B:195:ALA:HB3	2.06	0.56
1:C:90:GLN:O	1:C:93:ILE:HB	2.04	0.56
1:A:47:ASN:HD22	1:A:50:LEU:CB	2.16	0.56
1:D:179:PHE:CZ	1:D:205:VAL:HG21	2.41	0.56
1:A:12:THR:HG23	1:A:16:GLN:NE2	2.21	0.56
1:D:19:ALA:O	1:D:20:HIS:HB2	2.06	0.56
1:A:160:ARG:NH1	1:A:164:ARG:HE	2.02	0.56
1:C:203:GLU:O	1:C:207:GLN:HB2	2.06	0.56
1:D:79:GLN:O	1:D:83:GLN:HG2	2.06	0.55
1:D:155:ARG:CZ	1:D:158:MSE:HE3	2.37	0.55
1:A:127:ALA:O	1:A:178:LEU:HD22	2.07	0.55
1:B:200:VAL:HG21	1:C:207:GLN:NE2	2.22	0.55
1:B:65:LEU:HB2	1:B:66:MSE:HE2	1.89	0.55
1:B:106:PHE:C	1:B:108:GLY:H	2.11	0.55
1:D:11:GLN:HG3	1:D:56:TRP:CZ2	2.42	0.55
1:D:103:SER:HB3	1:D:163:TYR:CD2	2.41	0.54
1:C:6:GLN:O	1:C:9:ALA:HB3	2.07	0.54
1:A:12:THR:CG2	1:A:16:GLN:HE22	2.19	0.54
1:A:85:VAL:CG1	1:A:86:THR:N	2.60	0.54
1:B:16:GLN:HB3	2:B:3005:HOH:O	2.07	0.54
1:C:201:MSE:O	1:C:205:VAL:HG23	2.08	0.54
1:B:85:VAL:HG11	1:B:90:GLN:HG3	1.90	0.53
1:D:182:ALA:HA	1:D:185:MSE:HE2	1.89	0.53
1:A:174:PHE:HA	1:A:178:LEU:HB2	1.90	0.53
1:C:71:LYS:O	1:C:75:ASP:OD2	2.27	0.53
1:A:47:ASN:ND2	1:A:50:LEU:H	2.07	0.53
1:D:100:MSE:HG3	1:D:101:SER:N	2.22	0.53
1:C:5:THR:HG22	1:C:5:THR:O	2.08	0.53
1:D:57:LEU:HD12	1:D:93:ILE:HG21	1.91	0.53
1:D:165:HIS:ND1	1:D:166:GLN:N	2.56	0.53
1:D:57:LEU:HA	1:D:60:VAL:HG21	1.89	0.53
1:A:187:THR:HG22	1:A:189:THR:H	1.74	0.53
1:A:61:ILE:HG12	1:A:62:ASP:N	2.24	0.52
1:C:103:SER:HB2	1:C:160:ARG:NH1	2.25	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:96:ILE:HG22	1:B:97:ILE:N	2.25	0.52
1:C:85:VAL:HG11	1:C:90:GLN:OE1	2.10	0.52
1:D:16:GLN:O	1:D:19:ALA:HB3	2.09	0.52
1:B:47:ASN:ND2	1:B:50:LEU:CB	2.65	0.52
1:A:85:VAL:HG22	1:A:86:THR:H	1.74	0.52
1:B:79:GLN:NE2	1:B:83:GLN:HE21	2.08	0.52
1:C:48:LEU:O	1:C:51:THR:N	2.42	0.52
1:D:90:GLN:C	1:D:92:ALA:N	2.62	0.51
1:D:115:GLU:O	1:D:119:VAL:HG23	2.10	0.51
1:D:125:LEU:HD13	1:D:193:LEU:HD23	1.91	0.51
1:D:121:ASP:O	1:D:125:LEU:HG	2.10	0.51
1:A:213:THR:C	1:A:215:ASP:H	2.13	0.51
1:C:18:LEU:CD1	1:C:30:LEU:HD11	2.41	0.51
1:B:80:LEU:HB3	1:B:85:VAL:CG1	2.40	0.51
1:D:50:LEU:HD23	1:D:50:LEU:O	2.10	0.51
1:B:71:LYS:CE	1:B:74:GLN:HE21	2.12	0.51
1:D:103:SER:HB3	1:D:163:TYR:HD2	1.75	0.51
1:A:103:SER:O	1:A:106:PHE:HD2	1.94	0.51
1:A:11:GLN:HG3	1:A:56:TRP:CH2	2.46	0.51
1:C:143:VAL:HG12	1:C:143:VAL:O	2.10	0.51
1:D:143:VAL:O	1:D:143:VAL:CG1	2.58	0.51
