



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 09:00 PM GMT

PDB ID : 1N0F
Title : CRYSTAL STRUCTURE OF A CELL DIVISION AND CELL WALL BIOSYNTHESIS PROTEIN UPF0040 FROM MYCOPLASMA PNEUMONIAE: INDICATION OF A NOVEL FOLD WITH A POSSIBLE NEW CONSERVED SEQUENCE MOTIF
Authors : Chen, S.; Jancrick, J.; Yokota, H.; Kim, R.; Kim, S.-H.; Berkeley Structural Genomics Center (BSGC)
Deposited on : 2002-10-13
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
<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) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

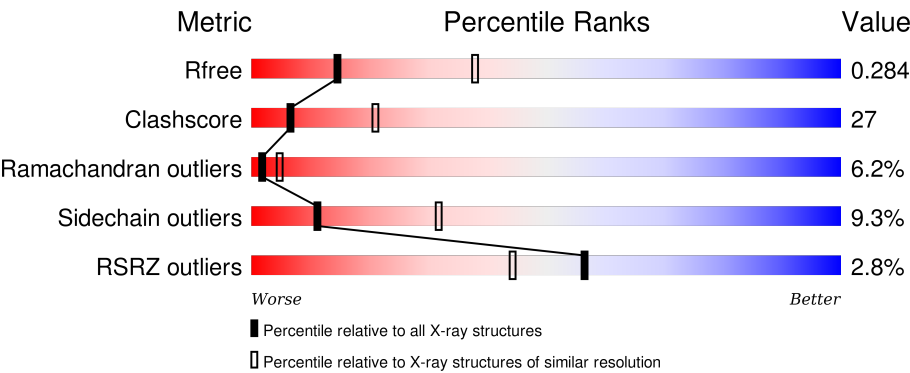
1 Overall quality at a glance i

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}	91344	2393 (2.80-2.80)
Clashscore	102246	2827 (2.80-2.80)
Ramachandran outliers	100387	2782 (2.80-2.80)
Sidechain outliers	100360	2784 (2.80-2.80)
RSRZ outliers	91569	2404 (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 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 <=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	166	<div><div>2%</div><div><div></div><div>39%</div><div>38%</div><div>7%</div><div>15%</div></div></div>
1	B	166	<div><div>%</div><div><div></div><div>44%</div><div>30%</div><div>9%</div><div>16%</div></div></div>
1	C	166	<div><div>%</div><div><div></div><div>47%</div><div>28%</div><div>7%</div><div>17%</div></div></div>
1	D	166	<div><div>%</div><div><div></div><div>43%</div><div>30%</div><div>9%</div><div>17%</div></div></div>
1	E	166	<div><div>5%</div><div><div></div><div>39%</div><div>36%</div><div>8%</div><div>17%</div></div></div>

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Mol	Chain	Length	Quality of chain
1	F	166	<div><div><div>%</div><div><div></div><div>46%</div><div>28%</div><div>7%</div><div>•</div><div>17%</div></div></div></div>
1	G	166	<div><div><div>4%</div><div><div></div><div>40%</div><div>34%</div><div>7%</div><div>•</div><div>17%</div></div></div></div>
1	H	166	<div><div><div>4%</div><div><div></div><div>37%</div><div>36%</div><div>7%</div><div>•</div><div>17%</div></div></div></div>

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 9184 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 mraZ.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	141	Total	C	N	O	S	0	0	0
			1153	739	197	214	3			
1	B	139	Total	C	N	O	S	0	0	0
			1133	725	194	211	3			
1	C	137	Total	C	N	O	S	0	0	0
			1119	717	190	209	3			
1	D	137	Total	C	N	O	S	0	0	0
			1119	717	190	209	3			
1	E	137	Total	C	N	O	S	0	0	0
			1119	717	190	209	3			
1	F	137	Total	C	N	O	S	0	0	0
			1119	717	190	209	3			
1	G	137	Total	C	N	O	S	0	0	0
			1119	717	190	209	3			
1	H	137	Total	C	N	O	S	0	0	0
			1119	717	190	209	3			

There are 200 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	EXPRESSION TAG	UNP P75467
A	2	GLY	-	EXPRESSION TAG	UNP P75467
A	3	SER	-	EXPRESSION TAG	UNP P75467
A	4	SER	-	EXPRESSION TAG	UNP P75467
A	5	HIS	-	EXPRESSION TAG	UNP P75467
A	6	HIS	-	EXPRESSION TAG	UNP P75467
A	7	HIS	-	EXPRESSION TAG	UNP P75467
A	8	HIS	-	EXPRESSION TAG	UNP P75467
A	9	HIS	-	EXPRESSION TAG	UNP P75467
A	10	HIS	-	EXPRESSION TAG	UNP P75467
A	11	ASP	-	EXPRESSION TAG	UNP P75467
A	12	TYR	-	EXPRESSION TAG	UNP P75467
A	13	ASP	-	EXPRESSION TAG	UNP P75467

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Chain	Residue	Modelled	Actual	Comment	Reference
A	14	ILE	-	EXPRESSION TAG	UNP P75467
A	15	PRO	-	EXPRESSION TAG	UNP P75467
A	16	THR	-	EXPRESSION TAG	UNP P75467
A	17	THR	-	EXPRESSION TAG	UNP P75467
A	18	GLU	-	EXPRESSION TAG	UNP P75467
A	19	ASN	-	EXPRESSION TAG	UNP P75467
A	20	LEU	-	EXPRESSION TAG	UNP P75467
A	21	TYR	-	EXPRESSION TAG	UNP P75467
A	22	PHE	-	EXPRESSION TAG	UNP P75467
A	23	GLN	-	EXPRESSION TAG	UNP P75467
A	24	GLY	-	EXPRESSION TAG	UNP P75467
A	25	HIS	-	EXPRESSION TAG	UNP P75467
B	1	MET	-	EXPRESSION TAG	UNP P75467
B	2	GLY	-	EXPRESSION TAG	UNP P75467
B	3	SER	-	EXPRESSION TAG	UNP P75467
B	4	SER	-	EXPRESSION TAG	UNP P75467
B	5	HIS	-	EXPRESSION TAG	UNP P75467
B	6	HIS	-	EXPRESSION TAG	UNP P75467
B	7	HIS	-	EXPRESSION TAG	UNP P75467
B	8	HIS	-	EXPRESSION TAG	UNP P75467
B	9	HIS	-	EXPRESSION TAG	UNP P75467
B	10	HIS	-	EXPRESSION TAG	UNP P75467
B	11	ASP	-	EXPRESSION TAG	UNP P75467
B	12	TYR	-	EXPRESSION TAG	UNP P75467
B	13	ASP	-	EXPRESSION TAG	UNP P75467
B	14	ILE	-	EXPRESSION TAG	UNP P75467
B	15	PRO	-	EXPRESSION TAG	UNP P75467
B	16	THR	-	EXPRESSION TAG	UNP P75467
B	17	THR	-	EXPRESSION TAG	UNP P75467
B	18	GLU	-	EXPRESSION TAG	UNP P75467
B	19	ASN	-	EXPRESSION TAG	UNP P75467
B	20	LEU	-	EXPRESSION TAG	UNP P75467
B	21	TYR	-	EXPRESSION TAG	UNP P75467
B	22	PHE	-	EXPRESSION TAG	UNP P75467
B	23	GLN	-	EXPRESSION TAG	UNP P75467
B	24	GLY	-	EXPRESSION TAG	UNP P75467
B	25	HIS	-	EXPRESSION TAG	UNP P75467
C	1	MET	-	EXPRESSION TAG	UNP P75467
C	2	GLY	-	EXPRESSION TAG	UNP P75467
C	3	SER	-	EXPRESSION TAG	UNP P75467
C	4	SER	-	EXPRESSION TAG	UNP P75467
C	5	HIS	-	EXPRESSION TAG	UNP P75467

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Chain	Residue	Modelled	Actual	Comment	Reference
C	6	HIS	-	EXPRESSION TAG	UNP P75467
C	7	HIS	-	EXPRESSION TAG	UNP P75467
C	8	HIS	-	EXPRESSION TAG	UNP P75467
C	9	HIS	-	EXPRESSION TAG	UNP P75467
C	10	HIS	-	EXPRESSION TAG	UNP P75467
C	11	ASP	-	EXPRESSION TAG	UNP P75467
C	12	TYR	-	EXPRESSION TAG	UNP P75467
C	13	ASP	-	EXPRESSION TAG	UNP P75467
C	14	ILE	-	EXPRESSION TAG	UNP P75467
C	15	PRO	-	EXPRESSION TAG	UNP P75467
C	16	THR	-	EXPRESSION TAG	UNP P75467
C	17	THR	-	EXPRESSION TAG	UNP P75467
C	18	GLU	-	EXPRESSION TAG	UNP P75467
C	19	ASN	-	EXPRESSION TAG	UNP P75467
C	20	LEU	-	EXPRESSION TAG	UNP P75467
C	21	TYR	-	EXPRESSION TAG	UNP P75467
C	22	PHE	-	EXPRESSION TAG	UNP P75467
C	23	GLN	-	EXPRESSION TAG	UNP P75467
C	24	GLY	-	EXPRESSION TAG	UNP P75467
C	25	HIS	-	EXPRESSION TAG	UNP P75467
D	1	MET	-	EXPRESSION TAG	UNP P75467
D	2	GLY	-	EXPRESSION TAG	UNP P75467
D	3	SER	-	EXPRESSION TAG	UNP P75467
D	4	SER	-	EXPRESSION TAG	UNP P75467
D	5	HIS	-	EXPRESSION TAG	UNP P75467
D	6	HIS	-	EXPRESSION TAG	UNP P75467
D	7	HIS	-	EXPRESSION TAG	UNP P75467
D	8	HIS	-	EXPRESSION TAG	UNP P75467
D	9	HIS	-	EXPRESSION TAG	UNP P75467
D	10	HIS	-	EXPRESSION TAG	UNP P75467
D	11	ASP	-	EXPRESSION TAG	UNP P75467
D	12	TYR	-	EXPRESSION TAG	UNP P75467
D	13	ASP	-	EXPRESSION TAG	UNP P75467
D	14	ILE	-	EXPRESSION TAG	UNP P75467
D	15	PRO	-	EXPRESSION TAG	UNP P75467
D	16	THR	-	EXPRESSION TAG	UNP P75467
D	17	THR	-	EXPRESSION TAG	UNP P75467
D	18	GLU	-	EXPRESSION TAG	UNP P75467
D	19	ASN	-	EXPRESSION TAG	UNP P75467
D	20	LEU	-	EXPRESSION TAG	UNP P75467
D	21	TYR	-	EXPRESSION TAG	UNP P75467
D	22	PHE	-	EXPRESSION TAG	UNP P75467

