



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 06:00 PM UTC

PDB ID : 2C45 / pdb_00002c45
Title : NATIVE PRECURSOR OF PYRUVATE DEHYDROGENASE
Authors : Gopalan, G.; Chopra, S.; Ranganathan, A.; Swaminathan, K.
Deposited on : 2005-10-15
Resolution : 2.99 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:

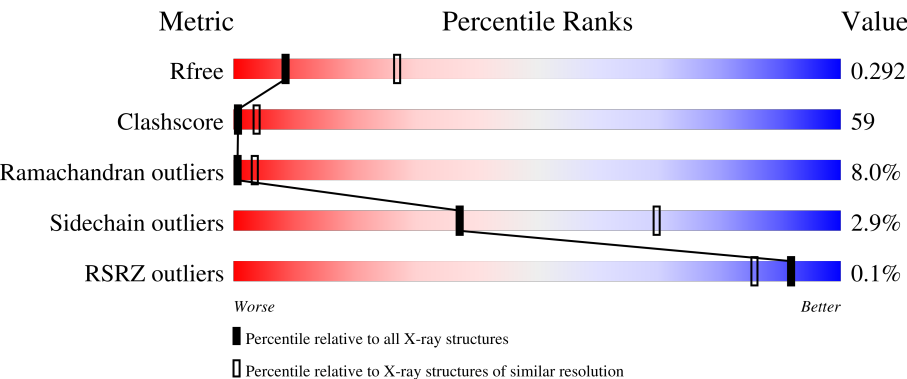
MolProbity	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)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

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.99 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	2672 (3.00-3.00)
Clashscore	190562	2977 (3.00-3.00)
Ramachandran outliers	187476	2877 (3.00-3.00)
Sidechain outliers	187428	2880 (3.00-3.00)
RSRZ outliers	180081	2671 (3.00-3.00)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments 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	139	33% 38% 9% • 18%
1	B	139	24% 48% 9% • 18%
1	C	139	31% 42% 7% • 18%
1	D	139	31% 40% 9% • 18%
1	E	139	% 28% 44% 9% • 18%

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Mol	Chain	Length	Quality of chain
1	F	139	32%42%8%18%
1	G	139	27%45%9%18%
1	H	139	25%47%8%18%

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 6881 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 Aspartate 1-decarboxylase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	114	Total	C	N	O	S	0	0	1
			854	535	151	163	5			
1	B	114	Total	C	N	O	S	0	0	1
			854	535	151	163	5			
1	C	114	Total	C	N	O	S	0	0	1
			854	535	151	163	5			
1	D	114	Total	C	N	O	S	0	0	1
			854	535	151	163	5			
1	E	114	Total	C	N	O	S	0	0	1
			854	535	151	163	5			
1	F	114	Total	C	N	O	S	0	0	1
			854	535	151	163	5			
1	G	114	Total	C	N	O	S	0	0	1
			854	535	151	163	5			
1	H	114	Total	C	N	O	S	0	0	1
			854	535	151	163	5			

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	9	Total	O	0	0
			9	9		
2	B	5	Total	O	0	0
			5	5		
2	C	5	Total	O	0	0
			5	5		
2	D	3	Total	O	0	0
			3	3		
2	E	9	Total	O	0	0
			9	9		
2	F	4	Total	O	0	0
			4	4		

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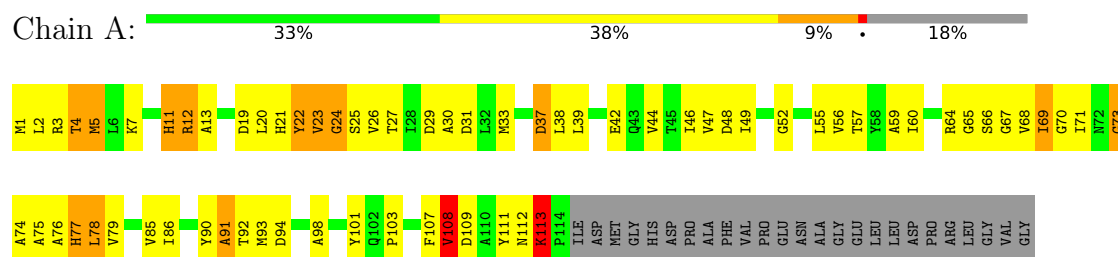
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	G	9	Total	O	0	0
			9	9		
2	H	5	Total	O	0	0
			5	5		

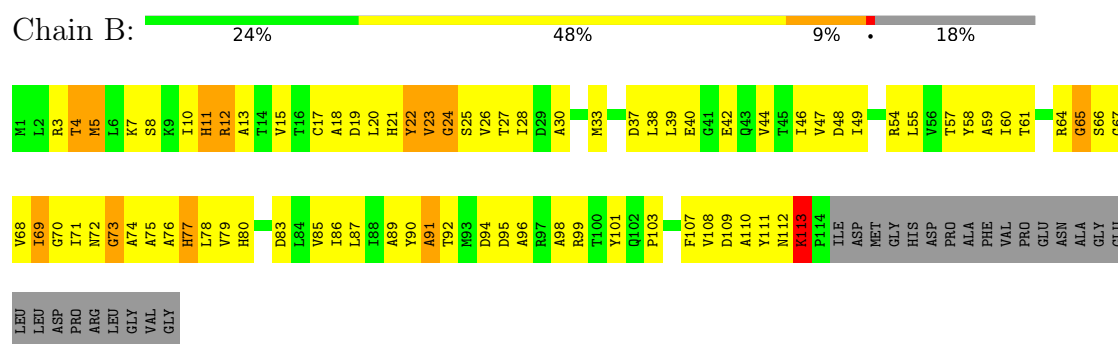
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry 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.

