



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 02:20 AM UTC

PDB ID : 3M2L / pdb_00003m2l
Title : Crystal structure of the M113F mutant of alpha-hemolysin
Authors : Montoya, M.; Gouaux, E.
Deposited on : 2010-03-07
Resolution : 2.10 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

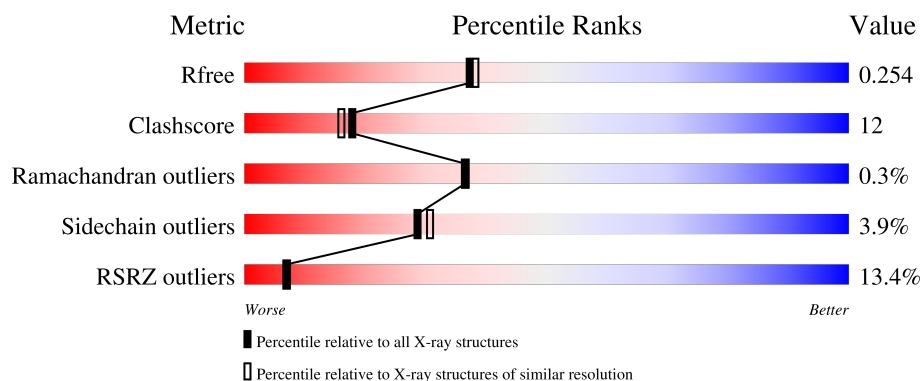
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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}	180053	6658 (2.10-2.10)
Clashscore	190562	7164 (2.10-2.10)
Ramachandran outliers	187476	7099 (2.10-2.10)
Sidechain outliers	187428	7100 (2.10-2.10)
RSRZ outliers	180081	6662 (2.10-2.10)

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	294	17% 76% 21% .
1	B	294	15% 70% 27% .
1	C	294	14% 78% 19% .
1	D	294	11% 69% 28% .
1	E	294	13% 77% 21% .

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Mol	Chain	Length	Quality of chain
1	F	294	13% 73% 24%
1	G	294	10% 76% 21%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 16733 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 Alpha-hemolysin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	293	Total	C	N	O	S	41	0	0
			2343	1472	400	465	6			
1	B	293	Total	C	N	O	S	45	0	0
			2348	1476	401	465	6			
1	C	293	Total	C	N	O	S	59	0	0
			2348	1476	401	465	6			
1	D	293	Total	C	N	O	S	66	0	0
			2348	1476	401	465	6			
1	E	293	Total	C	N	O	S	49	0	0
			2348	1476	401	465	6			
1	F	293	Total	C	N	O	S	62	0	0
			2348	1476	401	465	6			
1	G	293	Total	C	N	O	S	52	0	0
			2348	1476	401	465	6			

There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	MET	-	initiating methionine	UNP P09616
A	113	PHE	MET	engineered mutation	UNP P09616
B	0	MET	-	initiating methionine	UNP P09616
B	113	PHE	MET	engineered mutation	UNP P09616
C	0	MET	-	initiating methionine	UNP P09616
C	113	PHE	MET	engineered mutation	UNP P09616
D	0	MET	-	initiating methionine	UNP P09616
D	113	PHE	MET	engineered mutation	UNP P09616
E	0	MET	-	initiating methionine	UNP P09616
E	113	PHE	MET	engineered mutation	UNP P09616
F	0	MET	-	initiating methionine	UNP P09616
F	113	PHE	MET	engineered mutation	UNP P09616
G	0	MET	-	initiating methionine	UNP P09616
G	113	PHE	MET	engineered mutation	UNP P09616

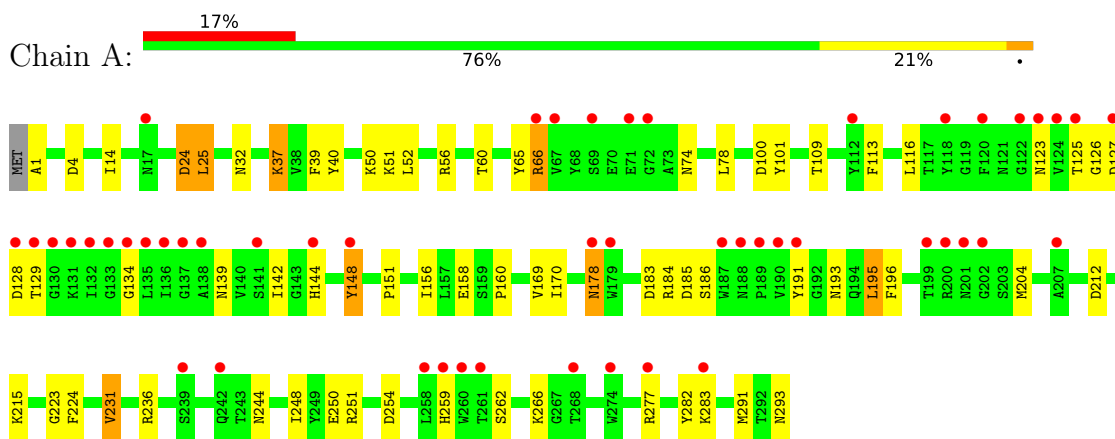
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	45	Total 45	O 45	0	0
2	B	45	Total 45	O 45	0	0
2	C	45	Total 45	O 45	0	0
2	D	40	Total 40	O 40	0	0
2	E	36	Total 36	O 36	0	0
2	F	52	Total 52	O 52	0	0
2	G	39	Total 39	O 39	0	0

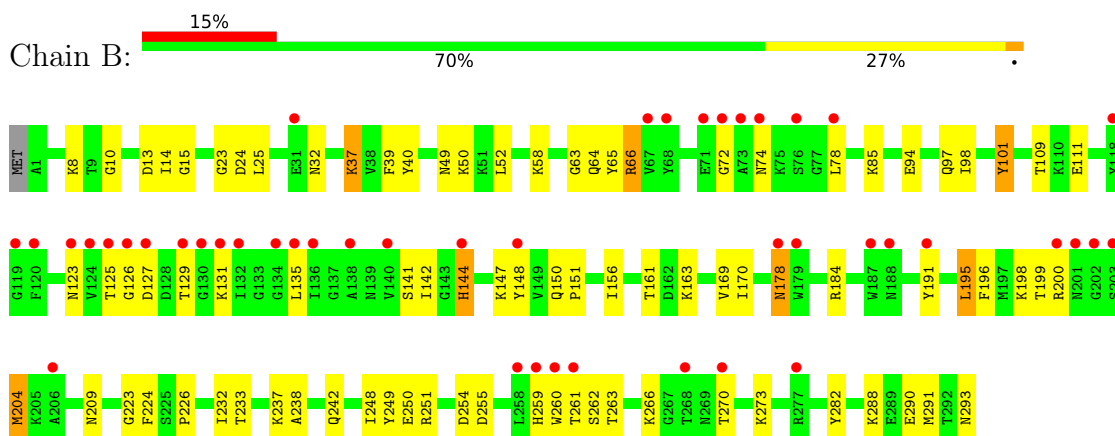
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