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Chain	Residue	Modelled	Actual	Comment	Reference
D	23	GLN	-	EXPRESSION TAG	UNP P75467
D	24	GLY	-	EXPRESSION TAG	UNP P75467
D	25	HIS	-	EXPRESSION TAG	UNP P75467
E	1	MET	-	EXPRESSION TAG	UNP P75467
E	2	GLY	-	EXPRESSION TAG	UNP P75467
E	3	SER	-	EXPRESSION TAG	UNP P75467
E	4	SER	-	EXPRESSION TAG	UNP P75467
E	5	HIS	-	EXPRESSION TAG	UNP P75467
E	6	HIS	-	EXPRESSION TAG	UNP P75467
E	7	HIS	-	EXPRESSION TAG	UNP P75467
E	8	HIS	-	EXPRESSION TAG	UNP P75467
E	9	HIS	-	EXPRESSION TAG	UNP P75467
E	10	HIS	-	EXPRESSION TAG	UNP P75467
E	11	ASP	-	EXPRESSION TAG	UNP P75467
E	12	TYR	-	EXPRESSION TAG	UNP P75467
E	13	ASP	-	EXPRESSION TAG	UNP P75467
E	14	ILE	-	EXPRESSION TAG	UNP P75467
E	15	PRO	-	EXPRESSION TAG	UNP P75467
E	16	THR	-	EXPRESSION TAG	UNP P75467
E	17	THR	-	EXPRESSION TAG	UNP P75467
E	18	GLU	-	EXPRESSION TAG	UNP P75467
E	19	ASN	-	EXPRESSION TAG	UNP P75467
E	20	LEU	-	EXPRESSION TAG	UNP P75467
E	21	TYR	-	EXPRESSION TAG	UNP P75467
E	22	PHE	-	EXPRESSION TAG	UNP P75467
E	23	GLN	-	EXPRESSION TAG	UNP P75467
E	24	GLY	-	EXPRESSION TAG	UNP P75467
E	25	HIS	-	EXPRESSION TAG	UNP P75467
F	1	MET	-	EXPRESSION TAG	UNP P75467
F	2	GLY	-	EXPRESSION TAG	UNP P75467
F	3	SER	-	EXPRESSION TAG	UNP P75467
F	4	SER	-	EXPRESSION TAG	UNP P75467
F	5	HIS	-	EXPRESSION TAG	UNP P75467
F	6	HIS	-	EXPRESSION TAG	UNP P75467
F	7	HIS	-	EXPRESSION TAG	UNP P75467
F	8	HIS	-	EXPRESSION TAG	UNP P75467
F	9	HIS	-	EXPRESSION TAG	UNP P75467
F	10	HIS	-	EXPRESSION TAG	UNP P75467
F	11	ASP	-	EXPRESSION TAG	UNP P75467
F	12	TYR	-	EXPRESSION TAG	UNP P75467
F	13	ASP	-	EXPRESSION TAG	UNP P75467
F	14	ILE	-	EXPRESSION TAG	UNP P75467

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Chain	Residue	Modelled	Actual	Comment	Reference
F	15	PRO	-	EXPRESSION TAG	UNP P75467
F	16	THR	-	EXPRESSION TAG	UNP P75467
F	17	THR	-	EXPRESSION TAG	UNP P75467
F	18	GLU	-	EXPRESSION TAG	UNP P75467
F	19	ASN	-	EXPRESSION TAG	UNP P75467
F	20	LEU	-	EXPRESSION TAG	UNP P75467
F	21	TYR	-	EXPRESSION TAG	UNP P75467
F	22	PHE	-	EXPRESSION TAG	UNP P75467
F	23	GLN	-	EXPRESSION TAG	UNP P75467
F	24	GLY	-	EXPRESSION TAG	UNP P75467
F	25	HIS	-	EXPRESSION TAG	UNP P75467
G	1	MET	-	EXPRESSION TAG	UNP P75467
G	2	GLY	-	EXPRESSION TAG	UNP P75467
G	3	SER	-	EXPRESSION TAG	UNP P75467
G	4	SER	-	EXPRESSION TAG	UNP P75467
G	5	HIS	-	EXPRESSION TAG	UNP P75467
G	6	HIS	-	EXPRESSION TAG	UNP P75467
G	7	HIS	-	EXPRESSION TAG	UNP P75467
G	8	HIS	-	EXPRESSION TAG	UNP P75467
G	9	HIS	-	EXPRESSION TAG	UNP P75467
G	10	HIS	-	EXPRESSION TAG	UNP P75467
G	11	ASP	-	EXPRESSION TAG	UNP P75467
G	12	TYR	-	EXPRESSION TAG	UNP P75467
G	13	ASP	-	EXPRESSION TAG	UNP P75467
G	14	ILE	-	EXPRESSION TAG	UNP P75467
G	15	PRO	-	EXPRESSION TAG	UNP P75467
G	16	THR	-	EXPRESSION TAG	UNP P75467
G	17	THR	-	EXPRESSION TAG	UNP P75467
G	18	GLU	-	EXPRESSION TAG	UNP P75467
G	19	ASN	-	EXPRESSION TAG	UNP P75467
G	20	LEU	-	EXPRESSION TAG	UNP P75467
G	21	TYR	-	EXPRESSION TAG	UNP P75467
G	22	PHE	-	EXPRESSION TAG	UNP P75467
G	23	GLN	-	EXPRESSION TAG	UNP P75467
G	24	GLY	-	EXPRESSION TAG	UNP P75467
G	25	HIS	-	EXPRESSION TAG	UNP P75467
H	1	MET	-	EXPRESSION TAG	UNP P75467
H	2	GLY	-	EXPRESSION TAG	UNP P75467
H	3	SER	-	EXPRESSION TAG	UNP P75467
H	4	SER	-	EXPRESSION TAG	UNP P75467
H	5	HIS	-	EXPRESSION TAG	UNP P75467
H	6	HIS	-	EXPRESSION TAG	UNP P75467

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Chain	Residue	Modelled	Actual	Comment	Reference
H	7	HIS	-	EXPRESSION TAG	UNP P75467
H	8	HIS	-	EXPRESSION TAG	UNP P75467
H	9	HIS	-	EXPRESSION TAG	UNP P75467
H	10	HIS	-	EXPRESSION TAG	UNP P75467
H	11	ASP	-	EXPRESSION TAG	UNP P75467
H	12	TYR	-	EXPRESSION TAG	UNP P75467
H	13	ASP	-	EXPRESSION TAG	UNP P75467
H	14	ILE	-	EXPRESSION TAG	UNP P75467
H	15	PRO	-	EXPRESSION TAG	UNP P75467
H	16	THR	-	EXPRESSION TAG	UNP P75467
H	17	THR	-	EXPRESSION TAG	UNP P75467
H	18	GLU	-	EXPRESSION TAG	UNP P75467
H	19	ASN	-	EXPRESSION TAG	UNP P75467
H	20	LEU	-	EXPRESSION TAG	UNP P75467
H	21	TYR	-	EXPRESSION TAG	UNP P75467
H	22	PHE	-	EXPRESSION TAG	UNP P75467
H	23	GLN	-	EXPRESSION TAG	UNP P75467
H	24	GLY	-	EXPRESSION TAG	UNP P75467
H	25	HIS	-	EXPRESSION TAG	UNP P75467

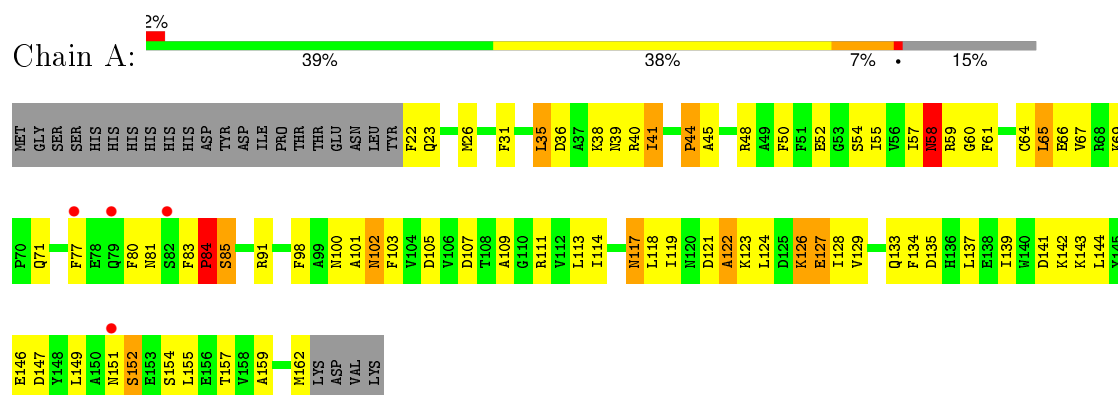
- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	21	Total O 21 21	0	0
2	B	31	Total O 31 31	0	0
2	C	23	Total O 23 23	0	0
2	D	30	Total O 30 30	0	0
2	E	15	Total O 15 15	0	0
2	F	10	Total O 10 10	0	0
2	G	14	Total O 14 14	0	0
2	H	40	Total O 40 40	0	0

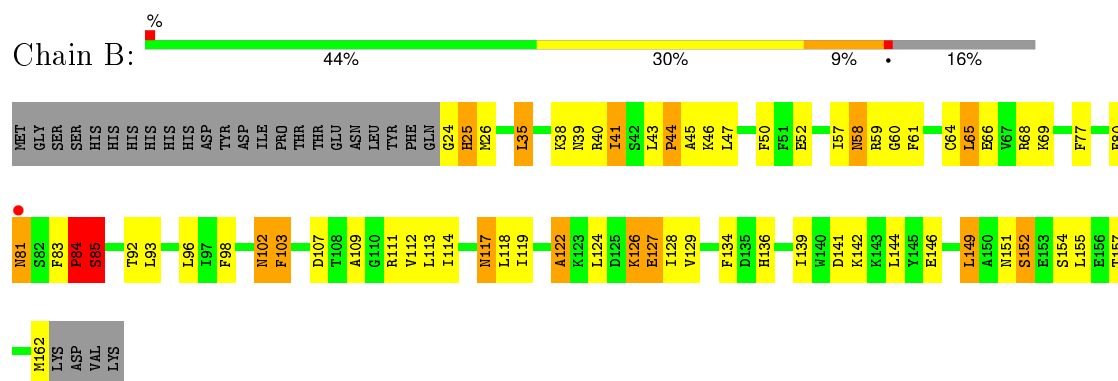
3 Residue-property plots [i](#)

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.