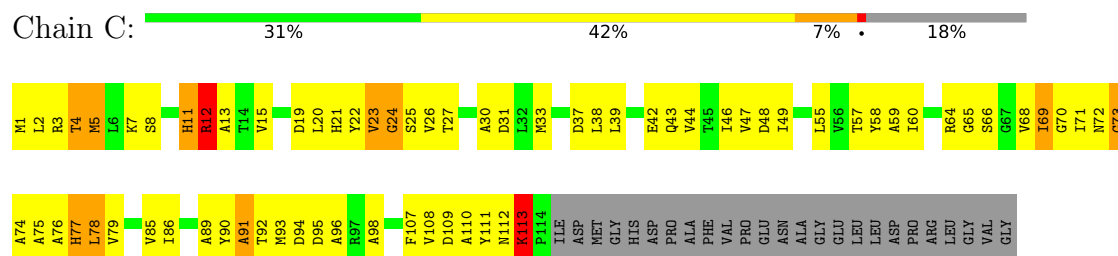
• Molecule 1: Aspartate 1-decarboxylase



• Molecule 1: Aspartate 1-decarboxylase

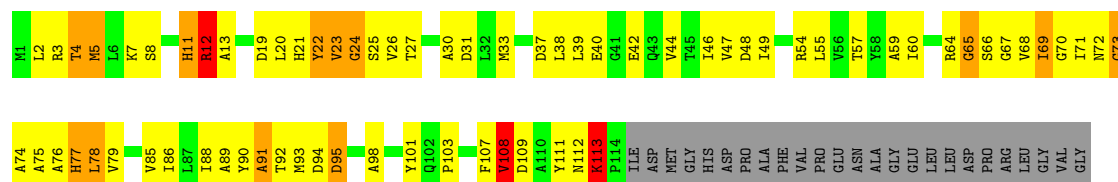


• Molecule 1: Aspartate 1-decarboxylase

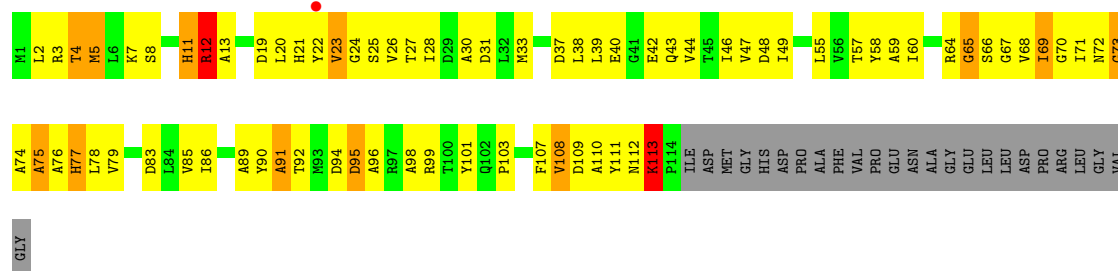


• Molecule 1: Aspartate 1-decarboxylase

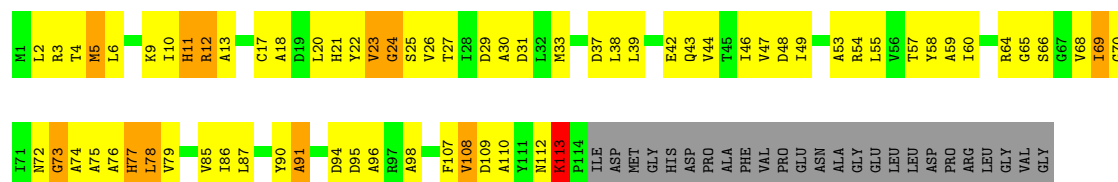
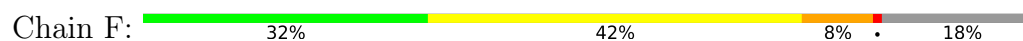




• Molecule 1: Aspartate 1-decarboxylase



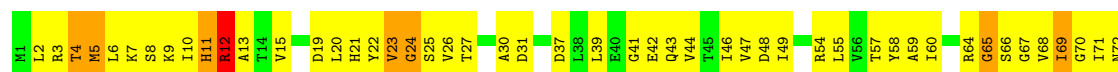
• Molecule 1: Aspartate 1-decarboxylase



• Molecule 1: Aspartate 1-decarboxylase



• Molecule 1: Aspartate 1-decarboxylase



G73	A74	A75	A76	H77	L78	V79	H80		D83	L84	V85	I86	L87	I88	A89	Y90	A91	T92	M93	D94	D95	A96	R97	A98	R99		F107	V108	D109	A110	Y111	N112	R113	P114	ILE	ASP	MET	GLY	HIS	ASP	PRO	ALA	PHE	VAL	PRO	GLU	ASN	ALA	GLY	GLU	LEU	LEU	ASP	PRO	ARG	LEU	GLY	VAL	GLY
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4 Data and refinement statistics

Property	Value	Source
Space group	P 31	Depositor
Cell constants a, b, c, α , β , γ	150.10Å 150.10Å 60.19Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	7.99 – 2.99 7.99 – 2.99	Depositor EDS
% Data completeness (in resolution range)	78.3 (7.99-2.99) 78.4 (7.99-2.99)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.93 (at 2.81Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.265 , 0.308 0.273 , 0.292	Depositor DCC
R_{free} test set	2095 reflections (8.20%)	wwPDB-VP
Wilson B-factor (Å ²)	49.7	Xtriage
Anisotropy	0.074	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 96.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.42$, $\langle L^2 \rangle = 0.24$	Xtriage
Estimated twinning fraction	0.097 for -h,-k,l 0.459 for h,-h-k,-l 0.095 for -k,-h,-l	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	6881	wwPDB-VP
Average B, all atoms (Å ²)	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 23.68 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 4.4487e-03.*

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 ⓘ

5.1 Standard geometry ⓘ

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.66	1/865 (0.1%)	1.13	6/1176 (0.5%)
1	B	0.64	1/865 (0.1%)	1.08	5/1176 (0.4%)
1	C	0.65	1/865 (0.1%)	1.10	6/1176 (0.5%)
1	D	0.69	1/865 (0.1%)	1.11	7/1176 (0.6%)
1	E	0.66	1/865 (0.1%)	1.13	7/1176 (0.6%)
1	F	0.65	1/865 (0.1%)	1.09	5/1176 (0.4%)
1	G	0.60	1/865 (0.1%)	1.12	8/1176 (0.7%)
1	H	0.68	1/865 (0.1%)	1.11	6/1176 (0.5%)
All	All	0.65	8/6920 (0.1%)	1.11	50/9408 (0.5%)