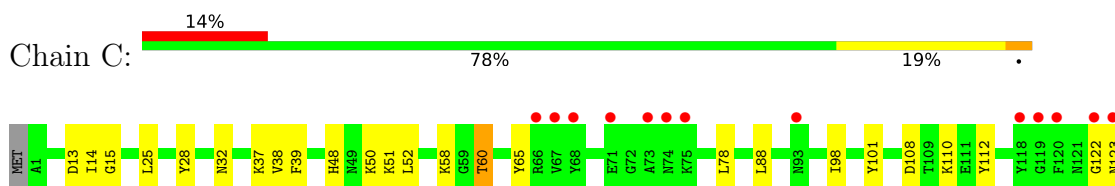
- Molecule 1: Alpha-hemolysin

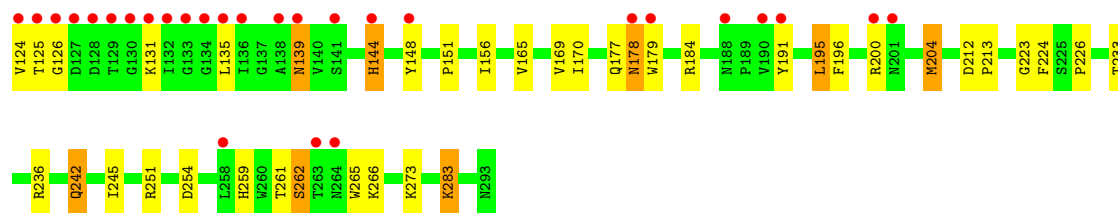


- Molecule 1: Alpha-hemolysin

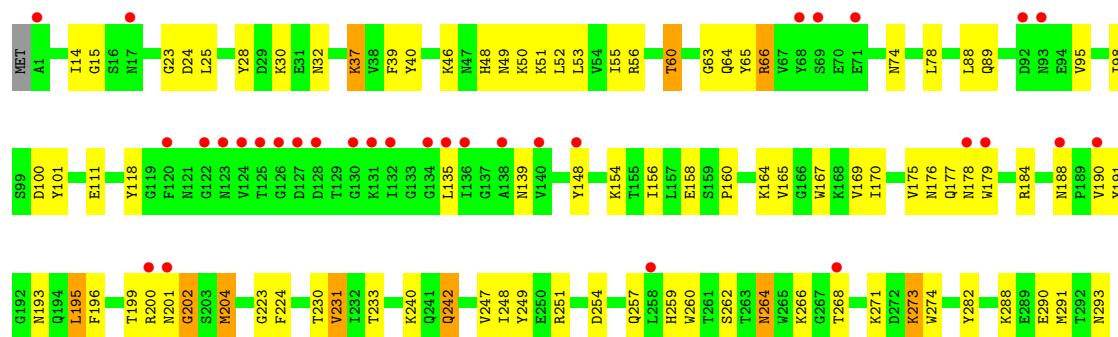


- Molecule 1: Alpha-hemolysin

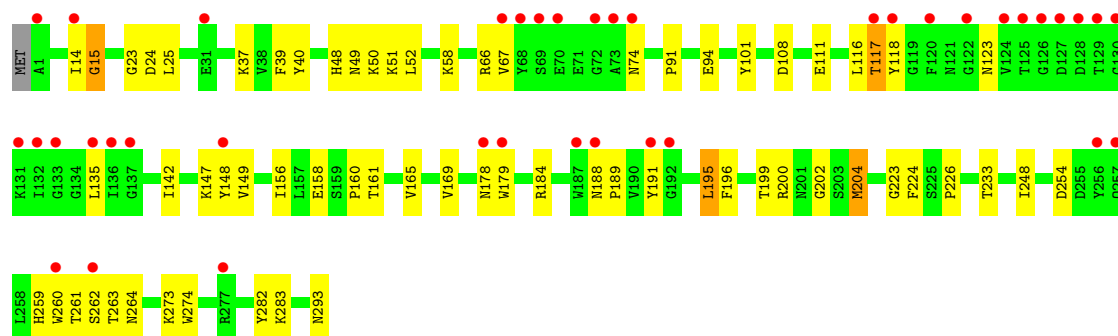
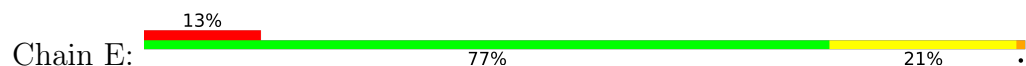




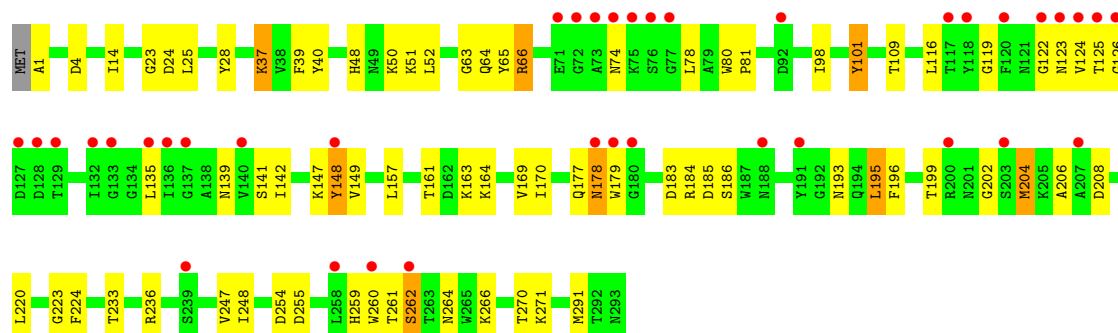
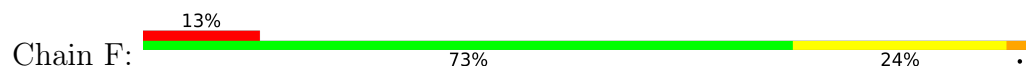
• Molecule 1: Alpha-hemolysin



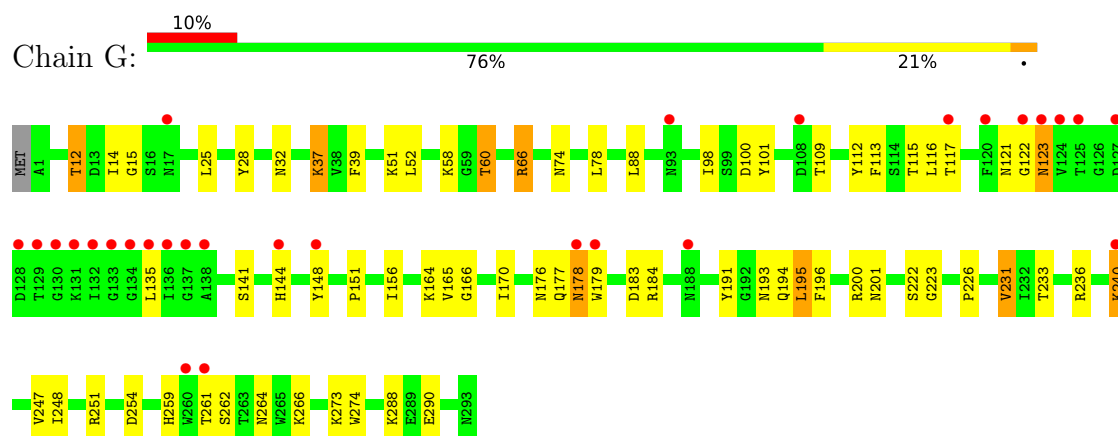
• Molecule 1: Alpha-hemolysin



• Molecule 1: Alpha-hemolysin



● Molecule 1: Alpha-hemolysin



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	151.19Å 134.80Å 132.89Å 90.00° 90.62° 90.00°	Depositor
Resolution (Å)	20.00 – 2.10 20.00 – 2.10	Depositor EDS
% Data completeness (in resolution range)	(Not available) (20.00-2.10) 87.0 (20.00-2.10)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.05 (at 2.10Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.241 , 0.275 0.256 , 0.254	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	32.2	Xtriage
Anisotropy	0.331	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 37.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.010 for -h,-k,l	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	16733	wwPDB-VP
Average B, all atoms (Å ²)	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.18% 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	0.38	0/2396	0.86	4/3243 (0.1%)
1	B	0.39	0/2401	0.88	8/3249 (0.2%)
1	C	0.39	0/2401	0.85	3/3249 (0.1%)
1	D	0.39	0/2401	0.87	7/3249 (0.2%)
1	E	0.38	0/2401	0.86	5/3249 (0.2%)
1	F	0.37	0/2401	0.85	4/3249 (0.1%)
1	G	0.39	0/2401	0.87	5/3249 (0.2%)
All	All	0.38	0/16802	0.86	36/22737 (0.2%)

There are no bond length outliers.