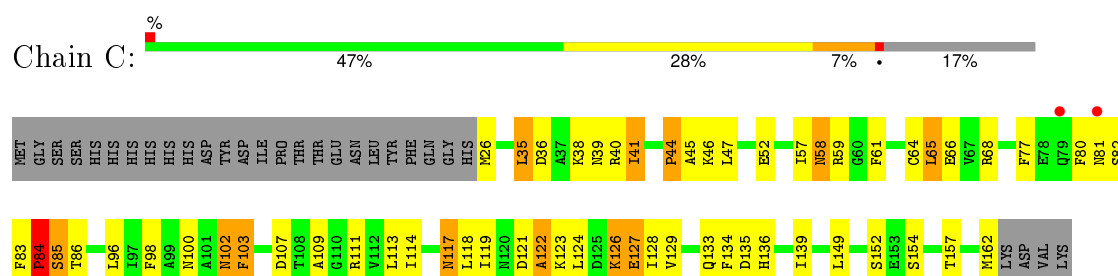
• Molecule 1: Protein mraZ



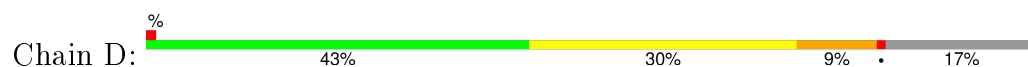
• Molecule 1: Protein mraZ

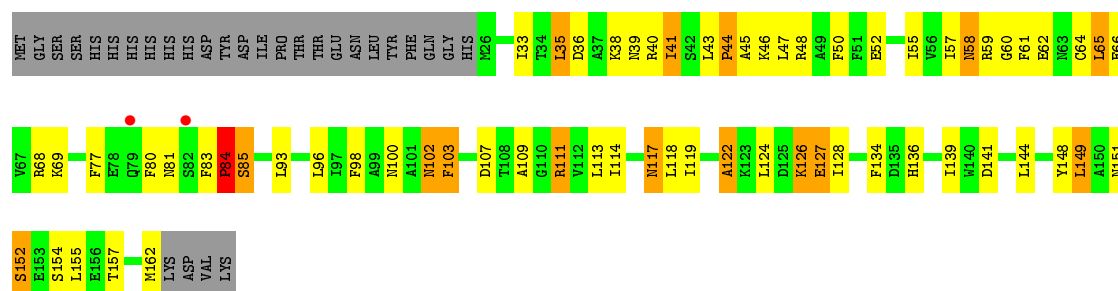


• Molecule 1: Protein mraZ

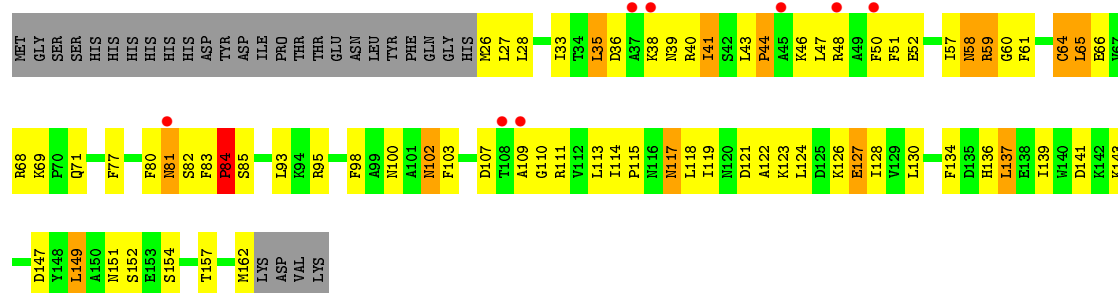


• Molecule 1: Protein mraZ

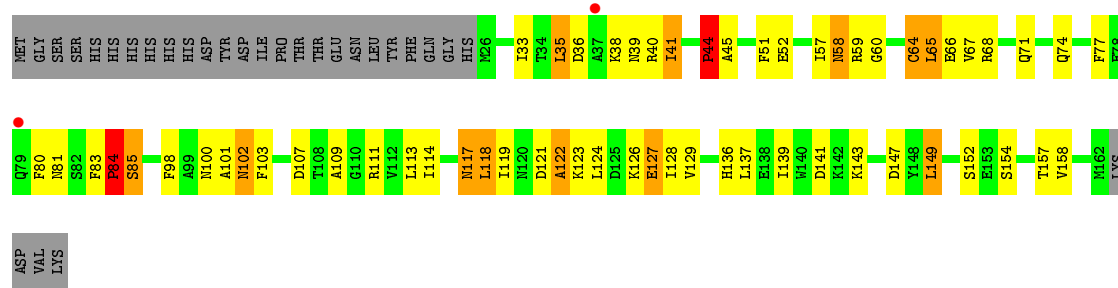




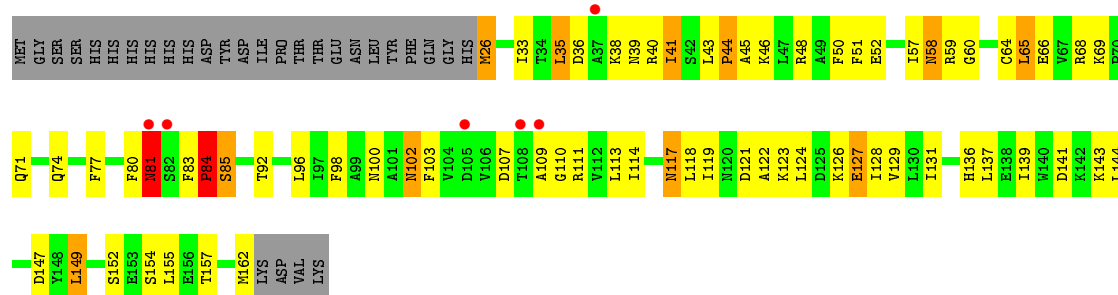
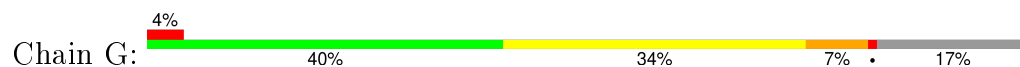
• Molecule 1: Protein mraZ



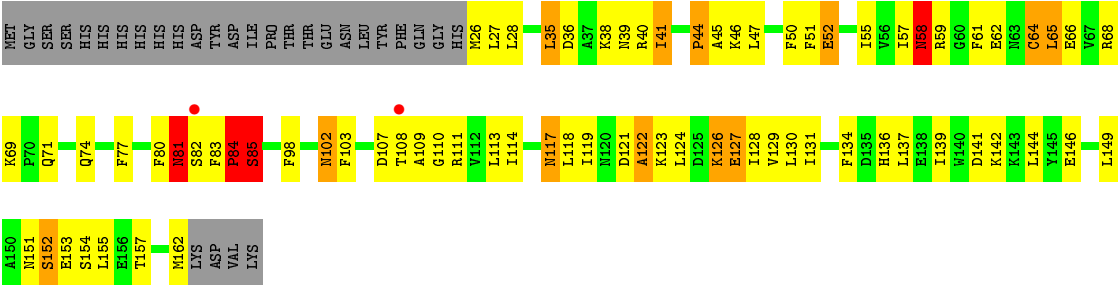
• Molecule 1: Protein mraZ



• Molecule 1: Protein mraZ



• Molecule 1: Protein mraZ



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	84.89Å 101.18Å 169.05Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	13.01 – 2.80 13.01 – 2.60	Depositor EDS
% Data completeness (in resolution range)	97.5 (13.01-2.80) 99.0 (13.01-2.60)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.10	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.64 (at 2.60Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.240 , 0.284 0.240 , 0.284	Depositor DCC
R_{free} test set	1786 reflections (5.06%)	DCC
Wilson B-factor (Å ²)	48.2	Xtriage
Anisotropy	0.039	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 57.6	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Outliers	0 of 44668 reflections	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	9184	wwPDB-VP
Average B, all atoms (Å ²)	48.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.38% 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, 0.375 respectively for untwinned datasets, and 0.333, 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	0.65	0/1175	0.89	4/1584 (0.3%)
1	B	0.74	0/1154	0.95	3/1556 (0.2%)
1	C	0.65	0/1139	0.90	3/1536 (0.2%)
1	D	0.68	0/1139	0.93	3/1536 (0.2%)
1	E	0.62	0/1139	0.87	3/1536 (0.2%)
1	F	0.57	0/1139	0.85	4/1536 (0.3%)
1	G	0.58	0/1139	0.84	1/1536 (0.1%)
1	H	0.70	0/1139	0.91	3/1536 (0.2%)
All	All	0.65	0/9163	0.89	24/12356 (0.2%)

There are no bond length outliers.