1:B:61:ILE:CD1	1:B:97:ILE:CG2	2.89	0.51
1:B:155:ARG:NH2	1:B:166:GLN:O	2.44	0.51
1:A:85:VAL:CG1	1:A:90:GLN:OE1	2.59	0.50
1:C:160:ARG:HH11	1:C:160:ARG:HG3	1.76	0.50
1:D:85:VAL:HG12	1:D:86:THR:N	2.25	0.50
1:D:182:ALA:HA	1:D:185:MSE:CE	2.41	0.50
1:A:128:ILE:HA	1:A:201:MSE:CE	2.41	0.50
1:B:205:VAL:O	1:B:209:LYS:HG3	2.12	0.50
1:A:212:TRP:O	1:A:215:ASP:O	2.30	0.50
1:C:54:ALA:CA	1:C:97:ILE:HD11	2.38	0.50
1:D:128:ILE:HA	1:D:201:MSE:HE1	1.92	0.50
1:A:185:MSE:HB3	1:A:191:LYS:HG2	1.94	0.50
1:D:85:VAL:O	1:D:86:THR:O	2.29	0.50
1:A:96:ILE:O	1:A:98:ASP:N	2.44	0.50
1:D:38:ARG:NH2	1:D:52:LEU:HD11	2.27	0.50
1:B:89:ASP:O	1:B:93:ILE:HG13	2.11	0.50
1:C:120:GLN:O	1:C:124:ARG:HG3	2.12	0.50
1:B:207:GLN:HG3	1:C:200:VAL:CG2	2.42	0.49
1:D:92:ALA:O	1:D:94:PHE:N	2.45	0.49
1:A:12:THR:CG2	1:A:16:GLN:NE2	2.75	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:148:TYR:CE2	1:B:150:PRO:HD3	2.47	0.49
1:A:7:LEU:O	1:A:10:ILE:N	2.45	0.49
1:A:213:THR:C	1:A:215:ASP:N	2.65	0.49
1:B:167:PRO:HD2	1:D:167:PRO:HD3	1.95	0.49
1:A:58:HIS:HA	1:A:97:ILE:HG23	1.95	0.49
1:A:124:ARG:HD2	1:A:181:LEU:HD22	1.93	0.49
1:C:12:THR:CG2	1:C:16:GLN:NE2	2.74	0.49
1:A:155:ARG:NE	1:A:158:MSE:HE3	2.28	0.49
1:A:11:GLN:O	1:A:12:THR:C	2.51	0.49
1:B:161:GLU:O	1:B:162:GLN:C	2.51	0.48
1:B:61:ILE:HD12	1:B:97:ILE:HG21	1.94	0.48
1:D:57:LEU:O	1:D:60:VAL:HB	2.13	0.48
1:C:40:LEU:HD22	1:C:122:ALA:HB2	1.94	0.48
1:D:61:ILE:HD11	1:D:97:ILE:HG22	1.95	0.48
1:A:185:MSE:HG3	1:A:190:ALA:CB	2.43	0.48
1:D:12:THR:HG23	1:D:16:GLN:HE22	1.77	0.48
1:D:80:LEU:O	1:D:83:GLN:HB2	2.14	0.48
1:B:57:LEU:HD22	1:B:76:LEU:HD13	1.95	0.48
1:A:85:VAL:CG1	1:A:86:THR:H	2.20	0.48
1:D:57:LEU:HB2	1:D:97:ILE:CD1	2.43	0.48
1:D:187:THR:HB	1:D:190:ALA:CB	2.43	0.48
1:A:18:LEU:HD12	1:A:30:LEU:HD11	1.95	0.48
1:D:61:ILE:O	1:D:62:ASP:O	2.32	0.48
1:D:179:PHE:HZ	1:D:205:VAL:HG21	1.77	0.48
1:D:19:ALA:O	1:D:20:HIS:CB	2.61	0.47
1:D:199:ALA:O	1:D:203:GLU:N	2.43	0.47
1:C:10:ILE:CG2	1:C:57:LEU:HD21	2.35	0.47
1:A:81:ASN:C	1:A:83:GLN:N	2.68	0.47
1:C:27:ARG:HH11	1:C:27:ARG:HB3	1.79	0.47
1:C:89:ASP:O	1:C:93:ILE:HG13	2.14	0.47
1:D:154:PRO:HD3	1:D:172:ASN:OD1	2.15	0.47
1:A:85:VAL:C	1:A:86:THR:CG2	2.83	0.47
1:B:115:GLU:H	1:B:115:GLU:CD	2.16	0.47
1:B:152:ILE:CG1	1:D:146:LYS:HE2	2.43	0.47
1:D:147:ILE:O	1:D:169:THR:HB	2.13	0.47
1:C:66:MSE:CA	1:C:66:MSE:HE2	2.44	0.47