All (36) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	223	GLY	N-CA-C	9.45	121.68	112.04
1	A	223	GLY	N-CA-C	8.75	120.96	112.04
1	E	223	GLY	N-CA-C	8.69	120.86	112.08
1	G	223	GLY	N-CA-C	8.47	120.63	112.08
1	F	223	GLY	N-CA-C	7.58	119.77	112.04
1	D	223	GLY	N-CA-C	7.34	119.53	112.04
1	B	223	GLY	N-CA-C	6.70	119.89	111.85
1	E	156	ILE	N-CA-C	6.25	116.87	108.11
1	B	170	ILE	N-CA-C	6.21	117.53	108.53
1	B	15	GLY	N-CA-C	6.10	121.74	114.48
1	B	98	ILE	N-CA-C	-5.89	101.06	108.84
1	A	66	ARG	N-CA-C	5.83	117.71	108.79
1	B	66	ARG	N-CA-C	5.72	117.81	108.55
1	D	156	ILE	N-CA-C	5.67	116.65	108.48
1	B	249	TYR	N-CA-C	-5.60	100.06	109.07
1	G	15	GLY	N-CA-C	5.57	121.39	114.37
1	A	170	ILE	N-CA-C	5.52	116.94	108.71
1	F	271	LYS	N-CA-C	5.49	118.60	110.48
1	D	170	ILE	N-CA-C	5.47	116.47	108.53
1	D	271	LYS	N-CA-C	5.45	118.19	110.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	249	TYR	N-CA-C	-5.39	100.11	108.90
1	F	66	ARG	N-CA-C	5.38	117.25	108.76
1	F	170	ILE	N-CA-C	5.35	116.68	108.71
1	G	66	ARG	N-CA-C	5.28	116.55	108.52
1	C	156	ILE	N-CA-C	5.25	116.03	108.48
1	A	156	ILE	N-CA-C	5.23	116.01	108.48
1	E	15	GLY	N-CA-C	5.18	120.90	114.37
1	E	66	ARG	N-CA-C	5.18	116.28	108.46
1	D	98	ILE	N-CA-C	-5.17	100.89	108.54
1	D	66	ARG	N-CA-C	5.15	116.35	108.52
1	E	51	LYS	N-CA-C	-5.12	102.90	110.48
1	C	15	GLY	N-CA-C	5.08	120.52	114.48
1	G	156	ILE	N-CA-C	5.05	115.75	108.48
1	G	115	THR	N-CA-C	5.05	117.13	108.90
1	B	156	ILE	N-CA-C	5.03	115.72	108.48
1	B	97	GLN	N-CA-C	5.00	116.98	109.23

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	2343	0	2258	56	0
1	B	2348	0	2270	68	0
1	C	2348	0	2270	60	0
1	D	2348	0	2270	80	0
1	E	2348	0	2270	51	0
1	F	2348	0	2270	67	0
1	G	2348	0	2270	67	0
2	A	45	0	0	1	0
2	B	45	0	0	1	0
2	C	45	0	0	1	0
2	D	40	0	0	3	0
2	E	36	0	0	0	0
2	F	52	0	0	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	G	39	0	0	0	0
All	All	16733	0	15878	387	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 12.