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	H	113	LYS	C-N	-5.96	1.25	1.34
1	A	113	LYS	C-N	-5.94	1.25	1.34
1	D	113	LYS	C-N	-5.93	1.25	1.34
1	F	113	LYS	C-N	-5.77	1.25	1.34
1	E	113	LYS	C-N	-5.62	1.25	1.34
1	G	113	LYS	C-N	-5.56	1.25	1.34
1	C	113	LYS	C-N	-5.47	1.25	1.34
1	B	113	LYS	C-N	-5.26	1.26	1.34

All (50) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	77	HIS	N-CA-C	-9.11	95.74	109.86
1	C	77	HIS	N-CA-C	-8.99	95.92	109.86
1	E	77	HIS	N-CA-C	-8.95	96.00	109.86
1	H	77	HIS	N-CA-C	-8.80	96.71	110.36
1	A	77	HIS	N-CA-C	-8.77	96.27	109.86
1	G	77	HIS	N-CA-C	-8.26	97.05	109.86
1	D	77	HIS	N-CA-C	-8.09	97.32	109.86
1	A	11	HIS	N-CA-C	7.67	120.57	108.67

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	77	HIS	N-CA-C	-7.52	98.20	109.86
1	B	11	HIS	N-CA-C	7.49	120.28	108.67
1	H	11	HIS	N-CA-C	7.44	120.20	108.67
1	A	23	VAL	N-CA-C	7.30	119.99	108.89
1	B	23	VAL	N-CA-C	7.20	119.83	108.89
1	G	5	MET	N-CA-C	7.14	120.03	109.24
1	A	5	MET	N-CA-C	7.02	120.11	109.23
1	G	23	VAL	N-CA-C	6.98	119.50	108.89
1	H	5	MET	N-CA-C	6.87	119.61	109.24
1	G	11	HIS	N-CA-C	6.81	119.67	109.25
1	C	11	HIS	N-CA-C	6.78	119.62	109.25
1	G	107	PHE	N-CA-C	-6.75	101.62	110.53
1	B	107	PHE	N-CA-C	-6.71	100.55	110.48
1	F	11	HIS	N-CA-C	6.70	119.06	108.67
1	C	23	VAL	N-CA-C	6.68	119.33	108.97
1	F	107	PHE	N-CA-C	-6.62	100.68	110.48
1	B	5	MET	N-CA-C	6.62	119.13	109.07
1	D	23	VAL	N-CA-C	6.61	119.22	108.97
1	E	23	VAL	N-CA-C	6.61	118.93	108.89
1	D	5	MET	N-CA-C	6.58	119.17	109.24
1	E	11	HIS	N-CA-C	6.57	119.30	109.25
1	H	107	PHE	N-CA-C	-6.57	100.76	110.48
1	C	5	MET	N-CA-C	6.40	118.90	109.24
1	E	5	MET	N-CA-C	6.40	119.14	109.23
1	G	12	ARG	N-CA-C	6.31	120.37	111.92
1	H	23	VAL	N-CA-C	6.31	118.75	108.97
1	F	5	MET	N-CA-C	6.26	118.59	109.07
1	E	107	PHE	N-CA-C	-6.24	101.25	110.48
1	C	12	ARG	N-CA-C	6.21	120.25	111.92
1	E	12	ARG	N-CA-C	5.99	119.94	111.92
1	D	11	HIS	N-CA-C	5.91	118.30	109.25
1	F	23	VAL	N-CA-C	5.87	118.07	108.97
1	D	12	ARG	N-CA-C	5.84	119.71	112.58
1	C	107	PHE	N-CA-C	-5.74	101.99	110.48
1	H	12	ARG	N-CA-C	5.66	119.50	111.92
1	G	75	ALA	N-CA-C	-5.51	106.39	113.01
1	A	107	PHE	N-CA-C	-5.51	102.33	110.48
1	D	107	PHE	N-CA-C	-5.47	102.38	110.48
1	E	75	ALA	N-CA-C	-5.46	106.32	112.87
1	G	106	VAL	N-CA-C	5.45	115.38	106.72
1	D	108	VAL	N-CA-C	5.41	117.88	108.90
1	A	108	VAL	N-CA-C	5.26	117.62	108.95

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	854	0	864	117	0
1	B	854	0	864	141	2
1	C	854	0	864	97	0
1	D	854	0	864	119	0
1	E	854	0	864	116	2
1	F	854	0	864	131	0
1	G	854	0	864	155	0
1	H	854	0	864	129	0
2	A	9	0	0	2	0
2	B	5	0	0	0	0
2	C	5	0	0	0	0
2	D	3	0	0	4	0
2	E	9	0	0	0	0
2	F	4	0	0	3	0
2	G	9	0	0	2	0
2	H	5	0	0	4	0
All	All	6881	0	6912	817	2

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 59.