1:B:121:ASP:OD2	1:B:186:ASN:HB2	2.14	0.47
1:C:20:HIS:HA	1:C:22:HIS:CE1	2.50	0.47
1:C:159:THR:OG1	1:C:162:GLN:HG3	2.14	0.47
1:C:97:ILE:HG22	1:C:97:ILE:O	2.14	0.47
1:D:41:ALA:O	1:D:45:GLY:N	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:77:ILE:HG23	1:D:90:GLN:NE2	2.30	0.47
1:C:212:TRP:CD1	1:C:212:TRP:C	2.88	0.47
1:D:76:LEU:O	1:D:80:LEU:HG	2.15	0.47
1:A:4:GLU:HA	1:A:49:ASN:HD21	1.79	0.47
1:B:213:THR:O	1:B:214:ALA:C	2.53	0.47
1:A:147:ILE:O	1:A:171:ILE:HG12	2.16	0.46
1:C:81:ASN:C	1:C:83:GLN:N	2.69	0.46
1:A:85:VAL:O	1:A:86:THR:HG22	2.15	0.46
1:B:67:ALA:O	1:B:69:PRO:HD3	2.16	0.46
1:B:159:THR:OG1	1:B:162:GLN:HG3	2.15	0.46
1:D:47:ASN:HD22	1:D:50:LEU:H	1.63	0.46
1:D:112:LEU:HB3	1:D:117:GLN:HG3	1.97	0.46
1:B:193:LEU:HD12	1:B:193:LEU:HA	1.72	0.46
2:A:3008:HOH:O	1:B:203:GLU:HG2	2.13	0.46
1:B:73:HIS:O	1:B:77:ILE:HD13	2.15	0.46
1:C:6:GLN:NE2	1:C:85:VAL:HA	2.30	0.46
1:D:182:ALA:O	1:D:185:MSE:HB2	2.16	0.46
1:D:196:HIS:O	1:D:196:HIS:CG	2.69	0.46
1:B:208:PHE:HA	1:C:130:ALA:HB3	1.98	0.46
1:D:127:ALA:O	1:D:178:LEU:HD22	2.15	0.46
1:A:21:ASP:O	1:A:22:HIS:HB2	2.15	0.46
1:A:120:GLN:NE2	1:A:186:ASN:HD21	2.13	0.46
1:D:16:GLN:OE1	1:D:16:GLN:N	2.48	0.46
1:D:46:ALA:HA	1:D:114:LEU:HD23	1.98	0.46
1:A:48:LEU:HD21	1:A:52:LEU:HD12	1.96	0.46
1:C:158:MSE:SE	1:C:163:TYR:HB2	2.66	0.46
1:A:107:ASN:ND2	1:B:202:HIS:HB3	2.30	0.46
1:B:130:ALA:HB3	1:C:208:PHE:HA	1.98	0.46
1:B:137:LEU:CD2	1:C:134:ALA:HB1	2.45	0.46
1:C:112:LEU:HG	1:C:113:SER:N	2.30	0.46
1:C:1:MSE:HA	1:C:89:ASP:OD1	2.16	0.46
1:D:120:GLN:HG2	1:D:124:ARG:HD2	1.97	0.46
1:B:13:TYR:CG	1:B:79:GLN:HG2	2.52	0.45
1:D:12:THR:HG23	1:D:16:GLN:NE2	2.31	0.45
1:B:47:ASN:HD22	1:B:50:LEU:HB3	1.81	0.45
1:D:58:HIS:C	1:D:60:VAL:H	2.18	0.45
1:A:128:ILE:HA	1:A:201:MSE:HE3	1.98	0.45
1:C:148:TYR:OH	1:C:209:LYS:HD2	2.16	0.45
1:D:146:LYS:O	1:D:169:THR:HA	2.16	0.45
1:A:108:GLY:O	1:A:110:GLN:NE2	2.50	0.45
1:B:141:GLY:HA3	1:C:138:TYR:O	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:12:THR:HG22	1:C:16:GLN:HE22	1.82	0.45
1:A:155:ARG:CZ	1:A:158:MSE:HE1	2.46	0.45
1:C:74:GLN:O	1:C:77:ILE:N	2.49	0.45
1:B:96:ILE:O	1:B:97:ILE:C	2.54	0.45
1:C:120:GLN:NE2	1:C:186:ASN:ND2	2.60	0.45
1:D:39:ARG:O	1:D:39:ARG:HG2	2.17	0.45
1:D:76:LEU:HG	1:D:80:LEU:HD11	1.98	0.45
1:D:185:MSE:HE3	1:D:194:ALA:HB2	1.97	0.45