All (387) 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:123:ASN:HB3	1:C:135:LEU:HB3	1.51	0.91
1:A:14:ILE:HD11	1:B:39:PHE:HE1	1.36	0.90
1:B:199:THR:H	1:B:209:ASN:HD21	1.20	0.89
1:G:123:ASN:HB3	1:G:135:LEU:HB3	1.54	0.89
1:B:123:ASN:HB3	1:B:135:LEU:HB3	1.54	0.88
1:A:212:ASP:HB3	1:A:215:LYS:HD2	1.59	0.84
1:G:51:LYS:HE3	1:G:236:ARG:HG2	1.62	0.81
1:B:178:ASN:N	1:B:178:ASN:HD22	1.79	0.81
1:D:52:LEU:HD22	1:D:233:THR:HG22	1.64	0.79
1:B:8:LYS:HD2	1:C:13:ASP:HB2	1.62	0.79
1:A:178:ASN:N	1:A:178:ASN:HD22	1.78	0.78
1:D:167:TRP:HH2	1:D:230:THR:HG22	1.50	0.77
1:D:230:THR:HG23	2:D:294:HOH:O	1.84	0.76
1:F:202:GLY:HA3	1:F:204:MET:HE3	1.66	0.76
1:C:242:GLN:HB2	1:C:283:LYS:HE3	1.68	0.75
1:A:39:PHE:HE1	1:G:14:ILE:HD11	1.50	0.75
1:E:91:PRO:HD2	1:E:94:GLU:HG3	1.69	0.74
1:F:123:ASN:HD21	1:G:135:LEU:HD11	1.52	0.74
1:A:14:ILE:HD11	1:B:39:PHE:CE1	2.22	0.74
1:G:100:ASP:HB3	1:G:231:VAL:CG1	2.18	0.73
1:F:148:TYR:OH	1:G:178:ASN:ND2	2.22	0.73
1:B:14:ILE:HD11	1:C:39:PHE:HE1	1.53	0.72
1:E:123:ASN:HB3	1:E:135:LEU:HB3	1.71	0.72
1:E:199:THR:OG1	1:E:204:MET:HE1	1.90	0.72
1:F:14:ILE:HD11	1:F:48:HIS:CE1	2.25	0.71
1:A:56:ARG:NH2	1:G:12:THR:HG21	2.05	0.71
1:B:52:LEU:CD2	1:B:233:THR:HG22	2.21	0.70
1:C:178:ASN:N	1:C:178:ASN:HD22	1.90	0.69
1:F:123:ASN:ND2	1:G:135:LEU:HD11	2.08	0.69
1:F:123:ASN:HB3	1:F:135:LEU:HB3	1.75	0.68
1:F:124:VAL:O	1:G:135:LEU:HD12	1.94	0.68
1:G:191:TYR:CE2	1:G:200:ARG:HB3	2.29	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:178:ASN:HD22	1:F:178:ASN:N	1.91	0.68
1:C:14:ILE:HD11	1:C:48:HIS:CE1	2.29	0.67
1:E:52:LEU:CD2	1:E:233:THR:HG22	2.23	0.67
1:D:264:ASN:C	1:D:264:ASN:HD22	2.00	0.67
1:G:100:ASP:HB3	1:G:231:VAL:HG11	1.75	0.67
1:G:52:LEU:HD23	1:G:233:THR:HG22	1.77	0.66
1:A:123:ASN:OD1	1:B:135:LEU:HD11	1.95	0.66
1:B:144:HIS:C	1:B:144:HIS:CD2	2.73	0.66
1:D:52:LEU:CD2	1:D:233:THR:HG22	2.26	0.66
1:D:148:TYR:OH	1:E:178:ASN:ND2	2.28	0.66
1:B:199:THR:H	1:B:209:ASN:ND2	1.92	0.66
1:F:199:THR:OG1	1:F:204:MET:HE1	1.96	0.65
1:D:202:GLY:HA3	1:D:204:MET:HE3	1.79	0.65
1:B:191:TYR:CE2	1:B:200:ARG:HB3	2.33	0.64
1:B:52:LEU:HD23	1:B:233:THR:HG22	1.79	0.64
1:D:167:TRP:CH2	1:D:230:THR:HG22	2.32	0.64
1:D:257:GLN:HB2	1:D:268:THR:CG2	2.29	0.63
1:C:148:TYR:OH	1:D:178:ASN:ND2	2.32	0.63
1:D:282:TYR:CD1	1:D:293:ASN:HB3	2.34	0.63
1:E:148:TYR:OH	1:F:178:ASN:ND2	2.32	0.63
1:A:148:TYR:OH	1:B:178:ASN:ND2	2.32	0.62
1:F:248:ILE:N	1:F:248:ILE:HD12	2.14	0.62
1:G:178:ASN:N	1:G:178:ASN:HD22	1.97	0.62
1:B:111:GLU:OE1	1:B:147:LYS:HD3	2.00	0.62
1:E:116:LEU:HD13	1:E:117:THR:N	2.15	0.62
1:A:100:ASP:HB3	1:A:231:VAL:HG13	1.83	0.61
1:B:259:HIS:CE1	1:B:266:LYS:HB3	2.36	0.61
1:D:240:LYS:HD2	1:D:242:GLN:NE2	2.16	0.61
1:F:66:ARG:C	1:F:78:LEU:HD12	2.25	0.61
1:C:37:LYS:HD2	1:C:37:LYS:C	2.26	0.60
1:C:14:ILE:HD11	1:D:39:PHE:HE1	1.65	0.60
1:F:177:GLN:O	1:F:179:TRP:HD1	1.84	0.60
1:A:56:ARG:HH22	1:G:12:THR:HG21	1.66	0.60
1:F:37:LYS:HD2	1:F:37:LYS:C	2.27	0.60
1:E:14:ILE:HD11	1:E:48:HIS:CE1	2.36	0.60
1:E:111:GLU:OE1	1:F:147:LYS:HE3	2.02	0.59
1:D:14:ILE:HD11	1:E:39:PHE:HE1	1.68	0.59
1:A:178:ASN:N	1:A:178:ASN:ND2	2.48	0.59
1:A:116:LEU:HD13	1:A:142:ILE:HD11	1.84	0.59
1:D:100:ASP:HB3	1:D:231:VAL:HG13	1.84	0.59
1:D:14:ILE:HD11	1:D:48:HIS:CE1	2.38	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:170:ILE:HD12	1:G:170:ILE:O	2.03	0.58
1:C:124:VAL:O	1:D:135:LEU:HD12	2.03	0.58
1:E:273:LYS:HD2	1:E:274:TRP:CE2	2.39	0.58
1:C:48:HIS:O	1:C:236:ARG:NH2	2.32	0.58
1:D:184:ARG:HD2	1:D:254:ASP:OD2	2.03	0.58
1:D:202:GLY:HA3	1:D:204:MET:CE	2.34	0.58
1:B:8:LYS:HD2	1:C:13:ASP:CB	2.32	0.57
1:D:195:LEU:HD13	1:D:196:PHE:CE2	2.39	0.57
1:D:49:ASN:O	1:D:50:LYS:HG3	2.05	0.57
1:A:244:ASN:OD1	1:A:283:LYS:HE2	2.05	0.57
1:F:74:ASN:O	1:F:259:HIS:HA	2.05	0.57
1:C:51:LYS:HG3	1:C:236:ARG:HG3	1.87	0.57
1:D:74:ASN:O	1:D:259:HIS:HA	2.04	0.56
1:A:116:LEU:HD13	1:A:142:ILE:CD1	2.35	0.56
1:A:178:ASN:ND2	1:G:148:TYR:OH	2.38	0.56
1:F:52:LEU:CD2	1:F:233:THR:HG22	2.34	0.56
1:G:117:THR:HG23	1:G:141:SER:HB3	1.86	0.56
1:F:261:THR:O	1:F:262:SER:CB	2.54	0.56
1:B:255:ASP:HB3	1:B:270:THR:OG1	2.06	0.56
1:C:259:HIS:CE1	1:C:266:LYS:HB3	2.41	0.56
1:D:240:LYS:CE	1:D:242:GLN:HE21	2.19	0.56
1:B:25:LEU:HD21	1:B:40:TYR:HE1	1.71	0.56
1:C:101:TYR:OH	1:D:60:THR:HG22	2.06	0.56
1:D:100:ASP:HB3	1:D:231:VAL:CG1	2.36	0.55
1:E:116:LEU:HD13	1:E:116:LEU:C	2.30	0.55
1:F:119:GLY:HA3	1:F:139:ASN:OD1	2.06	0.55
1:B:178:ASN:N	1:B:178:ASN:ND2	2.51	0.55
1:F:259:HIS:CE1	1:F:266:LYS:HB3	2.40	0.55
1:C:169:VAL:HG21	1:C:224:PHE:CZ	2.41	0.55
1:D:264:ASN:C	1:D:264:ASN:ND2	2.62	0.55
1:A:125:THR:HG22	1:A:126:GLY:H	1.71	0.55
1:C:261:THR:O	1:C:262:SER:HB3	2.07	0.55
1:B:148:TYR:OH	1:C:178:ASN:ND2	2.40	0.55
1:D:259:HIS:CE1	1:D:266:LYS:HB3	2.42	0.55
1:C:112:TYR:CE2	1:C:144:HIS:NE2	2.74	0.55
1:A:65:TYR:CE1	1:A:78:LEU:HD21	2.43	0.54
1:C:144:HIS:C	1:C:144:HIS:CD2	2.84	0.54
1:F:177:GLN:O	1:F:179:TRP:CD1	2.60	0.54
1:A:100:ASP:HB3	1:A:231:VAL:CG1	2.36	0.54
1:B:58:LYS:HA	1:B:226:PRO:O	2.07	0.54
1:C:52:LEU:CD2	1:C:233:THR:HG22	2.38	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:193:ASN:OD1	1:D:195:LEU:HB2	2.08	0.54
1:C:51:LYS:HE3	1:C:236:ARG:HG2	1.89	0.54
1:E:116:LEU:HD23	1:E:142:ILE:HG12	1.90	0.54
1:E:248:ILE:N	1:E:248:ILE:HD12	2.23	0.54
1:F:141:SER:C	1:F:142:ILE:HD12	2.32	0.54
1:B:199:THR:N	1:B:209:ASN:HD21	1.98	0.54
1:C:184:ARG:HD2	1:C:254:ASP:OD2	2.08	0.53
1:F:51:LYS:HG3	1:F:236:ARG:HG2	1.89	0.53
1:G:248:ILE:HD12	1:G:248:ILE:N	2.24	0.53
1:E:49:ASN:O	1:E:50:LYS:HG3	2.08	0.53
1:C:52:LEU:HD21	1:C:233:THR:HG22	1.89	0.53
1:A:191:TYR:O	1:A:266:LYS:HA	2.09	0.53
1:B:125:THR:HG22	1:C:135:LEU:HD13	1.91	0.53
1:E:169:VAL:HG21	1:E:224:PHE:CZ	2.44	0.53
1:C:126:GLY:HA2	1:C:131:LYS:O	2.08	0.53
1:D:32:ASN:O	1:D:251:ARG:NH2	2.35	0.53