All (817) 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:G:3:ARG:NH1	1:H:39:LEU:HG	1.51	1.26
1:A:23:VAL:HG21	1:B:86:ILE:CD1	1.71	1.19
1:C:86:ILE:HD11	1:D:23:VAL:HG21	1.30	1.14
1:B:23:VAL:HG21	1:D:86:ILE:CD1	1.80	1.10
1:B:23:VAL:HG21	1:D:86:ILE:HD11	1.27	1.10
1:A:23:VAL:HG21	1:B:86:ILE:HD11	1.08	1.07
1:A:39:LEU:HD12	1:B:5:MET:HE1	1.32	1.07

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:39:LEU:HD12	1:D:5:MET:HE1	1.38	1.03
1:G:5:MET:HE2	1:H:42:GLU:HG3	1.41	1.03
1:E:39:LEU:HG	1:H:3:ARG:NH1	1.73	1.02
1:E:42:GLU:HG3	1:H:5:MET:HE2	1.43	1.01
1:E:3:ARG:NH1	1:F:39:LEU:HG	1.76	1.00
1:B:39:LEU:HG	1:D:3:ARG:NH1	1.76	0.99
1:A:23:VAL:CG2	1:B:86:ILE:HD11	1.93	0.99
1:F:18:ALA:HB1	2:F:2003:HOH:O	1.63	0.98
1:F:5:MET:HE1	1:G:39:LEU:HD12	1.46	0.98
1:A:3:ARG:NH1	1:C:39:LEU:HG	1.81	0.96
1:F:12:ARG:HH12	1:G:21:HIS:CG	1.84	0.95
1:B:22:TYR:H	1:D:12:ARG:CZ	1.80	0.94
1:E:3:ARG:HH12	1:F:39:LEU:HG	1.28	0.94
1:E:23:VAL:HG23	1:H:11:HIS:HE1	1.31	0.93
1:G:13:ALA:HB1	1:G:69:ILE:HD13	1.50	0.92
1:C:86:ILE:CD1	1:D:23:VAL:HG21	2.00	0.91
1:A:39:LEU:HG	1:B:3:ARG:NH1	1.85	0.90
1:F:5:MET:HE1	1:F:98:ALA:HB1	1.49	0.90
1:A:22:TYR:H	1:B:12:ARG:CZ	1.83	0.90
1:F:12:ARG:HH22	1:G:21:HIS:HA	1.36	0.90
1:G:5:MET:HG2	1:H:42:GLU:HA	1.52	0.89
1:A:22:TYR:N	1:B:12:ARG:NH2	2.20	0.89
1:A:22:TYR:H	1:B:12:ARG:NH2	1.72	0.87
1:B:13:ALA:HB1	1:B:69:ILE:HD13	1.54	0.87
1:E:13:ALA:HB1	1:E:69:ILE:HD13	1.57	0.86
1:B:22:TYR:N	1:D:12:ARG:NH2	2.23	0.86
1:D:26:VAL:HG21	1:D:46:ILE:HD11	1.56	0.86
1:G:3:ARG:HH12	1:H:39:LEU:HG	1.34	0.86
1:E:39:LEU:HG	1:H:3:ARG:HH12	1.39	0.85
1:C:13:ALA:HB1	1:C:69:ILE:HD13	1.57	0.85
1:A:13:ALA:HB1	1:A:69:ILE:HD13	1.59	0.84
1:G:12:ARG:HH12	1:H:21:HIS:CD2	1.96	0.84
1:F:12:ARG:NH2	1:G:21:HIS:HA	1.92	0.83
1:F:11:HIS:CE1	1:G:23:VAL:HB	2.13	0.83
1:F:11:HIS:HE1	1:G:23:VAL:HG23	1.43	0.83
1:G:5:MET:HE1	1:H:39:LEU:HD12	1.59	0.83
1:B:13:ALA:HB1	1:B:69:ILE:CD1	2.09	0.83
1:H:13:ALA:HB1	1:H:69:ILE:HD13	1.59	0.82
1:D:13:ALA:HB1	1:D:69:ILE:HD13	1.59	0.82
1:F:11:HIS:CE1	1:G:23:VAL:H	1.97	0.81
1:F:13:ALA:HB1	1:F:69:ILE:HD13	1.61	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:3:ARG:NH1	1:G:39:LEU:HG	1.95	0.81
1:D:13:ALA:HB1	1:D:69:ILE:CD1	2.10	0.81
1:B:22:TYR:H	1:D:12:ARG:NH2	1.78	0.80
1:A:21:HIS:HA	1:B:12:ARG:HH22	1.45	0.80
1:B:26:VAL:HG21	1:B:46:ILE:HD11	1.63	0.80
1:C:5:MET:HE1	1:D:39:LEU:HD12	1.63	0.80
1:G:26:VAL:HG21	1:G:46:ILE:HD11	1.64	0.80
1:A:13:ALA:HB1	1:A:69:ILE:CD1	2.13	0.79
1:H:3:ARG:HD2	1:H:5:MET:CE	2.12	0.79
1:B:23:VAL:CG2	1:D:86:ILE:HD11	2.12	0.79
1:E:47:VAL:CG2	1:E:86:ILE:HB	2.13	0.79
1:D:108:VAL:HG22	1:D:113:LYS:H	1.47	0.79
1:E:23:VAL:HG23	1:H:11:HIS:CE1	2.17	0.79
1:H:13:ALA:HB1	1:H:69:ILE:CD1	2.12	0.79
1:A:3:ARG:HH12	1:C:39:LEU:HG	1.47	0.79
1:H:26:VAL:HG21	1:H:46:ILE:HD11	1.64	0.79
1:A:26:VAL:HG21	1:A:46:ILE:HD11	1.65	0.78
1:G:13:ALA:HB1	1:G:69:ILE:CD1	2.12	0.78
1:G:108:VAL:HG22	1:G:113:LYS:H	1.48	0.78
1:H:108:VAL:HG22	1:H:113:LYS:H	1.48	0.78
1:F:86:ILE:CD1	1:G:23:VAL:HG21	2.15	0.77