1:B:174:PHE:CE2	1:B:201:MSE:HE2	2.51	0.45
1:D:40:LEU:HD21	1:D:190:ALA:HB2	1.99	0.45
1:B:80:LEU:HD13	1:B:90:GLN:HG2	1.98	0.45
1:B:138:TYR:O	1:C:141:GLY:HA3	2.16	0.45
1:B:61:ILE:O	1:B:61:ILE:HG12	2.16	0.45
1:A:61:ILE:O	1:A:62:ASP:O	2.36	0.44
1:B:103:SER:O	1:B:106:PHE:HD1	2.00	0.44
1:C:54:ALA:HB1	1:C:97:ILE:HG13	1.99	0.44
1:C:142:HIS:CG	1:C:142:HIS:O	2.71	0.44
1:A:48:LEU:C	1:A:48:LEU:HD23	2.37	0.44
1:C:61:ILE:HD12	1:C:61:ILE:HG21	1.64	0.44
1:C:76:LEU:O	1:C:80:LEU:HG	2.18	0.44
1:B:10:ILE:HG23	1:B:57:LEU:HD21	1.99	0.44
1:D:140:SER:HB3	1:D:145:GLU:HB3	2.00	0.44
1:B:113:SER:O	1:B:117:GLN:HG3	2.17	0.44
1:C:71:LYS:NZ	1:C:74:GLN:NE2	2.66	0.44
1:C:121:ASP:OD1	1:C:186:ASN:N	2.45	0.44
1:C:12:THR:HG22	1:C:16:GLN:NE2	2.32	0.44
1:D:93:ILE:O	1:D:97:ILE:HB	2.17	0.44
1:D:148:TYR:CD1	1:D:171:ILE:HG13	2.53	0.44
1:D:187:THR:HB	1:D:190:ALA:HB2	1.99	0.44
1:A:6:GLN:NE2	1:A:84:ASN:O	2.51	0.43
1:A:149:ASP:HB3	1:A:152:ILE:HB	2.00	0.43
1:C:146:LYS:O	1:C:169:THR:HA	2.18	0.43
1:C:193:LEU:O	1:C:197:ARG:HG3	2.18	0.43
1:A:61:ILE:HA	1:A:72:ALA:HB1	2.00	0.43
1:A:85:VAL:HG22	1:A:86:THR:N	2.33	0.43
1:C:54:ALA:O	1:C:97:ILE:HD11	2.18	0.43
1:C:74:GLN:HG2	1:C:75:ASP:N	2.33	0.43
1:C:214:ALA:O	1:C:215:ASP:O	2.36	0.43
1:A:161:GLU:O	1:A:162:GLN:C	2.57	0.43
1:B:165:HIS:ND1	1:B:165:HIS:C	2.71	0.43
1:B:166:GLN:HE22	1:D:143:VAL:HG12	1.84	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:73:HIS:O	1:C:74:GLN:C	2.56	0.43
1:D:60:VAL:HG12	1:D:60:VAL:O	2.17	0.43
1:A:143:VAL:HG12	1:A:145:GLU:HB2	1.99	0.43
1:D:96:ILE:HG23	1:D:116:GLY:HA2	2.00	0.43
1:A:48:LEU:O	1:A:52:LEU:HG	2.18	0.43
1:C:165:HIS:ND1	1:C:165:HIS:C	2.72	0.43
1:C:205:VAL:O	1:C:209:LYS:HG3	2.19	0.43
1:A:7:LEU:HD11	1:A:52:LEU:HB2	2.01	0.43
1:C:1:MSE:HE2	1:C:1:MSE:N	2.33	0.43
1:C:28:ASP:HB3	1:C:32:ARG:HH12	1.83	0.43
1:D:37:ALA:HB2	1:D:122:ALA:CB	2.48	0.43
1:B:158:MSE:HE2	1:B:163:TYR:HA	2.01	0.43
1:C:28:ASP:HB3	1:C:32:ARG:NH1	2.33	0.43
1:D:213:THR:O	1:D:214:ALA:C	2.57	0.43
1:D:92:ALA:O	1:D:93:ILE:C	2.56	0.43
1:A:147:ILE:HA	1:A:170:ALA:HB3	2.01	0.43
1:B:77:ILE:HG22	1:B:81:ASN:HD22	1.82	0.43
1:B:182:ALA:HA	1:B:185:MSE:HE2	2.00	0.43
1:B:174:PHE:HA	1:B:178:LEU:HB2	2.01	0.42
1:C:81:ASN:HA	1:C:85:VAL:HG12	2.01	0.42
1:C:149:ASP:C	1:C:151:ALA:H	2.22	0.42
1:C:125:LEU:HD21	1:C:185:MSE:HE3	2.00	0.42