1:B:109:THR:HG22	1:C:151:PRO:HA	1.91	0.53
1:C:139:ASN:HD22	1:C:139:ASN:N	2.06	0.53
1:F:261:THR:O	1:F:262:SER:HB2	2.08	0.53
1:G:74:ASN:O	1:G:259:HIS:HA	2.08	0.53
1:B:141:SER:C	1:B:142:ILE:HD12	2.33	0.53
1:F:195:LEU:HD13	1:F:196:PHE:CE2	2.43	0.53
1:G:122:GLY:O	1:G:123:ASN:HB2	2.08	0.53
1:E:263:THR:HG23	1:E:264:ASN:OD1	2.09	0.52
1:G:184:ARG:HD2	1:G:254:ASP:OD2	2.09	0.52
1:C:242:GLN:CB	1:C:283:LYS:HE3	2.39	0.52
1:F:184:ARG:HD2	1:F:254:ASP:OD2	2.09	0.52
1:E:37:LYS:HD2	1:E:37:LYS:C	2.34	0.52
1:F:25:LEU:HD21	1:F:40:TYR:HE1	1.74	0.52
1:A:215:LYS:NZ	1:G:183:ASP:OD1	2.42	0.52
1:G:240:LYS:HB2	1:G:240:LYS:NZ	2.24	0.52
1:A:123:ASN:CG	1:B:135:LEU:HD11	2.34	0.52
1:F:123:ASN:CG	1:G:135:LEU:HD11	2.35	0.52
1:D:28:TYR:CE1	1:D:30:LYS:HG2	2.46	0.51
1:F:122:GLY:O	1:F:123:ASN:HB2	2.09	0.51
1:B:125:THR:HG22	1:C:135:LEU:CD1	2.40	0.51
1:E:14:ILE:HD11	1:F:39:PHE:HE1	1.75	0.51
1:E:178:ASN:N	1:E:178:ASN:HD22	2.08	0.51
1:F:116:LEU:HD23	1:G:144:HIS:CE1	2.45	0.51
1:A:148:TYR:OH	1:B:178:ASN:CG	2.54	0.51
1:C:178:ASN:N	1:C:178:ASN:ND2	2.57	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:74:ASN:O	1:E:259:HIS:HA	2.10	0.51
1:B:101:TYR:OH	1:C:60:THR:CG2	2.59	0.51
1:F:125:THR:HG22	1:F:126:GLY:N	2.25	0.51
1:A:1:ALA:HB3	1:A:4:ASP:OD1	2.11	0.50
1:A:248:ILE:N	1:A:248:ILE:HD12	2.26	0.50
1:D:247:VAL:C	1:D:248:ILE:HD12	2.37	0.50
1:G:37:LYS:HD2	1:G:37:LYS:C	2.36	0.50
1:B:101:TYR:OH	1:C:60:THR:HG22	2.11	0.50
1:A:178:ASN:CG	1:G:148:TYR:OH	2.54	0.50
1:B:85:LYS:HD2	1:B:250:GLU:OE1	2.11	0.50
1:C:170:ILE:O	1:C:170:ILE:HD12	2.10	0.50
1:F:123:ASN:OD1	1:G:135:LEU:HD11	2.11	0.50
1:B:10:GLY:HA2	1:B:13:ASP:OD2	2.11	0.50
1:C:58:LYS:HA	1:C:226:PRO:O	2.11	0.50
1:D:37:LYS:C	1:D:37:LYS:HD2	2.37	0.50
1:G:288:LYS:HE2	1:G:290:GLU:CD	2.37	0.50
1:A:66:ARG:C	1:A:78:LEU:HD12	2.37	0.50
1:E:191:TYR:CE1	1:E:200:ARG:HB3	2.47	0.49
1:A:40:TYR:CE1	1:A:291:MET:HB2	2.47	0.49
1:F:52:LEU:HD23	1:F:233:THR:HG22	1.94	0.49
1:A:123:ASN:ND2	1:B:135:LEU:HD11	2.27	0.49
1:A:24:ASP:O	1:A:25:LEU:HD13	2.11	0.49
1:B:37:LYS:HD2	1:B:37:LYS:C	2.38	0.49
1:D:111:GLU:OE1	1:E:147:LYS:HE3	2.13	0.49
1:D:178:ASN:HD22	1:D:178:ASN:N	2.08	0.49
1:E:184:ARG:HD2	1:E:254:ASP:OD2	2.13	0.49
1:A:37:LYS:HD2	1:A:37:LYS:C	2.37	0.49
1:C:110:LYS:HD3	1:D:175:VAL:HG23	1.94	0.49
1:E:195:LEU:HD13	1:E:196:PHE:CE2	2.47	0.49
1:A:39:PHE:CE1	1:G:14:ILE:HD11	2.40	0.49
1:D:56:ARG:NH2	2:D:298:HOH:O	2.46	0.49
1:D:177:GLN:O	1:D:179:TRP:HD1	1.96	0.48
1:C:101:TYR:OH	1:D:60:THR:CG2	2.62	0.48
1:E:191:TYR:CZ	1:E:200:ARG:HD3	2.49	0.48
1:F:178:ASN:N	1:F:178:ASN:ND2	2.57	0.48
1:B:169:VAL:HG21	1:B:224:PHE:CZ	2.48	0.48
1:B:184:ARG:HD2	1:B:254:ASP:OD2	2.13	0.48
1:B:195:LEU:HD13	1:B:196:PHE:CE2	2.48	0.48
1:A:193:ASN:OD1	1:A:195:LEU:HB2	2.13	0.48
1:B:282:TYR:CD1	1:B:293:ASN:HB3	2.48	0.48
1:C:177:GLN:O	1:C:179:TRP:HD1	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:125:THR:HG22	1:A:126:GLY:N	2.28	0.48
1:D:169:VAL:HG21	1:D:224:PHE:CZ	2.49	0.48
1:D:260:TRP:NE1	1:D:262:SER:HA	2.29	0.48
1:G:193:ASN:OD1	1:G:195:LEU:HB2	2.14	0.48
1:B:237:LYS:O	1:B:238:ALA:C	2.57	0.48
1:E:161:THR:HG22	1:F:28:TYR:CZ	2.48	0.48
1:G:123:ASN:HD22	1:G:135:LEU:HB3	1.79	0.48
1:A:51:LYS:HG3	1:A:236:ARG:HG2	1.96	0.48
1:A:144:HIS:CE1	1:G:116:LEU:HB3	2.49	0.48
1:E:261:THR:O	1:E:262:SER:HB2	2.14	0.48
1:B:49:ASN:O	1:B:50:LYS:HG3	2.13	0.47
1:B:23:GLY:HA3	1:B:40:TYR:CZ	2.49	0.47
1:G:32:ASN:O	1:G:251:ARG:NH1	2.43	0.47
1:A:50:LYS:NZ	2:A:303:HOH:O	2.48	0.47
1:B:50:LYS:NZ	2:B:325:HOH:O	2.47	0.47
1:D:118:TYR:HA	1:D:139:ASN:O	2.15	0.47
1:D:273:LYS:HD2	1:D:274:TRP:CE2	2.50	0.47
1:E:260:TRP:CD1	1:E:262:SER:H	2.32	0.47
1:B:74:ASN:O	1:B:259:HIS:HA	2.15	0.47
1:C:37:LYS:HD2	1:C:38:VAL:N	2.29	0.47
1:F:169:VAL:HG21	1:F:224:PHE:CZ	2.49	0.47
1:A:113:PHE:O	1:A:144:HIS:HA	2.14	0.47
1:D:177:GLN:O	1:D:179:TRP:CD1	2.68	0.47
1:E:118:TYR:O	1:F:141:SER:HB2	2.14	0.47
1:F:23:GLY:HA3	1:F:40:TYR:CZ	2.50	0.47
1:B:24:ASP:C	1:B:25:LEU:HD22	2.40	0.47
1:B:204:MET:HE3	1:B:209:ASN:HB2	1.97	0.47
1:B:248:ILE:HD12	1:B:248:ILE:N	2.29	0.47
1:C:204:MET:HE1	1:C:265:TRP:HE1	1.79	0.47
1:D:293:ASN:CG	1:D:293:ASN:O	2.58	0.47
1:F:98:ILE:HD12	1:F:164:LYS:N	2.30	0.47
1:D:23:GLY:HA3	1:D:40:TYR:CZ	2.50	0.47
1:B:161:THR:HG22	1:C:28:TYR:CZ	2.50	0.47
1:F:101:TYR:OH	1:G:60:THR:CG2	2.63	0.47
1:F:193:ASN:OD1	1:F:195:LEU:HB2	2.15	0.47
1:C:32:ASN:O	1:C:251:ARG:NH1	2.46	0.46
1:E:111:GLU:HG2	1:F:149:VAL:HG22	1.98	0.46
1:E:179:TRP:CD1	1:E:179:TRP:N	2.81	0.46
1:F:14:ILE:HD11	1:G:39:PHE:HE1	1.79	0.46
1:F:65:TYR:CE2	1:F:78:LEU:HD21	2.51	0.46
1:A:148:TYR:CD1	1:A:148:TYR:N	2.83	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:198:LYS:HB3	1:B:209:ASN:ND2	2.31	0.46
1:B:261:THR:C	1:B:263:THR:H	2.22	0.46
1:D:89:GLN:HG3	1:D:164:LYS:HB3	1.97	0.46
1:E:179:TRP:HZ3	1:E:200:ARG:NH2	2.13	0.46
1:G:123:ASN:HD22	1:G:135:LEU:CB	2.28	0.46
1:D:191:TYR:CE2	1:D:200:ARG:HB3	2.50	0.46
1:G:113:PHE:O	1:G:144:HIS:HA	2.15	0.46
1:B:288:LYS:HB2	1:B:290:GLU:HG2	1.98	0.46
1:D:202:GLY:CA	1:D:204:MET:HE3	2.44	0.46
1:F:260:TRP:CZ3	1:F:264:ASN:HA	2.50	0.46
1:G:14:ILE:HD13	1:G:52:LEU:HD11	1.98	0.46
1:C:148:TYR:N	1:C:148:TYR:CD1	2.83	0.46
1:D:158:GLU:O	1:D:160:PRO:HD3	2.16	0.46
1:G:58:LYS:HA	1:G:226:PRO:O	2.16	0.46
1:A:184:ARG:HD2	1:A:254:ASP:OD2	2.16	0.46
1:B:65:TYR:CE2	1:B:78:LEU:HD21	2.51	0.46
1:E:116:LEU:HD11	1:E:118:TYR:CZ	2.51	0.46
1:D:178:ASN:ND2	1:D:178:ASN:N	2.64	0.46
1:G:178:ASN:ND2	1:G:178:ASN:N	2.60	0.46
1:A:151:PRO:HA	1:G:109:THR:HG22	1.98	0.45
1:B:127:ASP:C	1:B:129:THR:H	2.24	0.45
1:D:63:GLY:O	1:D:64:GLN:HB2	2.16	0.45
1:D:260:TRP:CD1	1:D:262:SER:H	2.34	0.45
1:E:202:GLY:HA3	1:E:204:MET:HE3	1.98	0.45
1:F:63:GLY:O	1:F:64:GLN:HB2	2.16	0.45
1:G:98:ILE:HD12	1:G:164:LYS:N	2.31	0.45
1:B:40:TYR:CE1	1:B:291:MET:HB3	2.50	0.45