All (24) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	102	ASN	N-CA-C	6.72	129.15	111.00
1	B	102	ASN	N-CA-C	6.71	129.11	111.00
1	A	102	ASN	N-CA-C	6.62	128.86	111.00
1	C	102	ASN	N-CA-C	6.52	128.61	111.00
1	H	122	ALA	N-CA-C	-6.37	93.81	111.00
1	E	102	ASN	N-CA-C	6.27	127.92	111.00
1	H	102	ASN	N-CA-C	6.24	127.86	111.00
1	G	102	ASN	N-CA-C	6.02	127.25	111.00
1	C	122	ALA	N-CA-C	-5.93	94.99	111.00
1	F	102	ASN	N-CA-C	5.93	127.01	111.00
1	D	126	LYS	N-CA-C	-5.74	95.50	111.00
1	D	122	ALA	N-CA-C	-5.71	95.58	111.00
1	A	122	ALA	N-CA-C	-5.58	95.92	111.00
1	B	122	ALA	N-CA-C	-5.46	96.27	111.00
1	H	126	LYS	N-CA-C	-5.37	96.52	111.00
1	E	64	CYS	N-CA-C	5.24	125.14	111.00
1	F	64	CYS	N-CA-C	5.23	125.11	111.00
1	A	58	ASN	N-CA-C	5.19	125.01	111.00
1	F	122	ALA	N-CA-C	-5.18	97.00	111.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	141	ASP	N-CA-C	-5.16	97.06	111.00
1	A	126	LYS	N-CA-C	-5.13	97.15	111.00
1	E	141	ASP	N-CA-C	-5.11	97.21	111.00
1	C	126	LYS	N-CA-C	-5.07	97.31	111.00
1	B	126	LYS	N-CA-C	-5.01	97.47	111.00

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	1153	0	1148	64	1
1	B	1133	0	1131	64	0
1	C	1119	0	1121	58	0
1	D	1119	0	1121	62	0
1	E	1119	0	1121	77	0
1	F	1119	0	1121	59	0
1	G	1119	0	1121	61	0
1	H	1119	0	1121	75	1
2	A	21	0	0	1	0
2	B	31	0	0	3	0
2	C	23	0	0	0	0
2	D	30	0	0	3	0
2	E	15	0	0	2	0
2	F	10	0	0	0	0
2	G	14	0	0	2	0
2	H	40	0	0	2	0
All	All	9184	0	9005	489	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 27.