1:B:115:GLU:CD	1:B:115:GLU:N	2.72	0.42
1:B:77:ILE:N	1:B:77:ILE:HD12	2.35	0.42
1:D:54:ALA:O	1:D:97:ILE:HD11	2.20	0.42
1:B:149:ASP:O	1:B:152:ILE:N	2.51	0.42
1:C:28:ASP:O	1:C:32:ARG:HG3	2.20	0.42
1:A:118:VAL:O	1:A:121:ASP:HB2	2.20	0.42
1:C:61:ILE:HA	1:C:66:MSE:HE3	2.00	0.42
1:C:103:SER:CB	1:C:160:ARG:NH1	2.82	0.42
1:C:178:LEU:HD23	1:C:178:LEU:HA	1.83	0.42
1:B:50:LEU:CD1	1:B:115:GLU:HG3	2.40	0.42
1:B:125:LEU:HD23	1:B:125:LEU:HA	1.92	0.42
1:D:47:ASN:HD22	1:D:50:LEU:CB	2.29	0.41
1:C:13:TYR:CD1	1:C:79:GLN:HG2	2.55	0.41
1:B:138:TYR:CG	1:C:147:ILE:HD11	2.55	0.41
1:C:155:ARG:NH1	1:C:158:MSE:CE	2.83	0.41
1:D:74:GLN:O	1:D:78:VAL:HG23	2.20	0.41
1:A:102:PHE:CB	1:A:177:LYS:HE3	2.50	0.41
1:B:137:LEU:HD22	1:C:134:ALA:CA	2.45	0.41
1:C:53:ALA:O	1:C:57:LEU:HG	2.19	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:159:THR:O	1:D:161:GLU:N	2.53	0.41
1:B:38:ARG:O	1:B:42:LYS:HG3	2.20	0.41
1:C:174:PHE:O	1:C:179:PHE:N	2.53	0.41
1:D:85:VAL:O	1:D:86:THR:C	2.58	0.41
1:C:13:TYR:CG	1:C:79:GLN:HG2	2.55	0.41
1:C:96:ILE:HA	1:C:112:LEU:HD11	2.01	0.41
1:C:208:PHE:CD1	1:C:208:PHE:C	2.93	0.41
1:B:104:LYS:O	1:B:106:PHE:N	2.53	0.41
1:C:69:PRO:O	1:C:72:ALA:HB3	2.19	0.41
1:C:100:MSE:O	1:C:101:SER:C	2.58	0.41
1:A:103:SER:O	1:A:106:PHE:CD2	2.73	0.41
1:A:178:LEU:HD13	1:A:201:MSE:CE	2.49	0.41
1:D:120:GLN:NE2	1:D:186:ASN:ND2	2.57	0.41
1:D:191:LYS:O	1:D:192:ALA:C	2.58	0.41
1:B:57:LEU:HD13	1:B:76:LEU:HD11	2.03	0.41
1:C:7:LEU:O	1:C:10:ILE:HB	2.21	0.40
1:A:112:LEU:O	1:A:113:SER:O	2.40	0.40
1:B:121:ASP:CG	1:B:186:ASN:H	2.24	0.40
1:C:2:ILE:HG22	1:C:3:THR:N	2.36	0.40
1:C:171:ILE:HD13	1:C:171:ILE:HA	1.94	0.40
1:C:179:PHE:CZ	1:C:205:VAL:HG21	2.56	0.40
1:C:98:ASP:O	1:C:99:HIS:ND1	2.54	0.40
1:C:119:VAL:O	1:C:120:GLN:C	2.59	0.40
1:D:29:HIS:O	1:D:33:VAL:HG23	2.22	0.40
1:D:29:HIS:NE2	1:D:59:ASP:OD2	2.49	0.40
1:A:145:GLU:CG	1:A:168:GLY:O	2.66	0.40
1:C:83:GLN:O	1:C:84:ASN:C	2.59	0.40
1:A:185:MSE:HG3	1:A:190:ALA:HB1	2.03	0.40
1:C:166:GLN:HA	1:C:167:PRO:HD3	1.77	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	202/231 (87%)	171 (85%)	23 (11%)	8 (4%)	3	9
1	B	208/231 (90%)	179 (86%)	24 (12%)	5 (2%)	6	20
1	C	208/231 (90%)	172 (83%)	24 (12%)	12 (6%)	1	4
1	D	197/231 (85%)	163 (83%)	32 (16%)	2 (1%)	15	44
All	All	815/924 (88%)	685 (84%)	103 (13%)	27 (3%)	4	13