1:D:3:ARG:HD2	1:D:5:MET:CE	2.15	0.77
1:B:47:VAL:HG22	1:B:86:ILE:HB	1.64	0.77
1:F:5:MET:CE	1:F:98:ALA:HB1	2.14	0.77
1:F:13:ALA:HB1	1:F:69:ILE:CD1	2.15	0.77
1:A:5:MET:HE1	1:A:98:ALA:HB1	1.66	0.77
1:G:47:VAL:CG2	1:G:86:ILE:HB	2.15	0.77
1:H:93:MET:HB2	2:H:2005:HOH:O	1.85	0.76
1:C:13:ALA:HB1	1:C:69:ILE:CD1	2.14	0.76
1:C:25:SER:HB2	1:C:57:THR:OG1	1.85	0.76
1:E:13:ALA:HB1	1:E:69:ILE:CD1	2.16	0.76
1:F:12:ARG:HH12	1:G:21:HIS:HA	1.50	0.76
1:F:26:VAL:HG21	1:F:46:ILE:HD11	1.66	0.76
1:E:21:HIS:CG	1:H:12:ARG:HH12	2.03	0.76
1:C:26:VAL:HG21	1:C:46:ILE:HD11	1.67	0.75
1:B:23:VAL:HG21	1:D:86:ILE:HD13	1.68	0.75
1:E:43:GLN:HG3	1:H:90:TYR:CE2	2.21	0.75
1:G:11:HIS:HE1	1:H:23:VAL:HG23	1.52	0.75
1:F:108:VAL:HG22	1:F:113:LYS:H	1.51	0.74
1:F:11:HIS:CE1	1:G:23:VAL:CB	2.70	0.74
1:B:21:HIS:HA	1:D:12:ARG:HH22	1.51	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:68:VAL:O	1:E:69:ILE:HG13	1.88	0.73
1:H:68:VAL:O	1:H:69:ILE:HG13	1.88	0.73
1:C:47:VAL:HG22	1:C:86:ILE:HB	1.69	0.73
1:F:12:ARG:NH1	1:G:21:HIS:HA	2.02	0.73
1:G:47:VAL:HG22	1:G:86:ILE:HB	1.68	0.73
1:B:22:TYR:H	1:D:12:ARG:NH1	1.86	0.73
1:B:47:VAL:CG2	1:B:86:ILE:HB	2.19	0.72
1:C:49:ILE:HD11	1:C:86:ILE:HG13	1.72	0.72
1:E:23:VAL:CG2	1:H:11:HIS:HE1	2.01	0.72
1:E:23:VAL:CG2	1:H:11:HIS:CE1	2.72	0.72
1:C:47:VAL:CG2	1:C:86:ILE:HB	2.19	0.72
1:E:26:VAL:HG21	1:E:46:ILE:HD11	1.72	0.72
1:H:3:ARG:HB2	1:H:5:MET:HE3	1.72	0.71
1:H:98:ALA:HB2	2:H:2005:HOH:O	1.89	0.71
1:F:11:HIS:CE1	1:G:23:VAL:N	2.58	0.70
1:A:39:LEU:HG	1:B:3:ARG:HH11	1.54	0.70
1:G:49:ILE:HD11	1:G:86:ILE:HG13	1.72	0.70
1:E:49:ILE:HD11	1:E:86:ILE:HG13	1.73	0.69
1:F:47:VAL:CG2	1:F:86:ILE:HB	2.23	0.69
1:F:11:HIS:CE1	1:G:23:VAL:HG23	2.26	0.69
1:F:3:ARG:HB2	1:F:5:MET:HE3	1.73	0.69
1:G:66:SER:OG	1:G:68:VAL:HG23	1.92	0.69
1:G:25:SER:HB2	1:G:57:THR:OG1	1.93	0.69
1:H:47:VAL:CG2	1:H:86:ILE:HB	2.23	0.69
1:A:39:LEU:CD1	1:B:5:MET:HE1	2.18	0.68
1:F:12:ARG:CZ	1:G:21:HIS:HA	2.23	0.68
1:A:66:SER:OG	1:A:68:VAL:HG23	1.92	0.68
1:C:12:ARG:NH1	1:D:22:TYR:H	1.92	0.68
1:F:11:HIS:HE1	1:G:23:VAL:CG2	2.06	0.68
1:F:12:ARG:NH1	1:G:21:HIS:CG	2.60	0.68
1:A:39:LEU:HD12	1:B:5:MET:CE	2.18	0.68
1:E:21:HIS:CD2	1:H:12:ARG:HH12	2.12	0.68
1:C:12:ARG:CZ	1:D:22:TYR:H	2.07	0.68
1:D:26:VAL:CG2	1:D:46:ILE:HD11	2.24	0.68
1:D:30:ALA:HB3	1:D:64:ARG:HG2	1.76	0.68
1:H:49:ILE:HD11	1:H:86:ILE:HG13	1.74	0.68
1:E:73:GLY:HA3	2:H:2003:HOH:O	1.94	0.67
1:G:90:TYR:OH	1:H:57:THR:HA	1.94	0.67
1:E:27:THR:HA	1:E:60:ILE:O	1.95	0.67
1:D:30:ALA:HB3	1:D:64:ARG:CG	2.25	0.67
1:A:23:VAL:CG2	1:B:86:ILE:CD1	2.63	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:3:ARG:HD2	1:E:5:MET:CE	2.24	0.67
1:E:47:VAL:HG22	1:E:86:ILE:HB	1.74	0.67
1:A:5:MET:CE	1:A:98:ALA:HB1	2.24	0.67
1:C:108:VAL:HG22	1:C:113:LYS:H	1.59	0.67
1:A:5:MET:HE2	1:C:42:GLU:HG3	1.76	0.66
1:A:47:VAL:HG22	1:A:86:ILE:HB	1.77	0.66
1:G:54:ARG:CZ	1:H:55:LEU:HD22	2.25	0.66
1:H:47:VAL:HG22	1:H:86:ILE:HB	1.76	0.66
1:E:5:MET:HE1	1:E:98:ALA:HB1	1.76	0.66
1:F:49:ILE:HD11	1:F:86:ILE:HG13	1.77	0.66