All (489) 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:H:26:MET:CE	1:H:26:MET:SD	2.01	1.48
1:F:41:ILE:HD12	1:F:114:ILE:HD11	1.57	0.87
1:H:126:LYS:O	1:H:127:GLU:HB2	1.76	0.86
1:H:27:LEU:HA	2:H:169:HOH:O	1.75	0.85
1:H:109:ALA:HB3	1:H:111:ARG:HD2	1.58	0.83
1:B:107:ASP:OD1	1:B:111:ARG:HD3	1.77	0.83
1:A:126:LYS:O	1:A:127:GLU:HB2	1.78	0.83
1:G:41:ILE:HD12	1:G:114:ILE:HD11	1.60	0.82
1:E:102:ASN:O	1:E:103:PHE:HB2	1.77	0.82
1:F:109:ALA:HB3	1:F:111:ARG:HD2	1.60	0.82
1:B:126:LYS:O	1:B:127:GLU:HB2	1.77	0.81
1:C:117:ASN:H	1:C:117:ASN:HD22	1.29	0.81
1:D:107:ASP:OD1	1:D:111:ARG:HD3	1.81	0.81
1:D:126:LYS:O	1:D:127:GLU:HB2	1.79	0.80
1:F:102:ASN:O	1:F:103:PHE:HB2	1.83	0.79
1:C:107:ASP:OD1	1:C:111:ARG:HD3	1.82	0.79
1:H:107:ASP:OD1	1:H:111:ARG:HD3	1.82	0.79
1:F:117:ASN:HD22	1:F:117:ASN:H	1.31	0.78
1:D:117:ASN:HD22	1:D:117:ASN:H	1.31	0.78
1:D:109:ALA:HB3	1:D:111:ARG:HD2	1.64	0.78
1:E:126:LYS:O	1:E:127:GLU:HB2	1.83	0.78
1:F:126:LYS:O	1:F:127:GLU:HB2	1.82	0.78
1:E:117:ASN:H	1:E:117:ASN:HD22	1.30	0.78
1:A:109:ALA:HB3	1:A:111:ARG:HD2	1.65	0.78
1:A:117:ASN:HD22	1:A:117:ASN:H	1.31	0.78
1:B:25:HIS:N	1:B:25:HIS:ND1	2.30	0.77
1:G:102:ASN:O	1:G:103:PHE:HB2	1.83	0.77
1:C:126:LYS:O	1:C:127:GLU:HB2	1.84	0.77
1:G:64:CYS:O	1:G:65:LEU:HB2	1.83	0.77
1:H:64:CYS:O	1:H:139:ILE:O	2.02	0.76
1:G:117:ASN:HD22	1:G:117:ASN:H	1.32	0.76
1:H:117:ASN:H	1:H:117:ASN:HD22	1.32	0.76
1:C:26:MET:HG3	1:C:134:PHE:CE1	2.21	0.76
1:F:107:ASP:OD1	1:F:111:ARG:HD3	1.85	0.76
1:H:102:ASN:O	1:H:103:PHE:HB2	1.85	0.76
1:C:154:SER:OG	1:C:157:THR:OG1	2.03	0.75
1:B:64:CYS:O	1:B:139:ILE:O	2.05	0.74
1:B:64:CYS:O	1:B:65:LEU:HB2	1.87	0.74
1:E:107:ASP:OD1	1:E:111:ARG:HD3	1.88	0.74
1:B:109:ALA:HB3	1:B:111:ARG:HD2	1.70	0.74
1:E:64:CYS:O	1:E:65:LEU:HB2	1.88	0.73
1:A:41:ILE:HD12	1:A:114:ILE:HD11	1.71	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:26:MET:HG2	1:H:134:PHE:CZ	2.23	0.73
1:G:126:LYS:O	1:G:127:GLU:HB2	1.89	0.73
1:E:57:ILE:O	1:E:66:GLU:O	2.06	0.72
1:E:41:ILE:HD12	1:E:114:ILE:HD11	1.70	0.72
1:A:102:ASN:O	1:A:103:PHE:HB2	1.90	0.71
1:G:64:CYS:O	1:G:139:ILE:O	2.09	0.71
1:C:109:ALA:HB3	1:C:111:ARG:HD2	1.72	0.71
1:A:64:CYS:O	1:A:65:LEU:HB2	1.91	0.71
1:G:109:ALA:HB3	1:G:111:ARG:HD2	1.72	0.70
1:G:126:LYS:HD3	2:G:175:HOH:O	1.90	0.70
1:H:122:ALA:HB3	1:H:124:LEU:HD13	1.73	0.70
1:E:35:LEU:HD22	1:E:39:ASN:HA	1.75	0.69
1:H:57:ILE:O	1:H:66:GLU:O	2.11	0.69
1:B:35:LEU:HD11	1:B:119:ILE:HD12	1.75	0.69
1:A:64:CYS:O	1:A:139:ILE:O	2.10	0.69
1:F:64:CYS:O	1:F:65:LEU:HB2	1.93	0.68
1:E:109:ALA:HB3	1:E:111:ARG:HD2	1.76	0.68
1:C:64:CYS:O	1:C:139:ILE:O	2.13	0.68
1:D:117:ASN:ND2	1:D:117:ASN:H	1.92	0.67
1:G:107:ASP:OD1	1:G:111:ARG:HD3	1.94	0.67
1:H:121:ASP:O	1:H:123:LYS:HE3	1.94	0.67
1:D:64:CYS:O	1:D:139:ILE:O	2.13	0.67
1:E:28:LEU:HB3	1:F:101:ALA:HB3	1.77	0.67
1:E:40:ARG:HH22	1:E:111:ARG:NH2	1.93	0.66
1:A:77:PHE:HD1	1:A:98:PHE:CZ	2.14	0.66
1:B:40:ARG:NE	2:B:167:HOH:O	2.28	0.66
1:E:40:ARG:NH2	1:E:111:ARG:NH2	2.44	0.65
1:B:122:ALA:HB3	1:B:124:LEU:HD13	1.78	0.65
1:B:40:ARG:NH2	1:B:111:ARG:CZ	2.60	0.65
1:H:41:ILE:HD12	1:H:114:ILE:HD11	1.79	0.65
1:A:26:MET:HG2	1:A:134:PHE:CE1	2.32	0.65
1:B:57:ILE:O	1:B:66:GLU:O	2.15	0.65
1:H:154:SER:OG	1:H:157:THR:OG1	2.14	0.64
1:A:57:ILE:O	1:A:66:GLU:O	2.16	0.64
1:C:41:ILE:HD12	1:C:114:ILE:HD11	1.78	0.64
1:D:38:LYS:HB2	1:D:40:ARG:HD2	1.80	0.64
1:C:38:LYS:HB2	1:C:40:ARG:HD2	1.79	0.64
1:F:38:LYS:HB2	1:F:40:ARG:HD2	1.79	0.64
1:E:154:SER:OG	1:E:157:THR:OG1	2.16	0.64
1:G:38:LYS:HB2	1:G:40:ARG:HD2	1.79	0.64
1:E:64:CYS:O	1:E:139:ILE:O	2.17	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:41:ILE:HD11	1:G:128:ILE:HG13	1.80	0.63
1:A:117:ASN:ND2	1:A:117:ASN:H	1.96	0.63
1:D:57:ILE:O	1:D:66:GLU:O	2.16	0.63
1:F:64:CYS:O	1:F:139:ILE:O	2.16	0.63
1:G:84:PRO:O	1:G:85:SER:CB	2.47	0.63
1:C:40:ARG:NH2	1:C:111:ARG:NH2	2.46	0.62
1:B:40:ARG:NH2	1:B:111:ARG:NH2	2.46	0.62
1:B:117:ASN:HD22	1:B:117:ASN:H	1.47	0.62
1:G:40:ARG:NH2	1:G:111:ARG:NH2	2.47	0.62
1:D:41:ILE:HD11	1:D:128:ILE:HG13	1.81	0.62
1:A:77:PHE:CD2	1:H:134:PHE:CD2	2.87	0.62
1:C:57:ILE:O	1:C:66:GLU:O	2.17	0.62
1:B:44:PRO:O	1:B:45:ALA:HB3	1.99	0.62
1:E:59:ARG:NH2	1:E:100:ASN:ND2	2.48	0.62
1:G:38:LYS:HD2	1:G:40:ARG:NH1	2.16	0.61
1:G:33:ILE:HG13	1:G:128:ILE:HB	1.81	0.61
1:C:38:LYS:HD2	1:C:40:ARG:NH1	2.15	0.61
1:H:84:PRO:O	1:H:85:SER:HB2	2.00	0.61
1:H:26:MET:SD	1:H:134:PHE:CE1	2.94	0.61
1:H:47:LEU:HD12	2:H:170:HOH:O	2.01	0.61
1:F:109:ALA:CB	1:F:111:ARG:HD2	2.31	0.61
1:A:107:ASP:OD1	1:A:111:ARG:HD3	2.01	0.60
1:H:35:LEU:HD22	1:H:39:ASN:HA	1.84	0.60
1:G:57:ILE:O	1:G:58:ASN:O	2.20	0.60
1:F:154:SER:OG	1:F:157:THR:OG1	2.19	0.60
1:A:109:ALA:CB	1:A:111:ARG:HD2	2.32	0.60
1:C:77:PHE:HD1	1:C:98:PHE:CZ	2.20	0.60
1:H:117:ASN:H	1:H:117:ASN:ND2	1.99	0.60
1:F:57:ILE:O	1:F:58:ASN:O	2.19	0.60
1:C:35:LEU:HD22	1:C:39:ASN:HA	1.84	0.59
1:A:48:ARG:HD3	2:A:167:HOH:O	2.01	0.59
1:B:41:ILE:HD12	1:B:114:ILE:HD11	1.84	0.59
1:F:35:LEU:HD11	1:F:119:ILE:HD12	1.84	0.59
1:G:117:ASN:ND2	1:G:117:ASN:H	1.98	0.59
1:D:154:SER:OG	1:D:157:THR:OG1	2.16	0.59
1:C:122:ALA:HB3	1:C:124:LEU:HD13	1.84	0.59
1:E:84:PRO:O	1:E:85:SER:CB	2.48	0.59
1:D:102:ASN:O	1:D:103:PHE:HB2	2.02	0.59
1:F:126:LYS:O	1:F:127:GLU:CB	2.51	0.58
1:E:117:ASN:H	1:E:117:ASN:ND2	1.99	0.58
1:G:155:LEU:HG	1:H:61:PHE:CE1	2.39	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:152:SER:HA	2:B:176:HOH:O	2.03	0.58
1:F:57:ILE:O	1:F:66:GLU:O	2.20	0.58
1:A:40:ARG:NH2	1:A:111:ARG:CZ	2.67	0.58
1:E:38:LYS:HB2	1:E:40:ARG:HD2	1.84	0.58
1:C:64:CYS:O	1:C:65:LEU:HB2	2.02	0.58
1:D:84:PRO:O	1:D:85:SER:CB	2.49	0.58
1:G:40:ARG:NH2	1:G:111:ARG:CZ	2.66	0.58
1:F:121:ASP:O	1:F:123:LYS:HE3	2.03	0.58
1:B:151:ASN:O	1:B:152:SER:O	2.22	0.58
1:B:40:ARG:HH22	1:B:111:ARG:NH2	2.02	0.58
1:A:155:LEU:HG	1:B:61:PHE:CE1	2.39	0.57
1:A:126:LYS:O	1:A:127:GLU:CB	2.48	0.57
1:A:77:PHE:CD2	1:H:134:PHE:CE2	2.93	0.57
1:E:162:MET:HB3	1:F:83:PHE:CE1	2.39	0.57
1:E:33:ILE:HD13	1:E:130:LEU:HG	1.85	0.57
1:A:109:ALA:HB3	1:A:111:ARG:CD	2.34	0.57
1:C:40:ARG:HH22	1:C:111:ARG:NH2	2.01	0.57
1:E:126:LYS:O	1:E:127:GLU:CB	2.52	0.57
1:H:114:ILE:HB	1:H:119:ILE:HD11	1.87	0.57
1:D:148:TYR:CE2	1:E:95:ARG:HD3	2.40	0.57
1:F:38:LYS:HD2	1:F:40:ARG:NH1	2.20	0.57
1:A:60:GLY:H	1:A:65:LEU:H	1.53	0.57
1:E:143:LYS:HE2	1:E:147:ASP:OD1	2.05	0.57
1:B:68:ARG:HG2	1:B:136:HIS:HB3	1.86	0.57
1:E:40:ARG:NH2	1:E:111:ARG:CZ	2.68	0.57
1:C:44:PRO:O	1:C:45:ALA:HB3	2.05	0.57
1:D:64:CYS:O	1:D:65:LEU:HB2	2.05	0.56
1:E:48:ARG:NE	1:E:110:GLY:HA3	2.20	0.56
1:F:58:ASN:HA	1:F:100:ASN:O	2.05	0.56
1:H:51:PHE:CE2	1:H:137:LEU:HD22	2.40	0.56
1:A:35:LEU:HD22	1:A:39:ASN:HA	1.87	0.56
1:G:40:ARG:HH22	1:G:111:ARG:NH2	2.04	0.56
1:D:134:PHE:CD2	1:E:77:PHE:CD2	2.94	0.56
1:H:122:ALA:CB	1:H:124:LEU:HD13	2.34	0.56
1:H:77:PHE:HD1	1:H:98:PHE:CZ	2.24	0.56
1:G:35:LEU:HD22	1:G:39:ASN:HA	1.88	0.56
1:F:40:ARG:NH2	1:F:111:ARG:CZ	2.70	0.56
1:G:114:ILE:HB	1:G:119:ILE:HD11	1.88	0.55