All (27) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	85	VAL
1	A	97	ILE
1	A	113	SER
1	C	82	ALA
1	C	187	THR
1	D	84	ASN
1	A	75	ASP
1	A	82	ALA
1	B	97	ILE
1	B	105	SER
1	C	48	LEU
1	C	60	VAL
1	C	61	ILE
1	C	156	GLU
1	B	107	ASN
1	D	46	ALA
1	A	11	GLN
1	B	178	LEU
1	C	49	ASN
1	C	101	SER
1	C	103	SER
1	C	177	LYS
1	A	96	ILE
1	B	96	ILE
1	C	74	GLN
1	A	152	ILE
1	C	109	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	165/178 (93%)	151 (92%)	14 (8%)	10	31
1	B	169/178 (95%)	156 (92%)	13 (8%)	13	35
1	C	169/178 (95%)	156 (92%)	13 (8%)	13	35
1	D	163/178 (92%)	156 (96%)	7 (4%)	29	62
All	All	666/712 (94%)	619 (93%)	47 (7%)	14	39

All (47) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	4	GLU
1	A	7	LEU
1	A	8	THR
1	A	16	GLN
1	A	40	LEU
1	A	50	LEU
1	A	61	ILE
1	A	78	VAL
1	A	86	THR
1	A	115	GLU
1	A	143	VAL
1	A	157	HIS
1	A	160	ARG
1	A	207	GLN
1	B	4	GLU
1	B	7	LEU
1	B	16	GLN
1	B	27	ARG
1	B	40	LEU
1	B	50	LEU
1	B	61	ILE
1	B	66	MSE
1	B	71	LYS
1	B	74	GLN
1	B	115	GLU
1	B	157	HIS
1	B	187	THR
1	C	7	LEU