1:C:52:LEU:HD23	1:C:52:LEU:HA	1.78	0.45
1:D:204:MET:HB2	2:D:317:HOH:O	2.15	0.45
1:F:157:LEU:O	1:G:222:SER:HB3	2.16	0.45
1:A:169:VAL:HG21	1:A:224:PHE:CZ	2.52	0.45
1:F:50:LYS:NZ	2:F:325:HOH:O	2.48	0.45
1:F:101:TYR:OH	1:G:60:THR:HG22	2.17	0.45
1:A:32:ASN:O	1:A:251:ARG:NH1	2.48	0.44
1:A:139:ASN:HB3	1:G:121:ASN:CB	2.47	0.44
1:A:282:TYR:CD1	1:A:293:ASN:HB3	2.52	0.44
1:D:160:PRO:HB3	1:D:165:VAL:HG23	1.98	0.44
1:B:260:TRP:CD1	1:B:262:SER:H	2.35	0.44
1:F:116:LEU:HD23	1:G:144:HIS:HE1	1.83	0.44
1:A:123:ASN:HD21	1:B:135:LEU:HD11	1.82	0.44
1:A:139:ASN:HB3	1:G:121:ASN:HB2	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:66:ARG:C	1:D:78:LEU:HD12	2.42	0.44
1:D:260:TRP:CZ3	1:D:264:ASN:HA	2.53	0.44
1:A:109:THR:HG22	1:B:151:PRO:HA	2.00	0.44
1:E:158:GLU:O	1:E:160:PRO:HD3	2.17	0.44
1:A:195:LEU:HD13	1:A:196:PHE:CE2	2.53	0.44
1:F:202:GLY:HA3	1:F:204:MET:CE	2.41	0.44
1:F:206:ALA:C	1:F:208:ASP:H	2.25	0.44
1:B:63:GLY:O	1:B:64:GLN:HB2	2.18	0.44
1:B:94:GLU:O	1:B:163:LYS:NZ	2.48	0.44
1:C:50:LYS:NZ	2:C:315:HOH:O	2.51	0.43
1:D:202:GLY:C	1:D:204:MET:HE3	2.42	0.43
1:F:148:TYR:N	1:F:148:TYR:CD1	2.86	0.43
1:G:273:LYS:HD3	1:G:274:TRP:CZ2	2.53	0.43
1:D:55:ILE:HD13	1:D:291:MET:HE1	1.99	0.43
1:D:199:THR:OG1	1:D:204:MET:HE1	2.19	0.43
1:D:201:ASN:O	1:D:202:GLY:C	2.61	0.43
1:G:261:THR:O	1:G:262:SER:HB3	2.18	0.43
1:C:139:ASN:HD22	1:C:139:ASN:H	1.64	0.43
1:D:111:GLU:HG2	1:E:149:VAL:HG22	2.00	0.43
1:G:259:HIS:CE1	1:G:266:LYS:HB3	2.53	0.43
1:B:126:GLY:HA2	1:B:131:LYS:O	2.19	0.43
1:C:195:LEU:HD13	1:C:196:PHE:CE2	2.54	0.43
1:D:65:TYR:CE2	1:D:78:LEU:HD21	2.54	0.43
1:E:282:TYR:CD1	1:E:293:ASN:HB3	2.53	0.43
1:E:293:ASN:OD1	1:E:293:ASN:C	2.61	0.43
1:F:161:THR:HG22	1:G:28:TYR:CZ	2.54	0.43
1:B:66:ARG:HG3	1:B:66:ARG:HH11	1.84	0.43
1:C:191:TYR:CE2	1:C:200:ARG:HB3	2.53	0.43
1:E:14:ILE:CG2	1:E:15:GLY:N	2.81	0.43
1:D:177:GLN:O	1:D:178:ASN:HB2	2.19	0.43
1:D:288:LYS:HB2	1:D:290:GLU:HG2	2.00	0.43
1:B:232:ILE:N	1:B:232:ILE:HD12	2.33	0.43
1:B:32:ASN:O	1:B:251:ARG:NH1	2.41	0.42
1:G:176:ASN:OD1	1:G:177:GLN:HG3	2.19	0.42
1:B:52:LEU:HD21	1:B:233:THR:HG22	1.96	0.42
1:C:212:ASP:OD1	1:C:213:PRO:HD2	2.18	0.42
1:G:12:THR:O	1:G:12:THR:CG2	2.67	0.42
1:G:247:VAL:C	1:G:248:ILE:HD12	2.44	0.42
1:A:183:ASP:OD2	1:A:183:ASP:C	2.63	0.42
1:A:282:TYR:C	1:A:283:LYS:HD2	2.44	0.42
1:D:14:ILE:HG22	1:D:15:GLY:N	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:51:LYS:O	1:D:52:LEU:HD23	2.19	0.42
1:E:148:TYR:N	1:E:148:TYR:CD1	2.87	0.42
1:F:52:LEU:HD21	1:F:233:THR:HG22	1.99	0.42
1:G:170:ILE:HD12	1:G:170:ILE:C	2.44	0.42
1:C:123:ASN:HB3	1:C:135:LEU:HD23	2.01	0.42
1:E:58:LYS:HA	1:E:226:PRO:O	2.20	0.42
1:C:98:ILE:HD13	1:C:165:VAL:HG12	2.01	0.42
1:D:248:ILE:HD12	1:D:248:ILE:N	2.34	0.42
1:D:88:LEU:HD13	1:D:230:THR:HG21	2.00	0.42
1:F:1:ALA:O	1:F:4:ASP:HB2	2.20	0.42
1:D:240:LYS:HE3	1:D:242:GLN:HE21	1.83	0.42
1:E:23:GLY:HA3	1:E:40:TYR:CZ	2.55	0.42
1:E:178:ASN:ND2	1:E:178:ASN:N	2.66	0.42
1:C:125:THR:HG22	1:C:126:GLY:N	2.34	0.42
1:F:81:PRO:CG	1:F:220:LEU:HA	2.50	0.42
1:G:112:TYR:OH	1:G:144:HIS:CD2	2.73	0.42
1:C:122:GLY:HA2	1:C:135:LEU:O	2.20	0.41
1:D:46:LYS:HA	1:D:46:LYS:HD3	1.88	0.41
1:D:188:ASN:OD1	1:D:190:VAL:N	2.51	0.41
1:B:142:ILE:HD12	1:B:142:ILE:N	2.35	0.41
1:F:109:THR:HG22	1:G:151:PRO:HA	2.01	0.41
1:G:66:ARG:C	1:G:78:LEU:HD12	2.44	0.41
1:A:74:ASN:O	1:A:259:HIS:HA	2.21	0.41
1:A:127:ASP:C	1:A:129:THR:H	2.28	0.41
1:C:52:LEU:HD21	1:C:233:THR:CG2	2.49	0.41
1:D:240:LYS:HD2	1:D:242:GLN:HE22	1.81	0.41
1:F:98:ILE:HD12	1:F:163:LYS:C	2.45	0.41
1:G:100:ASP:N	1:G:231:VAL:HG13	2.34	0.41
1:A:158:GLU:O	1:A:160:PRO:HD3	2.19	0.41
1:B:72:GLY:C	1:B:74:ASN:H	2.29	0.41
1:D:23:GLY:HA3	1:D:40:TYR:CE1	2.55	0.41
1:A:250:GLU:OE2	1:A:277:ARG:HD2	2.20	0.41
1:C:139:ASN:N	1:C:139:ASN:ND2	2.68	0.41
1:F:247:VAL:C	1:F:248:ILE:HD12	2.45	0.41
1:G:165:VAL:HG22	1:G:166:GLY:N	2.36	0.41
1:C:88:LEU:HB3	1:C:245:ILE:HD11	2.03	0.41
1:D:242:GLN:HE21	1:D:242:GLN:HB2	1.72	0.41
1:E:188:ASN:HA	1:E:189:PRO:HD3	1.94	0.41
1:E:202:GLY:HA3	1:E:204:MET:CE	2.50	0.41
1:C:14:ILE:CD1	1:D:39:PHE:HE1	2.30	0.41
1:C:65:TYR:CE2	1:C:78:LEU:HD21	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:14:ILE:HG22	1:E:15:GLY:N	2.35	0.41
1:F:185:ASP:O	1:F:186:SER:C	2.64	0.41
1:C:148:TYR:OH	1:D:178:ASN:CG	2.64	0.41
1:D:154:LYS:O	1:D:169:VAL:HA	2.20	0.41
1:D:257:GLN:HB2	1:D:268:THR:HG22	2.02	0.41
1:F:14:ILE:CD1	1:F:48:HIS:CE1	3.02	0.41
1:G:201:ASN:HD22	1:G:264:ASN:HB3	1.85	0.41
1:G:240:LYS:NZ	1:G:240:LYS:CB	2.83	0.41
1:A:123:ASN:O	1:A:134:GLY:HA2	2.21	0.41
1:B:64:GLN:NE2	1:B:251:ARG:CZ	2.84	0.41
1:F:80:TRP:CE2	1:F:254:ASP:HB2	2.56	0.41
1:G:117:THR:CG2	1:G:141:SER:HB3	2.48	0.41
1:A:185:ASP:O	1:A:186:SER:C	2.61	0.40
1:C:170:ILE:HD12	1:C:170:ILE:C	2.45	0.40
1:D:176:ASN:OD1	1:D:176:ASN:C	2.64	0.40
1:E:261:THR:C	1:E:263:THR:H	2.29	0.40
1:F:255:ASP:HB3	1:F:270:THR:HB	2.03	0.40
1:G:194:GLN:O	1:G:195:LEU:C	2.65	0.40
1:D:40:TYR:HB2	1:D:53:LEU:HD11	2.02	0.40
1:E:260:TRP:CZ3	1:E:264:ASN:HA	2.56	0.40
1:F:177:GLN:O	1:F:178:ASN:HB2	2.21	0.40
1:G:88:LEU:HD12	1:G:88:LEU:N	2.37	0.40
1:F:183:ASP:HB2	2:F:339:HOH:O	2.21	0.40
1:B:66:ARG:C	1:B:78:LEU:HD12	2.47	0.40
1:E:116:LEU:C	1:E:116:LEU:CD1	2.95	0.40
1:E:160:PRO:HB3	1:E:165:VAL:HG23	2.03	0.40
1:G:195:LEU:HD13	1:G:196:PHE:CE2	2.57	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	291/294 (99%)	273 (94%)	16 (6%)	2 (1%)	18	15
1	B	291/294 (99%)	272 (94%)	19 (6%)	0	100	100
1	C	291/294 (99%)	274 (94%)	16 (6%)	1 (0%)	36	36
1	D	291/294 (99%)	277 (95%)	13 (4%)	1 (0%)	36	36
1	E	291/294 (99%)	276 (95%)	15 (5%)	0	100	100
1	F	291/294 (99%)	276 (95%)	14 (5%)	1 (0%)	36	36
1	G	291/294 (99%)	276 (95%)	14 (5%)	1 (0%)	36	36
All	All	2037/2058 (99%)	1924 (94%)	107 (5%)	6 (0%)	36	36