1:E:114:ILE:HB	1:E:119:ILE:HD11	1.88	0.55
1:C:35:LEU:HD11	1:C:119:ILE:HD12	1.88	0.55
1:A:44:PRO:O	1:A:45:ALA:HB3	2.05	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:107:ASP:OD2	1:A:107:ASP:C	2.43	0.55
1:E:65:LEU:HD13	1:E:122:ALA:HB2	1.88	0.55
1:H:84:PRO:O	1:H:85:SER:CB	2.54	0.55
1:C:117:ASN:ND2	1:C:117:ASN:H	2.02	0.55
1:G:57:ILE:O	1:G:66:GLU:O	2.24	0.55
1:B:141:ASP:OD2	1:B:144:LEU:HD13	2.06	0.55
1:G:126:LYS:O	1:G:127:GLU:CB	2.55	0.55
1:H:38:LYS:HB2	1:H:40:ARG:HD2	1.88	0.55
1:A:35:LEU:CD2	1:A:39:ASN:HA	2.37	0.54
1:H:50:PHE:O	1:H:69:LYS:HD3	2.08	0.54
1:H:44:PRO:O	1:H:46:LYS:N	2.36	0.54
1:H:51:PHE:CZ	1:H:137:LEU:HD22	2.42	0.54
1:G:71:GLN:O	1:G:74:GLN:HB3	2.07	0.54
1:F:41:ILE:HD11	1:F:128:ILE:HG13	1.90	0.54
1:F:84:PRO:O	1:F:85:SER:CB	2.55	0.54
1:H:109:ALA:CB	1:H:111:ARG:HD2	2.33	0.54
1:A:57:ILE:O	1:A:58:ASN:O	2.26	0.54
1:D:41:ILE:HD12	1:D:114:ILE:HD11	1.89	0.54
1:B:126:LYS:O	1:B:127:GLU:CB	2.51	0.54
1:B:122:ALA:CB	1:B:124:LEU:HD13	2.36	0.54
1:B:142:LYS:O	1:B:146:GLU:HG3	2.07	0.54
1:G:121:ASP:O	1:G:123:LYS:HE3	2.07	0.54
1:E:51:PHE:CE2	1:E:137:LEU:HD22	2.43	0.54
1:E:27:LEU:HD21	1:E:50:PHE:CG	2.43	0.53
1:A:77:PHE:O	1:A:80:PHE:HB2	2.08	0.53
1:F:60:GLY:H	1:F:65:LEU:H	1.55	0.53
1:A:40:ARG:HH22	1:A:111:ARG:NH2	2.05	0.53
1:A:141:ASP:OD2	1:A:144:LEU:HD13	2.09	0.53
1:C:40:ARG:NH2	1:C:111:ARG:CZ	2.71	0.53
1:A:38:LYS:HB2	1:A:40:ARG:HD2	1.91	0.53
1:B:117:ASN:ND2	1:B:117:ASN:H	2.06	0.53
1:B:41:ILE:HD11	1:B:128:ILE:HG13	1.91	0.53
1:E:44:PRO:O	1:E:46:LYS:N	2.40	0.53
1:E:41:ILE:HD11	1:E:128:ILE:HG13	1.91	0.53
1:F:114:ILE:HB	1:F:119:ILE:HD11	1.91	0.53
1:H:27:LEU:HD11	1:H:50:PHE:CE2	2.44	0.52
1:D:122:ALA:HB3	1:D:124:LEU:HD13	1.90	0.52
1:D:126:LYS:O	1:D:127:GLU:CB	2.51	0.52
1:A:35:LEU:HD11	1:A:119:ILE:HD12	1.91	0.52
1:F:117:ASN:N	1:F:117:ASN:HD22	2.04	0.52
1:D:114:ILE:HB	1:D:119:ILE:HD11	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:51:PHE:CZ	1:E:137:LEU:HD22	2.45	0.52
1:G:60:GLY:H	1:G:65:LEU:H	1.57	0.52
1:A:107:ASP:OD2	1:A:109:ALA:N	2.43	0.52
1:D:107:ASP:C	1:D:107:ASP:OD2	2.49	0.52
1:B:84:PRO:O	1:B:85:SER:CB	2.58	0.52
1:G:154:SER:OG	1:G:157:THR:OG1	2.27	0.52
1:A:84:PRO:O	1:A:85:SER:CB	2.58	0.52
1:D:40:ARG:NH2	1:D:111:ARG:CZ	2.74	0.51
1:A:58:ASN:HA	1:A:100:ASN:O	2.10	0.51
1:G:109:ALA:CB	1:G:111:ARG:HD2	2.38	0.51
1:F:40:ARG:NH2	1:F:111:ARG:NH2	2.58	0.51
1:A:40:ARG:NH2	1:A:111:ARG:NH2	2.58	0.51
1:D:57:ILE:O	1:D:58:ASN:O	2.28	0.51
1:F:117:ASN:ND2	1:F:117:ASN:H	2.01	0.51
1:G:77:PHE:HD1	1:G:98:PHE:CZ	2.28	0.51
1:F:77:PHE:HD1	1:F:98:PHE:CZ	2.29	0.51
1:B:162:MET:HB3	1:C:83:PHE:CE1	2.44	0.51
1:F:128:ILE:HG22	1:F:129:VAL:N	2.25	0.51
1:F:77:PHE:O	1:F:80:PHE:HB2	2.11	0.51
1:B:24:GLY:N	1:B:25:HIS:ND1	2.59	0.51
1:G:64:CYS:O	1:G:65:LEU:CB	2.55	0.51
1:E:107:ASP:OD2	1:E:107:ASP:C	2.48	0.51
1:H:44:PRO:HG2	1:H:47:LEU:HD22	1.92	0.51
1:D:155:LEU:HD12	1:E:93:LEU:HD12	1.93	0.51
1:C:128:ILE:HG21	1:C:139:ILE:HG23	1.93	0.51
1:B:102:ASN:O	1:B:103:PHE:O	2.28	0.51
1:A:117:ASN:N	1:A:117:ASN:ND2	2.59	0.50
1:E:77:PHE:HD1	1:E:98:PHE:CZ	2.29	0.50
1:C:126:LYS:O	1:C:127:GLU:CB	2.56	0.50
1:C:68:ARG:HG2	1:C:136:HIS:HB3	1.93	0.50
1:H:126:LYS:O	1:H:127:GLU:CB	2.50	0.50
1:H:35:LEU:HD11	1:H:119:ILE:HD12	1.92	0.50
1:H:64:CYS:O	1:H:65:LEU:HB2	2.11	0.50
1:E:122:ALA:O	1:E:124:LEU:N	2.42	0.50
1:F:109:ALA:HB3	1:F:111:ARG:CD	2.39	0.50
1:G:128:ILE:HG22	1:G:129:VAL:N	2.27	0.50
1:B:40:ARG:HH22	1:B:111:ARG:HH22	1.59	0.50
1:C:102:ASN:O	1:C:103:PHE:O	2.29	0.50
1:E:35:LEU:CD2	1:E:39:ASN:HA	2.41	0.50
1:F:117:ASN:ND2	1:F:117:ASN:N	2.59	0.49
1:F:40:ARG:HH22	1:F:111:ARG:NH2	2.10	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:142:LYS:O	1:H:146:GLU:HG3	2.12	0.49
1:C:133:GLN:O	1:C:135:ASP:N	2.43	0.49
1:B:50:PHE:CE2	1:B:69:LYS:HG3	2.47	0.49
1:A:77:PHE:CE1	1:H:134:PHE:HB3	2.47	0.49
1:G:84:PRO:O	1:G:85:SER:HB2	2.13	0.49
1:H:68:ARG:HG2	1:H:136:HIS:HB3	1.94	0.49
1:E:117:ASN:ND2	1:E:117:ASN:N	2.59	0.49
1:C:57:ILE:HG23	1:C:58:ASN:N	2.27	0.49
1:E:128:ILE:CG2	1:E:139:ILE:HG23	2.43	0.49
1:E:35:LEU:HD11	1:E:119:ILE:HD12	1.94	0.49
1:E:33:ILE:HG13	1:E:128:ILE:HB	1.94	0.49
1:G:109:ALA:HB3	1:G:111:ARG:CD	2.40	0.49
1:C:35:LEU:CD2	1:C:39:ASN:HA	2.43	0.49
1:C:117:ASN:ND2	1:C:117:ASN:N	2.60	0.49
1:E:80:PHE:O	1:E:83:PHE:N	2.44	0.49
1:D:141:ASP:OD2	1:D:144:LEU:HD13	2.13	0.49
1:F:35:LEU:HD22	1:F:39:ASN:HA	1.93	0.49
1:C:117:ASN:HD22	1:C:117:ASN:N	2.02	0.49
1:C:122:ALA:CB	1:C:124:LEU:HD13	2.42	0.49
1:A:119:ILE:O	1:A:122:ALA:O	2.31	0.49
1:A:50:PHE:O	1:A:69:LYS:HD3	2.12	0.49
1:A:61:PHE:CE1	1:H:155:LEU:HG	2.48	0.49
1:B:60:GLY:H	1:B:65:LEU:H	1.60	0.48
1:B:77:PHE:CZ	1:B:81:ASN:OD1	2.66	0.48
1:D:38:LYS:HD2	1:D:40:ARG:NH1	2.29	0.48
1:D:96:LEU:O	1:D:100:ASN:ND2	2.46	0.48
1:D:155:LEU:HG	1:E:61:PHE:CE1	2.48	0.48
1:G:96:LEU:O	1:G:100:ASN:ND2	2.46	0.48
1:G:48:ARG:NE	1:G:110:GLY:HA3	2.29	0.48
1:E:27:LEU:HD11	1:E:50:PHE:CE2	2.48	0.48
1:A:162:MET:HB3	1:B:83:PHE:CE1	2.48	0.48
1:E:60:GLY:H	1:E:65:LEU:H	1.61	0.48
1:H:57:ILE:O	1:H:58:ASN:O	2.32	0.48
1:D:50:PHE:CE2	1:D:69:LYS:HG3	2.48	0.48
1:H:151:ASN:O	1:H:152:SER:O	2.31	0.48
1:D:35:LEU:HD11	1:D:119:ILE:HD12	1.96	0.48
1:F:33:ILE:HG13	1:F:128:ILE:HB	1.96	0.47
1:E:26:MET:N	2:E:167:HOH:O	2.47	0.47
1:C:128:ILE:CG2	1:C:139:ILE:HG23	2.44	0.47
1:C:128:ILE:HG22	1:C:129:VAL:N	2.28	0.47
1:C:36:ASP:OD2	1:C:36:ASP:C	2.53	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:64:CYS:O	1:E:65:LEU:CB	2.56	0.47
1:B:134:PHE:CD2	1:C:77:PHE:CD2	3.02	0.47
1:D:44:PRO:O	1:D:46:LYS:N	2.45	0.47
1:H:141:ASP:HB3	1:H:144:LEU:HB2	1.95	0.47
1:B:46:LYS:HG3	2:B:180:HOH:O	2.13	0.47
1:D:149:LEU:HA	1:D:149:LEU:HD12	1.69	0.47
1:C:77:PHE:O	1:C:80:PHE:HB2	2.15	0.47
1:A:67:VAL:HB	1:A:137:LEU:HB3	1.96	0.47
1:A:143:LYS:HE2	1:A:147:ASP:OD1	2.14	0.47
1:B:35:LEU:HD22	1:B:39:ASN:HA	1.96	0.47
1:C:41:ILE:HD11	1:C:128:ILE:HG13	1.96	0.47
1:G:80:PHE:O	1:G:83:PHE:N	2.43	0.47
1:F:68:ARG:HG2	1:F:136:HIS:HB3	1.95	0.47
1:A:55:ILE:HD12	1:A:55:ILE:C	2.35	0.47
1:H:26:MET:SD	1:H:134:PHE:CZ	3.08	0.47
1:G:65:LEU:HD13	1:G:122:ALA:HB2	1.95	0.47
1:E:28:LEU:HD13	1:F:101:ALA:HB1	1.97	0.47
1:D:162:MET:HB3	1:E:83:PHE:CE1	2.50	0.47
1:B:77:PHE:O	1:B:80:PHE:HB2	2.15	0.47
1:C:134:PHE:CD2	1:D:77:PHE:CD2	3.02	0.47
1:G:77:PHE:O	1:G:80:PHE:HB2	2.15	0.47
1:A:91:ARG:HD3	1:H:61:PHE:CD2	2.50	0.47
1:B:109:ALA:CB	1:B:111:ARG:HD2	2.44	0.46
1:A:77:PHE:CE2	1:H:134:PHE:CD2	3.03	0.46
1:D:77:PHE:HD1	1:D:98:PHE:CZ	2.34	0.46
1:C:119:ILE:O	1:C:122:ALA:O	2.33	0.46
1:G:141:ASP:OD2	1:G:144:LEU:HD13	2.15	0.46
1:E:134:PHE:CD2	1:F:77:PHE:CD2	3.04	0.46
1:E:57:ILE:O	1:E:58:ASN:O	2.33	0.46
1:H:80:PHE:O	1:H:83:PHE:N	2.42	0.46
1:A:128:ILE:HG22	1:A:129:VAL:N	2.30	0.46
1:E:59:ARG:NH2	1:E:100:ASN:HD21	2.13	0.46
1:H:52:GLU:HG3	1:H:52:GLU:H	1.50	0.46
1:C:57:ILE:HG23	1:C:58:ASN:H	1.81	0.46
1:B:40:ARG:NH2	1:B:111:ARG:NH1	2.64	0.46
1:B:38:LYS:HD2	1:B:40:ARG:NH1	2.31	0.46
1:G:38:LYS:HD2	1:G:40:ARG:HH11	1.80	0.46
1:G:44:PRO:O	1:G:46:LYS:N	2.47	0.46