1:B:39:LEU:HG	1:D:3:ARG:HH12	1.57	0.66
1:B:77:HIS:O	1:B:79:VAL:N	2.29	0.66
1:E:108:VAL:HG22	1:E:113:LYS:H	1.60	0.66
1:F:3:ARG:HD2	1:F:5:MET:CE	2.25	0.66
1:G:5:MET:HE1	1:G:98:ALA:HB1	1.76	0.66
1:E:44:VAL:HG21	1:E:59:ALA:HB2	1.79	0.65
1:E:25:SER:HB2	1:E:57:THR:OG1	1.96	0.65
1:A:49:ILE:HD11	1:A:86:ILE:HG13	1.78	0.65
1:D:47:VAL:HG22	1:D:86:ILE:HB	1.78	0.65
1:F:12:ARG:HH12	1:G:21:HIS:CB	2.10	0.65
1:E:24:GLY:CA	1:E:60:ILE:HD12	2.27	0.65
1:F:12:ARG:HH12	1:G:21:HIS:CA	2.08	0.65
1:B:44:VAL:HG21	1:B:59:ALA:HB2	1.79	0.65
1:E:58:TYR:CD1	1:H:6:LEU:HD22	2.32	0.65
1:F:55:LEU:HD21	1:F:78:LEU:HD13	1.79	0.65
1:F:11:HIS:CE1	1:G:23:VAL:CG2	2.80	0.65
1:G:24:GLY:CA	1:G:60:ILE:HD12	2.26	0.64
1:H:24:GLY:CA	1:H:60:ILE:HD12	2.26	0.64
1:G:12:ARG:NH1	1:H:21:HIS:CD2	2.65	0.64
1:H:108:VAL:HG22	1:H:113:LYS:N	2.12	0.64
1:G:98:ALA:HB1	1:H:39:LEU:HD12	1.79	0.64
1:F:47:VAL:HG22	1:F:86:ILE:HB	1.78	0.64
1:F:68:VAL:O	1:F:69:ILE:HG13	1.98	0.64
1:G:26:VAL:CG2	1:G:46:ILE:HD11	2.27	0.64
1:E:5:MET:CE	1:E:98:ALA:HB1	2.28	0.64
1:F:12:ARG:NH2	1:G:20:LEU:O	2.31	0.64
1:F:66:SER:OG	1:F:68:VAL:HG23	1.98	0.63
1:A:30:ALA:HB3	1:A:64:ARG:HG2	1.79	0.63
1:F:86:ILE:HD13	1:G:23:VAL:HG21	1.81	0.63
1:G:5:MET:SD	1:H:41:GLY:O	2.57	0.63
1:B:26:VAL:HA	1:B:70:GLY:O	1.99	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:12:ARG:HH12	1:H:21:HIS:CG	2.16	0.63
1:H:5:MET:HE1	1:H:98:ALA:HB1	1.80	0.63
1:D:49:ILE:HD11	1:D:86:ILE:HG13	1.80	0.63
1:C:27:THR:HA	1:C:60:ILE:O	1.97	0.63
1:A:23:VAL:HG11	1:B:86:ILE:HD13	1.80	0.63
1:A:108:VAL:HG22	1:A:113:LYS:H	1.63	0.63
1:B:26:VAL:CG2	1:B:46:ILE:HD11	2.28	0.63
1:F:108:VAL:HG22	1:F:113:LYS:N	2.14	0.63
1:A:22:TYR:N	1:B:12:ARG:HH22	1.96	0.63
1:E:39:LEU:HD13	1:H:99:ARG:HA	1.80	0.63
1:A:30:ALA:HB3	1:A:64:ARG:CG	2.29	0.63
1:C:48:ASP:HA	1:C:85:VAL:HG12	1.79	0.63
1:A:3:ARG:HB2	1:A:5:MET:HE3	1.79	0.62
1:B:49:ILE:HD11	1:B:86:ILE:HG13	1.80	0.62
1:C:86:ILE:HD11	1:D:23:VAL:CG2	2.19	0.62
1:A:47:VAL:CG2	1:A:86:ILE:HB	2.29	0.62
2:A:2001:HOH:O	1:C:21:HIS:HB3	1.98	0.62
1:C:24:GLY:CA	1:C:60:ILE:HD12	2.29	0.62
1:G:5:MET:CE	1:G:98:ALA:HB1	2.29	0.62
1:D:3:ARG:HB2	1:D:5:MET:HE3	1.80	0.62
1:D:66:SER:OG	1:D:68:VAL:HG23	2.00	0.62
1:F:27:THR:HA	1:F:60:ILE:O	1.99	0.62
1:G:20:LEU:O	1:G:73:GLY:HA2	1.99	0.62
1:H:5:MET:CE	1:H:98:ALA:HB1	2.29	0.62
1:C:11:HIS:CE1	1:D:23:VAL:HB	2.35	0.62
1:A:24:GLY:CA	1:A:60:ILE:HD12	2.30	0.62
1:B:108:VAL:HG22	1:B:113:LYS:H	1.63	0.62
1:D:108:VAL:HG22	1:D:113:LYS:N	2.14	0.62
1:F:86:ILE:HD11	1:G:23:VAL:HG21	1.82	0.62
1:A:22:TYR:H	1:B:12:ARG:NH1	1.98	0.61
1:B:27:THR:HA	1:B:60:ILE:O	2.00	0.61
1:A:68:VAL:O	1:A:69:ILE:HG13	2.01	0.61
1:F:24:GLY:CA	1:F:60:ILE:HD12	2.30	0.61
1:G:44:VAL:HG21	1:G:59:ALA:HB2	1.81	0.61
1:C:3:ARG:NH1	1:D:39:LEU:HG	2.15	0.61
1:E:30:ALA:HB3	1:E:64:ARG:CG	2.30	0.61
1:E:75:ALA:O	1:E:77:HIS:O	2.18	0.61
1:B:108:VAL:HG22	1:B:112:ASN:HA	1.83	0.61
1:D:47:VAL:CG2	1:D:86:ILE:HB	2.31	0.61
1:E:20:LEU:O	1:E:73:GLY:HA2	2.01	0.61
1:E:57:THR:HA	1:H:90:TYR:OH	2.01	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:26:VAL:CG2	1:F:46:ILE:HD11	2.30	0.61