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Mol	Chain	Res	Type
1	C	27	ARG
1	C	50	LEU
1	C	58	HIS
1	C	59	ASP
1	C	61	ILE
1	C	62	ASP
1	C	71	LYS
1	C	113	SER
1	C	137	LEU
1	C	157	HIS
1	C	188	ASP
1	C	209	LYS
1	D	4	GLU
1	D	7	LEU
1	D	16	GLN
1	D	86	THR
1	D	137	LEU
1	D	155	ARG
1	D	157	HIS

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

Mol	Chain	Res	Type
1	A	11	GLN
1	A	16	GLN
1	A	47	ASN
1	A	49	ASN
1	A	58	HIS
1	A	79	GLN
1	A	99	HIS
1	A	120	GLN
1	A	162	GLN
1	B	25	HIS
1	B	47	ASN
1	B	58	HIS
1	B	74	GLN
1	B	79	GLN
1	B	81	ASN
1	B	90	GLN
1	B	99	HIS
1	B	110	GLN
1	B	120	GLN

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Mol	Chain	Res	Type
1	B	162	GLN
1	C	6	GLN
1	C	16	GLN
1	C	29	HIS
1	C	47	ASN
1	C	74	GLN
1	C	79	GLN
1	C	120	GLN
1	C	162	GLN
1	C	186	ASN
1	D	47	ASN
1	D	79	GLN
1	D	90	GLN
1	D	99	HIS
1	D	110	GLN
1	D	120	GLN
1	D	162	GLN

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, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	201/231 (87%)	-0.14	5 (2%) 57 47	2, 17, 44, 63	0
1	B	206/231 (89%)	0.03	10 (4%) 29 20	1, 18, 82, 97	0
1	C	206/231 (89%)	0.37	15 (7%) 15 8	3, 36, 77, 101	0
1	D	198/231 (85%)	0.59	20 (10%) 7 4	3, 38, 83, 89	0
All	All	811/924 (87%)	0.21	50 (6%) 20 13	1, 26, 78, 101	0

All (50) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	164	ARG	8.0
1	C	108	GLY	7.9
1	C	107	ASN	6.0
1	C	110	GLN	6.0
1	B	157	HIS	5.4
1	A	215	ASP	5.2
1	D	110	GLN	4.9
1	D	101	SER	4.8
1	A	214	ALA	4.5
1	C	109	PRO	4.2
1	B	110	GLN	4.0
1	D	74	GLN	3.9
1	A	213	THR	3.9
1	A	72	ALA	3.7
1	D	37	ALA	3.7
1	D	4	GLU	3.6
1	B	109	PRO	3.6
1	D	62	ASP	3.5
1	B	160	ARG	3.5
1	D	157	HIS	3.5
1	B	163	TYR	3.4

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Mol	Chain	Res	Type	RSRZ
1	C	164	ARG	3.0
1	C	115	GLU	2.9
1	D	103	SER	2.9
1	D	104	LYS	2.9
1	D	167	PRO	2.8
1	B	106	PHE	2.8
1	D	161	GLU	2.7
1	C	84	ASN	2.7
1	C	161	GLU	2.6
1	B	107	ASN	2.6
1	D	165	HIS	2.6
1	D	166	GLN	2.6
1	A	188	ASP	2.5
1	D	80	LEU	2.4
1	D	40	LEU	2.4
1	D	44	GLU	2.3
1	B	111	LYS	2.3
1	B	196	HIS	2.3
1	C	44	GLU	2.2
1	C	106	PHE	2.2
1	C	79	GLN	2.2
1	D	163	TYR	2.2
1	C	196	HIS	2.1
1	D	6	GLN	2.1
1	C	3	THR	2.1
1	C	99	HIS	2.0
1	C	5	THR	2.0
1	D	109	PRO	2.0
1	D	111	LYS	2.0

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

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

6.3 Carbohydrates ⓘ

There are no monosaccharides in this entry.

6.4 Ligands ⓘ

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.