1:E:26:MET:HB3	1:E:134:PHE:CE1	2.51	0.46
1:B:50:PHE:O	1:B:69:LYS:HD3	2.16	0.46
1:E:68:ARG:HG2	1:E:136:HIS:HB3	1.96	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:58:ASN:ND2	2:D:169:HOH:O	2.49	0.46
1:C:80:PHE:O	1:C:83:PHE:N	2.45	0.46
1:G:143:LYS:HE2	1:G:147:ASP:OD1	2.16	0.46
1:C:96:LEU:O	1:C:100:ASN:ND2	2.47	0.45
1:D:61:PHE:O	1:D:62:GLU:HB2	2.15	0.45
1:H:26:MET:CG	1:H:134:PHE:CZ	2.97	0.45
1:A:41:ILE:HD12	1:A:114:ILE:CD1	2.45	0.45
1:A:64:CYS:O	1:A:65:LEU:CB	2.57	0.45
1:H:107:ASP:C	1:H:107:ASP:OD2	2.55	0.45
1:E:109:ALA:CB	1:E:111:ARG:HD2	2.45	0.45
1:H:41:ILE:HD11	1:H:128:ILE:HG21	1.99	0.45
1:D:68:ARG:HG2	1:D:136:HIS:HB3	1.99	0.45
1:F:119:ILE:O	1:F:122:ALA:O	2.35	0.45
1:G:107:ASP:OD2	1:G:107:ASP:C	2.54	0.45
1:D:119:ILE:O	1:D:122:ALA:O	2.34	0.45
1:E:77:PHE:O	1:E:80:PHE:HB2	2.16	0.45
1:A:101:ALA:HB3	1:H:28:LEU:HB3	1.98	0.45
1:E:149:LEU:O	1:E:151:ASN:O	2.34	0.45
1:H:130:LEU:CD2	1:H:139:ILE:HG12	2.46	0.45
1:A:159:ALA:HB1	1:C:86:THR:HB	1.98	0.45
1:D:77:PHE:O	1:D:80:PHE:HB2	2.16	0.45
1:H:44:PRO:CG	1:H:47:LEU:HD22	2.47	0.45
1:A:122:ALA:HB3	1:A:124:LEU:HD13	1.98	0.45
1:E:43:LEU:HA	1:E:44:PRO:HD3	1.81	0.45
1:F:44:PRO:O	1:F:45:ALA:HB3	2.17	0.45
1:D:122:ALA:CB	1:D:124:LEU:HD13	2.47	0.45
1:F:41:ILE:HD12	1:F:114:ILE:CD1	2.40	0.44
1:H:128:ILE:HG22	1:H:129:VAL:N	2.32	0.44
1:H:80:PHE:O	1:H:82:SER:N	2.50	0.44
1:G:68:ARG:HG2	1:G:136:HIS:HB3	1.99	0.44
1:B:57:ILE:O	1:B:58:ASN:O	2.35	0.44
1:E:121:ASP:O	1:E:123:LYS:HE3	2.18	0.44
1:H:71:GLN:O	1:H:74:GLN:HB3	2.18	0.44
1:E:26:MET:HB3	1:E:134:PHE:CZ	2.52	0.44
1:C:102:ASN:O	1:C:103:PHE:HB2	2.17	0.44
1:A:38:LYS:HB2	1:A:40:ARG:CD	2.47	0.44
1:A:41:ILE:HD11	1:A:128:ILE:HG13	1.98	0.44
1:H:55:ILE:C	1:H:55:ILE:HD12	2.38	0.44
1:B:38:LYS:O	1:B:39:ASN:HB2	2.16	0.44
1:E:26:MET:N	2:E:178:HOH:O	2.51	0.44
1:D:39:ASN:HD22	1:D:39:ASN:HA	1.50	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:80:PHE:HE1	1:B:93:LEU:HD21	1.83	0.44
1:E:36:ASP:C	1:E:36:ASP:OD2	2.56	0.44
1:G:35:LEU:CD2	1:G:39:ASN:HA	2.48	0.44
1:F:36:ASP:OD2	1:F:36:ASP:C	2.56	0.44
1:F:51:PHE:CE2	1:F:137:LEU:HD22	2.53	0.44
1:D:55:ILE:C	1:D:55:ILE:HD12	2.38	0.44
1:A:23:GLN:OE1	1:A:23:GLN:N	2.51	0.44
1:H:109:ALA:HB3	1:H:111:ARG:CD	2.40	0.43
1:C:109:ALA:CB	1:C:111:ARG:HD2	2.44	0.43
1:B:124:LEU:HG	1:B:128:ILE:CD1	2.48	0.43
1:E:80:PHE:O	1:E:82:SER:N	2.51	0.43
1:D:151:ASN:O	1:D:152:SER:O	2.36	0.43
1:C:84:PRO:O	1:C:85:SER:CB	2.65	0.43
1:G:122:ALA:O	1:G:124:LEU:N	2.45	0.43
1:B:128:ILE:HG22	1:B:129:VAL:N	2.33	0.43
1:H:44:PRO:O	1:H:45:ALA:HB3	2.18	0.43
1:A:83:PHE:CE1	1:H:162:MET:HB3	2.53	0.43
1:G:128:ILE:CG2	1:G:139:ILE:HG23	2.48	0.43
1:H:117:ASN:N	1:H:117:ASN:ND2	2.65	0.43
1:D:80:PHE:O	1:D:83:PHE:N	2.50	0.43
1:E:124:LEU:HG	1:E:128:ILE:HD12	1.99	0.43
1:C:65:LEU:HD13	1:C:122:ALA:HB2	2.00	0.43
1:B:84:PRO:O	1:B:85:SER:HB2	2.16	0.43
1:F:158:VAL:HG21	1:G:92:THR:HG21	1.99	0.43
1:C:121:ASP:O	1:C:123:LYS:HE3	2.18	0.43
1:B:154:SER:OG	1:B:157:THR:OG1	2.26	0.43
1:F:107:ASP:OD2	1:F:107:ASP:C	2.57	0.43
1:D:117:ASN:N	1:D:117:ASN:ND2	2.60	0.43
1:B:44:PRO:O	1:B:45:ALA:CB	2.64	0.43
1:H:77:PHE:CZ	1:H:81:ASN:OD1	2.71	0.43
1:H:80:PHE:C	1:H:82:SER:H	2.21	0.43
1:G:149:LEU:HA	1:G:149:LEU:HD12	1.79	0.43
1:A:133:GLN:O	1:A:135:ASP:N	2.48	0.43
1:G:43:LEU:O	1:G:45:ALA:N	2.46	0.43
1:B:155:LEU:HG	1:C:61:PHE:CE1	2.54	0.43
1:A:121:ASP:O	1:A:123:LYS:HE3	2.19	0.43
1:F:35:LEU:CD2	1:F:39:ASN:HA	2.48	0.43
1:F:80:PHE:O	1:F:83:PHE:HB2	2.19	0.43
1:C:162:MET:HG3	1:D:93:LEU:HD22	2.01	0.43
1:B:40:ARG:HA	1:B:112:VAL:O	2.19	0.43
1:F:128:ILE:CG2	1:F:129:VAL:N	2.81	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:117:ASN:ND2	2:D:192:HOH:O	2.47	0.43
1:G:44:PRO:O	1:G:45:ALA:HB3	2.18	0.43
1:D:33:ILE:HG13	1:D:128:ILE:HB	2.01	0.43
1:D:60:GLY:H	1:D:65:LEU:H	1.67	0.42
1:F:67:VAL:HB	1:F:137:LEU:HB3	2.00	0.42
1:F:143:LYS:HE2	1:F:147:ASP:OD1	2.19	0.42
1:A:31:PHE:N	1:A:31:PHE:CD2	2.87	0.42
1:E:26:MET:HG3	1:F:103:PHE:CE2	2.54	0.42
1:E:124:LEU:HG	1:E:128:ILE:CD1	2.49	0.42
1:H:80:PHE:C	1:H:82:SER:N	2.71	0.42
1:G:117:ASN:ND2	1:G:117:ASN:N	2.62	0.42
1:B:80:PHE:O	1:B:83:PHE:N	2.48	0.42
1:B:92:THR:O	1:B:96:LEU:HG	2.20	0.42
1:G:102:ASN:O	1:G:103:PHE:CB	2.56	0.42
1:E:109:ALA:HB3	1:E:111:ARG:CD	2.47	0.42
1:H:131:ILE:HG13	1:H:131:ILE:O	2.20	0.42
1:A:142:LYS:O	1:A:146:GLU:HG3	2.19	0.42
1:C:36:ASP:OD1	1:C:40:ARG:HD3	2.20	0.42
1:E:38:LYS:HB2	1:E:40:ARG:CD	2.47	0.42
1:H:119:ILE:O	1:H:122:ALA:O	2.38	0.42
1:D:48:ARG:HD3	2:D:195:HOH:O	2.19	0.42
1:F:149:LEU:HA	1:F:149:LEU:HD12	1.79	0.42
1:A:151:ASN:O	1:A:152:SER:O	2.38	0.42
1:E:26:MET:CB	1:E:134:PHE:CE1	3.02	0.42
1:C:26:MET:HE2	1:C:134:PHE:CE1	2.54	0.42
1:D:80:PHE:O	1:D:83:PHE:HB2	2.20	0.42
1:B:80:PHE:O	1:B:83:PHE:HB2	2.20	0.42
1:D:44:PRO:O	1:D:45:ALA:HB3	2.20	0.42
1:F:65:LEU:HD13	1:F:122:ALA:HB2	2.01	0.42
1:C:107:ASP:OD2	1:C:107:ASP:C	2.58	0.42
1:G:36:ASP:OD1	1:G:40:ARG:HD3	2.20	0.42
1:E:80:PHE:C	1:E:82:SER:N	2.72	0.42
1:H:108:THR:C	1:H:110:GLY:H	2.23	0.42
1:D:126:LYS:HB2	1:D:126:LYS:HE3	1.92	0.41
1:G:162:MET:HB3	1:H:83:PHE:CE1	2.55	0.41
1:G:50:PHE:O	1:G:69:LYS:HD3	2.19	0.41
1:B:35:LEU:CD2	1:B:39:ASN:HA	2.50	0.41
1:D:84:PRO:O	1:D:85:SER:HB2	2.19	0.41
1:G:77:PHE:CZ	1:G:81:ASN:OD1	2.73	0.41
1:D:41:ILE:HD11	1:D:128:ILE:HG21	2.03	0.41
1:B:43:LEU:HA	1:B:44:PRO:HD3	1.88	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:27:LEU:HD13	1:E:137:LEU:HD13	2.01	0.41
1:F:38:LYS:HB2	1:F:40:ARG:CD	2.47	0.41
1:B:117:ASN:ND2	1:B:117:ASN:N	2.68	0.41
1:D:122:ALA:O	1:D:124:LEU:N	2.51	0.41
1:D:36:ASP:OD1	1:D:40:ARG:HD3	2.21	0.41
1:C:38:LYS:HD2	1:C:40:ARG:HH11	1.86	0.41
1:E:119:ILE:O	1:E:122:ALA:O	2.38	0.41
1:C:44:PRO:O	1:C:46:LYS:N	2.49	0.41
1:D:155:LEU:CD1	1:E:93:LEU:HD12	2.50	0.41
1:B:102:ASN:O	1:B:103:PHE:C	2.59	0.41
1:E:84:PRO:O	1:E:85:SER:HB3	2.20	0.41
1:B:122:ALA:O	1:B:124:LEU:N	2.52	0.41
1:D:35:LEU:HD22	1:D:39:ASN:HA	2.03	0.41
1:E:50:PHE:CE2	1:E:69:LYS:HG3	2.55	0.41
1:G:131:ILE:O	1:G:131:ILE:HG13	2.21	0.41
1:A:154:SER:OG	1:A:157:THR:OG1	2.34	0.41
1:C:57:ILE:O	1:C:58:ASN:O	2.39	0.41
1:F:71:GLN:O	1:F:74:GLN:HB3	2.21	0.41
1:A:36:ASP:C	1:A:36:ASP:OD2	2.59	0.41
1:G:26:MET:N	2:G:170:HOH:O	2.54	0.41
1:F:102:ASN:O	1:F:103:PHE:CB	2.56	0.40
1:B:64:CYS:O	1:B:65:LEU:CB	2.58	0.40
1:D:35:LEU:HA	1:D:35:LEU:HD23	1.91	0.40
1:H:57:ILE:HG23	1:H:58:ASN:N	2.36	0.40
1:A:54:SER:HB3	1:A:105:ASP:OD1	2.21	0.40
1:F:124:LEU:HG	1:F:128:ILE:HD11	2.03	0.40
1:F:57:ILE:HG23	1:F:118:LEU:CD2	2.51	0.40
1:H:36:ASP:OD2	1:H:36:ASP:C	2.60	0.40
1:G:51:PHE:CE2	1:G:137:LEU:HD22	2.56	0.40
1:C:80:PHE:O	1:C:82:SER:N	2.55	0.40
1:B:77:PHE:HD1	1:B:98:PHE:CZ	2.39	0.40
1:B:149:LEU:HD12	1:B:149:LEU:HA	1.79	0.40
1:H:61:PHE:O	1:H:62:GLU:HB2	2.20	0.40
1:D:162:MET:HG3	1:E:93:LEU:HD22	2.04	0.40
1:H:77:PHE:O	1:H:80:PHE:HB2	2.21	0.40
1:H:36:ASP:OD1	1:H:40:ARG:HD3	2.22	0.40
1:D:43:LEU:HA	1:D:44:PRO:HD3	1.90	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:48:ARG:NH2	1:H:153:GLU:OE2[4_456]	2.19	0.01