1:B:30:ALA:HB3	1:B:64:ARG:CG	2.30	0.61
1:G:108:VAL:HG22	1:G:113:LYS:N	2.16	0.61
1:B:39:LEU:HG	1:D:3:ARG:HH11	1.63	0.61
1:E:3:ARG:HB2	1:E:5:MET:HE3	1.83	0.61
1:E:11:HIS:HE1	1:F:23:VAL:HG23	1.65	0.61
1:G:20:LEU:HD13	1:G:76:ALA:HB3	1.83	0.60
1:G:12:ARG:HH22	1:H:21:HIS:HA	1.66	0.60
1:D:68:VAL:O	1:D:69:ILE:HG13	2.01	0.60
1:C:20:LEU:O	1:C:73:GLY:HA2	2.01	0.60
1:B:3:ARG:HD2	1:B:5:MET:CE	2.31	0.60
1:E:26:VAL:CG2	1:E:46:ILE:HD11	2.31	0.60
1:A:26:VAL:CG2	1:A:46:ILE:HD11	2.31	0.60
1:A:48:ASP:HA	1:A:85:VAL:HG12	1.84	0.60
1:E:77:HIS:O	1:E:79:VAL:N	2.33	0.60
1:E:21:HIS:HA	1:H:12:ARG:NH2	2.17	0.59
1:E:90:TYR:CE2	1:F:43:GLN:HG3	2.37	0.59
1:C:77:HIS:O	1:C:79:VAL:N	2.34	0.59
1:H:8:SER:OG	1:H:89:ALA:HB3	2.02	0.59
1:E:12:ARG:HH22	1:F:21:HIS:HA	1.66	0.59
1:C:55:LEU:HD13	1:C:75:ALA:HB1	1.84	0.59
1:D:20:LEU:HD13	1:D:76:ALA:HB3	1.85	0.59
1:A:23:VAL:HG21	1:B:86:ILE:HD13	1.74	0.59
1:A:90:TYR:O	1:A:91:ALA:HB2	2.02	0.59
1:F:25:SER:HB2	1:F:57:THR:OG1	2.03	0.59
1:A:56:VAL:HG11	2:A:2004:HOH:O	2.03	0.58
1:C:12:ARG:NH2	1:D:22:TYR:N	2.51	0.58
1:H:90:TYR:O	1:H:91:ALA:HB2	2.03	0.58
1:C:75:ALA:O	1:C:77:HIS:O	2.20	0.58
1:E:21:HIS:HA	1:H:12:ARG:HH22	1.68	0.58
1:F:64:ARG:C	1:F:66:SER:H	2.11	0.58
1:H:109:ASP:C	1:H:111:TYR:H	2.11	0.58
1:A:39:LEU:CG	1:B:3:ARG:NH1	2.65	0.58
1:C:5:MET:CE	1:C:98:ALA:HB1	2.34	0.58
1:A:86:ILE:CD1	1:C:23:VAL:HG21	2.34	0.58
1:C:20:LEU:HD13	1:C:76:ALA:HB3	1.85	0.58
1:C:90:TYR:O	1:C:91:ALA:HB2	2.02	0.58
1:G:108:VAL:HG22	1:G:112:ASN:HA	1.85	0.58
1:C:26:VAL:CG2	1:C:46:ILE:HD11	2.34	0.58
1:D:26:VAL:HA	1:D:70:GLY:O	2.02	0.58
1:F:11:HIS:ND1	1:G:23:VAL:HB	2.18	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:98:ALA:HB1	1:G:39:LEU:HD12	1.86	0.58
1:G:27:THR:HA	1:G:60:ILE:O	2.04	0.58
1:G:77:HIS:O	1:G:79:VAL:N	2.37	0.58
1:A:90:TYR:CE2	1:C:43:GLN:HG3	2.39	0.57
1:D:24:GLY:CA	1:D:60:ILE:HD12	2.35	0.57
1:G:48:ASP:HA	1:G:85:VAL:HG12	1.87	0.57
1:A:75:ALA:O	1:A:77:HIS:O	2.21	0.57
1:B:10:ILE:HD12	1:B:87:LEU:HD12	1.85	0.57
1:G:5:MET:HE2	1:H:42:GLU:CG	2.26	0.57
1:A:22:TYR:N	1:B:12:ARG:CZ	2.60	0.57
1:C:26:VAL:HA	1:C:70:GLY:O	2.05	0.57
1:A:55:LEU:HD13	1:A:75:ALA:HB1	1.86	0.57
1:C:108:VAL:HG22	1:C:113:LYS:N	2.20	0.57
1:G:12:ARG:NH2	1:H:21:HIS:HA	2.20	0.57
1:A:108:VAL:HG22	1:A:112:ASN:HA	1.86	0.57
1:B:48:ASP:HA	1:B:85:VAL:HG12	1.87	0.57
1:C:5:MET:HE1	1:C:98:ALA:HB1	1.86	0.57
1:E:30:ALA:HB3	1:E:64:ARG:HG2	1.85	0.57
1:A:27:THR:HG22	1:A:60:ILE:CG2	2.35	0.57
1:B:64:ARG:C	1:B:66:SER:H	2.13	0.57
1:E:8:SER:OG	1:E:89:ALA:HB3	2.04	0.57
1:E:39:LEU:HD12	1:H:98:ALA:HB1	1.87	0.57
1:E:71:ILE:HD13	1:E:79:VAL:HB	1.87	0.56
1:F:20:LEU:HD13	1:F:76:ALA:HB3	1.86	0.56
1:F:44:VAL:HG21	1:F:59:ALA:HB2	1.86	0.56
1:C:11:HIS:HE1	1:D:23:VAL:HB	1.70	0.56
1:E:39:LEU:HD12	1:H:5:MET:HE1	1.87	0.56
1:H:26:VAL:CG2	1:H:46:ILE:HD11	2.33	0.56
1:A:27:THR:HA	1:A:60:ILE:O	2.05	0.56
1:E:5:MET:HE2	1:F:42:GLU:HG3	1.88	0.56
1:G:25:SER:CB	1:G:57:THR:OG1	2.53	0.56
1:B:24:GLY:CA	1:B:60:ILE:HD12	2.35	0.56