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	262	SER
1	C	262	SER
1	G	123	ASN
1	F	262	SER
1	A	128	ASP
1	D	202	GLY

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	258/260 (99%)	247 (96%)	11 (4%)	26	27
1	B	259/260 (100%)	250 (96%)	9 (4%)	32	35
1	C	259/260 (100%)	248 (96%)	11 (4%)	26	28
1	D	259/260 (100%)	247 (95%)	12 (5%)	24	25
1	E	259/260 (100%)	250 (96%)	9 (4%)	32	35
1	F	259/260 (100%)	251 (97%)	8 (3%)	35	39
1	G	259/260 (100%)	249 (96%)	10 (4%)	28	31
All	All	1812/1820 (100%)	1742 (96%)	70 (4%)	28	31

All (70) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	24	ASP
1	A	25	LEU
1	A	37	LYS
1	A	52	LEU
1	A	60	THR
1	A	101	TYR
1	A	148	TYR
1	A	178	ASN
1	A	195	LEU
1	A	204	MET
1	A	231	VAL
1	B	37	LYS
1	B	101	TYR
1	B	144	HIS
1	B	150	GLN
1	B	178	ASN
1	B	195	LEU
1	B	204	MET
1	B	242	GLN
1	B	273	LYS
1	C	25	LEU
1	C	60	THR
1	C	108	ASP
1	C	139	ASN
1	C	144	HIS
1	C	178	ASN
1	C	195	LEU
1	C	204	MET
1	C	242	GLN
1	C	273	LYS
1	C	283	LYS
1	D	24	ASP
1	D	25	LEU
1	D	37	LYS
1	D	60	THR
1	D	95	VAL
1	D	101	TYR
1	D	195	LEU
1	D	204	MET
1	D	231	VAL
1	D	242	GLN
1	D	264	ASN

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Mol	Chain	Res	Type
1	D	273	LYS
1	E	24	ASP
1	E	25	LEU
1	E	67	VAL
1	E	101	TYR
1	E	108	ASP
1	E	117	THR
1	E	195	LEU
1	E	204	MET
1	E	283	LYS
1	F	24	ASP
1	F	37	LYS
1	F	101	TYR
1	F	148	TYR
1	F	178	ASN
1	F	195	LEU
1	F	204	MET
1	F	291	MET
1	G	12	THR
1	G	25	LEU
1	G	37	LYS
1	G	60	THR
1	G	101	TYR
1	G	178	ASN
1	G	179	TRP
1	G	195	LEU
1	G	231	VAL
1	G	240	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (51) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	17	ASN
1	A	64	GLN
1	A	74	ASN
1	A	144	HIS
1	A	178	ASN
1	A	242	GLN
1	A	259	HIS
1	B	17	ASN
1	B	64	GLN
1	B	74	ASN

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Mol	Chain	Res	Type
1	B	89	GLN
1	B	144	HIS
1	B	178	ASN
1	B	209	ASN
1	B	242	GLN
1	B	259	HIS
1	C	64	GLN
1	C	74	ASN
1	C	139	ASN
1	C	178	ASN
1	C	201	ASN
1	C	242	GLN
1	C	259	HIS
1	D	74	ASN
1	D	178	ASN
1	D	242	GLN
1	D	244	ASN
1	D	257	GLN
1	D	259	HIS
1	D	264	ASN
1	E	64	GLN
1	E	74	ASN
1	E	139	ASN
1	E	144	HIS
1	E	178	ASN
1	E	242	GLN
1	F	74	ASN
1	F	89	GLN
1	F	123	ASN
1	F	144	HIS
1	F	178	ASN
1	F	242	GLN
1	F	259	HIS
1	G	17	ASN
1	G	64	GLN
1	G	74	ASN
1	G	89	GLN
1	G	123	ASN
1	G	144	HIS
1	G	178	ASN
1	G	201	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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	293/294 (99%)	1.11	50 (17%) 4 4	12, 34, 62, 84	13 (4%)
1	B	292/294 (99%)	0.96	45 (15%) 5 5	16, 33, 64, 79	12 (4%)
1	C	293/294 (99%)	0.63	41 (13%) 6 6	14, 31, 63, 83	16 (5%)
1	D	292/294 (99%)	0.75	32 (10%) 10 11	15, 31, 57, 70	19 (6%)
1	E	293/294 (99%)	1.09	39 (13%) 7 7	18, 32, 57, 79	17 (5%)
1	F	293/294 (99%)	0.77	38 (12%) 7 7	19, 32, 60, 80	19 (6%)
1	G	292/294 (99%)	0.59	29 (9%) 13 13	14, 33, 56, 80	16 (5%)
All	All	2048/2058 (99%)	0.84	274 (13%) 7 7	12, 32, 61, 84	112 (5%)

All (274) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	127	ASP	9.9
1	F	127	ASP	9.1
1	D	128	ASP	7.5
1	A	132	ILE	7.1
1	G	132	ILE	7.0
1	F	179	TRP	6.7
1	G	125	THR	6.6
1	G	127	ASP	6.5
1	A	144	HIS	6.2
1	G	179	TRP	6.2
1	B	129	THR	6.0
1	F	135	LEU	6.0
1	D	130	GLY	5.8
1	A	135	LEU	5.8
1	B	120	PHE	5.8
1	D	127	ASP	5.8
1	A	148	TYR	5.7

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Mol	Chain	Res	Type	RSRZ
1	E	118	TYR	5.6
1	A	179	TRP	5.5
1	B	144	HIS	5.4
1	E	179	TRP	5.4
1	E	124	VAL	5.4
1	D	179	TRP	5.3
1	G	148	TYR	5.3
1	G	128	ASP	5.2
1	C	118	TYR	5.1
1	C	132	ILE	5.1
1	C	179	TRP	5.1
1	C	127	ASP	5.0
1	E	126	GLY	5.0
1	A	127	ASP	4.9
1	B	124	VAL	4.9
1	F	136	ILE	4.9
1	A	120	PHE	4.9
1	F	148	TYR	4.9
1	D	123	ASN	4.9
1	B	132	ILE	4.8
1	C	126	GLY	4.8
1	A	136	ILE	4.8
1	C	136	ILE	4.8
1	F	132	ILE	4.7
1	C	130	GLY	4.7
1	G	144	HIS	4.7
1	F	118	TYR	4.6
1	D	124	VAL	4.6
1	E	68	TYR	4.6
1	B	127	ASP	4.5
1	C	144	HIS	4.5
1	F	126	GLY	4.5
1	B	148	TYR	4.5
1	F	128	ASP	4.4
1	E	67	VAL	4.4
1	G	124	VAL	4.4
1	E	120	PHE	4.3
1	A	131	LYS	4.3
1	F	129	THR	4.3
1	B	258	LEU	4.3
1	C	124	VAL	4.3
1	A	129	THR	4.3