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	139/166 (84%)	118 (85%)	13 (9%)	8 (6%)	2	5
1	B	137/166 (82%)	116 (85%)	12 (9%)	9 (7%)	1	4
1	C	135/166 (81%)	112 (83%)	14 (10%)	9 (7%)	1	4
1	D	135/166 (81%)	115 (85%)	12 (9%)	8 (6%)	2	5
1	E	135/166 (81%)	114 (84%)	13 (10%)	8 (6%)	2	5
1	F	135/166 (81%)	111 (82%)	16 (12%)	8 (6%)	2	5
1	G	135/166 (81%)	110 (82%)	17 (13%)	8 (6%)	2	5
1	H	135/166 (81%)	111 (82%)	15 (11%)	9 (7%)	1	4
All	All	1086/1328 (82%)	907 (84%)	112 (10%)	67 (6%)	2	5

All (67) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	44	PRO
1	A	58	ASN
1	A	127	GLU
1	B	58	ASN
1	B	152	SER
1	C	44	PRO
1	C	58	ASN
1	D	58	ASN
1	E	44	PRO
1	E	58	ASN
1	E	127	GLU
1	F	44	PRO

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Mol	Chain	Res	Type
1	F	58	ASN
1	F	127	GLU
1	G	44	PRO
1	G	58	ASN
1	H	44	PRO
1	H	52	GLU
1	H	58	ASN
1	H	84	PRO
1	H	152	SER
1	A	152	SER
1	B	44	PRO
1	B	103	PHE
1	B	127	GLU
1	C	127	GLU
1	D	44	PRO
1	D	127	GLU
1	D	152	SER
1	E	52	GLU
1	E	152	SER
1	F	52	GLU
1	F	84	PRO
1	F	152	SER
1	G	52	GLU
1	G	127	GLU
1	G	152	SER
1	H	127	GLU
1	A	84	PRO
1	B	52	GLU
1	B	84	PRO
1	C	52	GLU
1	C	65	LEU
1	C	103	PHE
1	C	152	SER
1	D	52	GLU
1	D	65	LEU
1	D	84	PRO
1	E	84	PRO
1	G	84	PRO
1	H	65	LEU
1	C	81	ASN
1	C	84	PRO
1	E	81	ASN

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Mol	Chain	Res	Type
1	F	65	LEU
1	A	85	SER
1	B	85	SER
1	D	103	PHE
1	E	65	LEU
1	F	85	SER
1	G	65	LEU
1	G	81	ASN
1	H	81	ASN
1	A	52	GLU
1	A	65	LEU
1	B	65	LEU
1	H	85	SER

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	126/150 (84%)	115 (91%)	11 (9%)	13	35
1	B	124/150 (83%)	111 (90%)	13 (10%)	8	24
1	C	123/150 (82%)	113 (92%)	10 (8%)	15	39
1	D	123/150 (82%)	111 (90%)	12 (10%)	10	28
1	E	123/150 (82%)	110 (89%)	13 (11%)	8	24
1	F	123/150 (82%)	113 (92%)	10 (8%)	15	39
1	G	123/150 (82%)	112 (91%)	11 (9%)	12	34
1	H	123/150 (82%)	111 (90%)	12 (10%)	10	28
All	All	988/1200 (82%)	896 (91%)	92 (9%)	11	32

All (92) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	22	PHE
1	A	35	LEU

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Mol	Chain	Res	Type
1	A	41	ILE
1	A	59	ARG
1	A	71	GLN
1	A	81	ASN
1	A	84	PRO
1	A	113	LEU
1	A	117	ASN
1	A	118	LEU
1	A	149	LEU
1	B	25	HIS
1	B	26	MET
1	B	35	LEU
1	B	41	ILE
1	B	47	LEU
1	B	59	ARG
1	B	81	ASN
1	B	84	PRO
1	B	85	SER
1	B	113	LEU
1	B	117	ASN
1	B	118	LEU
1	B	149	LEU
1	C	35	LEU
1	C	41	ILE
1	C	47	LEU
1	C	59	ARG
1	C	84	PRO
1	C	85	SER
1	C	113	LEU
1	C	117	ASN
1	C	118	LEU
1	C	149	LEU
1	D	35	LEU
1	D	41	ILE
1	D	47	LEU
1	D	59	ARG
1	D	81	ASN
1	D	84	PRO
1	D	85	SER
1	D	111	ARG
1	D	113	LEU
1	D	117	ASN

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Mol	Chain	Res	Type
1	D	118	LEU
1	D	149	LEU
1	E	35	LEU
1	E	41	ILE
1	E	47	LEU
1	E	59	ARG
1	E	71	GLN
1	E	81	ASN
1	E	84	PRO
1	E	113	LEU
1	E	115	PRO
1	E	117	ASN
1	E	118	LEU
1	E	137	LEU
1	E	149	LEU
1	F	35	LEU
1	F	41	ILE
1	F	44	PRO
1	F	59	ARG
1	F	81	ASN
1	F	84	PRO
1	F	113	LEU
1	F	117	ASN
1	F	118	LEU
1	F	149	LEU
1	G	26	MET
1	G	35	LEU
1	G	41	ILE
1	G	59	ARG
1	G	81	ASN
1	G	84	PRO
1	G	85	SER
1	G	113	LEU
1	G	117	ASN
1	G	118	LEU
1	G	149	LEU
1	H	35	LEU
1	H	41	ILE
1	H	58	ASN
1	H	59	ARG
1	H	64	CYS
1	H	81	ASN

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Mol	Chain	Res	Type
1	H	84	PRO
1	H	85	SER
1	H	113	LEU
1	H	117	ASN
1	H	118	LEU
1	H	149	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (25) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	39	ASN
1	A	117	ASN
1	A	151	ASN
1	B	39	ASN
1	B	117	ASN
1	C	39	ASN
1	C	58	ASN
1	C	117	ASN
1	C	133	GLN
1	D	39	ASN
1	D	58	ASN
1	D	117	ASN
1	E	39	ASN
1	E	100	ASN
1	E	117	ASN
1	E	133	GLN
1	F	39	ASN
1	F	100	ASN
1	F	117	ASN
1	G	39	ASN
1	G	117	ASN
1	G	151	ASN
1	H	39	ASN
1	H	58	ASN
1	H	117	ASN

5.3.3 RNA ⓘ

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 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 ⓘ

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	141/166 (84%)	-0.13	4 (2%) 56 44	26, 46, 71, 95	0
1	B	139/166 (83%)	-0.41	1 (0%) 89 84	19, 36, 59, 80	0
1	C	137/166 (82%)	-0.31	2 (1%) 76 68	23, 42, 70, 80	0
1	D	137/166 (82%)	-0.35	2 (1%) 76 68	24, 39, 66, 83	0
1	E	137/166 (82%)	0.22	8 (5%) 26 16	26, 53, 84, 102	0
1	F	137/166 (82%)	0.00	2 (1%) 76 68	31, 57, 76, 85	0
1	G	137/166 (82%)	0.14	6 (4%) 38 26	31, 58, 80, 91	0
1	H	137/166 (82%)	-0.22	6 (4%) 38 26	20, 38, 74, 91	0
All	All	1102/1328 (82%)	-0.13	31 (2%) 56 44	19, 46, 77, 102	0

All (31) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	50	PHE	6.1
1	G	108	THR	5.1
1	H	50	PHE	4.8
1	E	48	ARG	4.6
1	A	82	SER	4.6
1	E	109	ALA	4.0
1	G	82	SER	4.0
1	G	109	ALA	3.9
1	E	45	ALA	3.7
1	D	79	GLN	3.7
1	E	81	ASN	3.5
1	G	81	ASN	3.1
1	A	79	GLN	3.1
1	F	37	ALA	3.0
1	E	108	THR	3.0
1	E	37	ALA	2.9

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Mol	Chain	Res	Type	RSRZ
1	H	47	LEU	2.8
1	H	108	THR	2.7
1	G	37	ALA	2.7
1	C	81	ASN	2.5
1	H	51	PHE	2.5
1	C	79	GLN	2.5
1	A	151	ASN	2.4
1	B	81	ASN	2.4
1	F	79	GLN	2.4
1	E	38	LYS	2.3
1	D	82	SER	2.2
1	A	77	PHE	2.2
1	G	105	ASP	2.1
1	H	45	ALA	2.1
1	H	82	SER	2.1

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

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

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.