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Mol	Chain	Res	Type	RSRZ
1	E	148	TYR	4.3
1	B	260	TRP	4.2
1	F	124	VAL	4.2
1	B	118	TYR	4.2
1	C	148	TYR	4.2
1	E	125	THR	4.1
1	E	128	ASP	4.1
1	F	258	LEU	4.1
1	F	120	PHE	4.1
1	E	132	ILE	4.1
1	A	133	GLY	4.0
1	E	136	ILE	4.0
1	B	179	TRP	3.9
1	G	133	GLY	3.9
1	G	120	PHE	3.8
1	G	135	LEU	3.8
1	A	124	VAL	3.8
1	E	122	GLY	3.8
1	F	262	SER	3.8
1	B	135	LEU	3.8
1	E	135	LEU	3.8
1	E	262	SER	3.7
1	A	188	ASN	3.7
1	G	136	ILE	3.7
1	E	133	GLY	3.7
1	G	131	LYS	3.6
1	A	261	THR	3.6
1	A	138	ALA	3.6
1	C	125	THR	3.6
1	B	138	ALA	3.6
1	B	123	ASN	3.6
1	G	129	THR	3.5
1	C	123	ASN	3.5
1	C	122	GLY	3.5
1	D	148	TYR	3.5
1	E	131	LYS	3.5
1	B	201	ASN	3.4
1	G	137	GLY	3.4
1	D	135	LEU	3.4
1	C	119	GLY	3.3
1	D	93	ASN	3.3
1	C	200	ARG	3.3

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Mol	Chain	Res	Type	RSRZ
1	A	258	LEU	3.3
1	A	260	TRP	3.3
1	C	73	ALA	3.2
1	E	191	TYR	3.2
1	C	120	PHE	3.2
1	E	129	THR	3.2
1	F	133	GLY	3.2
1	A	202	GLY	3.2
1	D	120	PHE	3.1
1	G	134	GLY	3.1
1	A	67	VAL	3.1
1	C	135	LEU	3.1
1	D	136	ILE	3.1
1	B	202	GLY	3.1
1	E	130	GLY	3.1
1	C	131	LYS	3.1
1	F	72	GLY	3.0
1	C	263	THR	3.0
1	A	200	ARG	3.0
1	A	199	THR	3.0
1	A	191	TYR	3.0
1	C	138	ALA	3.0
1	G	138	ALA	3.0
1	A	130	GLY	3.0
1	B	178	ASN	3.0
1	D	71	GLU	3.0
1	C	178	ASN	3.0
1	F	178	ASN	3.0
1	G	93	ASN	3.0
1	D	122	GLY	3.0
1	F	125	THR	3.0
1	A	71	GLU	2.9
1	B	73	ALA	2.9
1	C	133	GLY	2.9
1	D	200	ARG	2.9
1	C	68	TYR	2.9
1	A	66	ARG	2.9
1	F	122	GLY	2.9
1	B	72	GLY	2.8
1	C	128	ASP	2.8
1	G	261	THR	2.8
1	B	68	TYR	2.8

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Mol	Chain	Res	Type	RSRZ
1	E	137	GLY	2.8
1	B	268	THR	2.8
1	A	190	VAL	2.8
1	B	131	LYS	2.8
1	A	134	GLY	2.8
1	D	178	ASN	2.7
1	D	92	ASP	2.7
1	F	117	THR	2.7
1	F	77	GLY	2.7
1	B	31	GLU	2.7
1	F	200	ARG	2.7
1	D	125	THR	2.7
1	A	178	ASN	2.7
1	G	178	ASN	2.7
1	B	71	GLU	2.6
1	F	71	GLU	2.6
1	B	136	ILE	2.6
1	F	137	GLY	2.6
1	B	188	ASN	2.6
1	C	264	ASN	2.6
1	E	178	ASN	2.6
1	F	73	ALA	2.6
1	D	131	LYS	2.6
1	C	188	ASN	2.6
1	F	203	SER	2.6
1	B	67	VAL	2.5
1	A	112	TYR	2.5
1	G	130	GLY	2.5
1	A	201	ASN	2.5
1	B	74	ASN	2.5
1	F	123	ASN	2.5
1	A	125	THR	2.5
1	A	189	PRO	2.5
1	A	207	ALA	2.5
1	E	260	TRP	2.5
1	C	191	TYR	2.5
1	F	188	ASN	2.5
1	G	123	ASN	2.5
1	G	260	TRP	2.5
1	D	140	VAL	2.5
1	E	14	ILE	2.5
1	B	203	SER	2.5

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Mol	Chain	Res	Type	RSRZ
1	B	270	THR	2.5
1	D	258	LEU	2.5
1	E	74	ASN	2.5
1	F	260	TRP	2.5
1	D	132	ILE	2.5
1	E	70	GLU	2.4
1	F	207	ALA	2.4
1	C	71	GLU	2.4
1	E	31	GLU	2.4
1	A	268	THR	2.4
1	D	268	THR	2.4
1	G	108	ASP	2.4
1	D	69	SER	2.4
1	A	118	TYR	2.4
1	B	191	TYR	2.4
1	C	258	LEU	2.4
1	A	122	GLY	2.4
1	A	123	ASN	2.4
1	D	188	ASN	2.4
1	B	277	ARG	2.4
1	C	141	SER	2.4
1	C	129	THR	2.4
1	C	93	ASN	2.3
1	E	192	GLY	2.3
1	A	72	GLY	2.3
1	C	134	GLY	2.3
1	D	134	GLY	2.3
1	B	259	HIS	2.3
1	G	117	THR	2.3
1	C	139	ASN	2.3
1	F	74	ASN	2.3
1	B	206	ALA	2.3
1	B	187	TRP	2.3
1	B	200	ARG	2.3
1	C	66	ARG	2.3
1	A	128	ASP	2.3
1	A	137	GLY	2.3
1	A	242	GLN	2.2
1	G	17	ASN	2.2
1	A	283	LYS	2.2
1	B	130	GLY	2.2
1	A	69	SER	2.2

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Mol	Chain	Res	Type	RSRZ
1	E	69	SER	2.2
1	B	140	VAL	2.2
1	D	126	GLY	2.2
1	E	73	ALA	2.2
1	D	68	TYR	2.2
1	D	201	ASN	2.2
1	E	72	GLY	2.2
1	E	1	ALA	2.2
1	B	78	LEU	2.2
1	A	277	ARG	2.2
1	F	75	LYS	2.2
1	G	240	LYS	2.2
1	C	201	ASN	2.2
1	E	188	ASN	2.2
1	A	187	TRP	2.2
1	E	187	TRP	2.2
1	E	277	ARG	2.1
1	A	239	SER	2.1
1	C	74	ASN	2.1
1	D	17	ASN	2.1
1	F	92	ASP	2.1
1	E	257	GLN	2.1
1	B	126	GLY	2.1
1	C	67	VAL	2.1
1	C	190	VAL	2.1
1	C	75	LYS	2.1
1	F	239	SER	2.1
1	A	17	ASN	2.1
1	F	191	TYR	2.1
1	B	119	GLY	2.1
1	F	180	GLY	2.1
1	B	125	THR	2.1
1	B	261	THR	2.1
1	E	117	THR	2.1
1	E	256	TYR	2.1
1	D	190	VAL	2.1
1	F	140	VAL	2.1
1	D	1	ALA	2.1
1	D	138	ALA	2.1
1	F	76	SER	2.1
1	G	188	ASN	2.0
1	B	134	GLY	2.0

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Mol	Chain	Res	Type	RSRZ
1	G	122	GLY	2.0
1	A	141	SER	2.0
1	B	76	SER	2.0
1	A	274	TRP	2.0
1	A	259	HIS	2.0

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides 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.