1:F:25:SER:OG	1:F:26:VAL:N	2.36	0.56
1:F:90:TYR:OH	1:G:57:THR:HA	2.05	0.56
1:G:90:TYR:O	1:G:91:ALA:HB2	2.05	0.56
1:F:12:ARG:CZ	1:G:22:TYR:H	2.19	0.56
1:G:100:THR:HB	2:G:2008:HOH:O	2.06	0.56
1:B:22:TYR:N	1:D:12:ARG:HH22	1.99	0.56
1:E:21:HIS:CD2	1:H:12:ARG:NH1	2.73	0.56
1:B:5:MET:CE	1:B:98:ALA:HB1	2.36	0.56
1:F:11:HIS:HE1	1:G:23:VAL:N	2.02	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:21:HIS:CA	1:B:12:ARG:HH22	2.17	0.55
1:C:44:VAL:HG21	1:C:59:ALA:HB2	1.87	0.55
1:H:48:ASP:HA	1:H:85:VAL:HG12	1.88	0.55
1:B:47:VAL:CG2	1:B:86:ILE:HD12	2.36	0.55
1:E:27:THR:HG22	1:E:60:ILE:CG2	2.37	0.55
1:A:77:HIS:O	1:A:79:VAL:N	2.40	0.55
1:G:75:ALA:O	1:G:77:HIS:O	2.25	0.55
1:B:25:SER:HB2	1:B:57:THR:OG1	2.06	0.55
1:G:3:ARG:HB2	1:G:5:MET:HE3	1.88	0.55
1:A:37:ASP:OD1	1:B:3:ARG:NH2	2.40	0.55
1:B:75:ALA:O	1:B:77:HIS:O	2.25	0.55
1:D:64:ARG:C	1:D:66:SER:H	2.15	0.55
1:E:90:TYR:O	1:E:91:ALA:HB2	2.07	0.55
1:G:19:ASP:OD2	1:G:21:HIS:O	2.24	0.55
1:G:108:VAL:CG2	1:G:113:LYS:H	2.18	0.55
1:D:88:ILE:HD13	2:D:2002:HOH:O	2.06	0.55
1:B:20:LEU:HD13	1:B:76:ALA:HB3	1.88	0.54
1:F:74:ALA:C	1:F:76:ALA:H	2.15	0.54
1:B:5:MET:HE1	1:B:98:ALA:HB1	1.90	0.54
1:F:6:LEU:HD22	1:G:58:TYR:CG	2.43	0.54
1:H:19:ASP:OD2	1:H:21:HIS:O	2.25	0.54
1:G:30:ALA:HB3	1:G:64:ARG:CG	2.37	0.54
1:B:30:ALA:HB3	1:B:64:ARG:HG2	1.88	0.54
1:H:25:SER:HB2	1:H:57:THR:OG1	2.07	0.54
1:C:12:ARG:HH22	1:D:21:HIS:HA	1.73	0.54
1:A:3:ARG:HD2	1:A:5:MET:CE	2.38	0.54
1:B:90:TYR:O	1:B:91:ALA:HB2	2.07	0.54
1:C:30:ALA:HB3	1:C:64:ARG:CG	2.37	0.54
1:C:68:VAL:O	1:C:69:ILE:HG13	2.07	0.54
1:B:3:ARG:HB2	1:B:5:MET:HE3	1.90	0.54
1:H:44:VAL:HG21	1:H:59:ALA:HB2	1.89	0.54
1:H:49:ILE:HD12	1:H:49:ILE:H	1.72	0.54
1:A:27:THR:HG22	1:A:60:ILE:HB	1.90	0.54
1:C:2:LEU:HD23	1:C:94:ASP:HA	1.89	0.54
1:A:5:MET:HE1	1:C:39:LEU:HD12	1.90	0.54
1:E:42:GLU:HG3	1:H:5:MET:CE	2.30	0.54
1:E:108:VAL:HG22	1:E:113:LYS:N	2.23	0.54
1:G:26:VAL:HA	1:G:70:GLY:O	2.08	0.54
1:C:64:ARG:C	1:C:66:SER:H	2.16	0.54
1:E:64:ARG:C	1:E:66:SER:H	2.16	0.54
1:G:3:ARG:HD2	1:G:5:MET:CE	2.37	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:24:GLY:H	1:C:72:ASN:HB2	1.73	0.53
1:E:5:MET:HE1	1:F:39:LEU:HD12	1.90	0.53
1:G:55:LEU:HD13	1:G:75:ALA:HB1	1.89	0.53
1:A:55:LEU:CD1	1:A:75:ALA:HB1	2.38	0.53
1:B:66:SER:OG	1:B:68:VAL:HG23	2.07	0.53
1:C:7:LYS:NZ	1:C:42:GLU:OE2	2.40	0.53
1:E:58:TYR:CG	1:H:6:LEU:HD22	2.42	0.53
1:F:90:TYR:O	1:F:91:ALA:HB2	2.07	0.53
1:E:19:ASP:OD2	1:E:21:HIS:O	2.25	0.53
1:G:42:GLU:O	1:G:44:VAL:HG23	2.07	0.53
1:A:108:VAL:HG22	1:A:113:LYS:N	2.23	0.53
1:D:19:ASP:OD2	1:D:21:HIS:O	2.26	0.53
1:E:55:LEU:HD13	1:E:75:ALA:HB1	1.89	0.53
1:B:108:VAL:HG22	1:B:113:LYS:N	2.23	0.53
1:C:33:MET:O	1:C:38:LEU:N	2.40	0.53
1:E:55:LEU:HD22	1:H:54:ARG:CZ	2.39	0.53
1:H:64:ARG:C	1:H:66:SER:H	2.16	0.53
1:D:101:TYR:O	1:D:103:PRO:HD3	2.09	0.53
1:A:55:LEU:HD13	1:A:75:ALA:CB	2.39	0.53
1:D:74:ALA:C	1:D:76:ALA:H	2.17	0.53
1:F:27:THR:HG22	1:F:60:ILE:HB	1.90	0.53
1:B:30:ALA:HB3	1:B:64:ARG:HG3	1.90	0.53
1:F:30:ALA:HB3	1:F:64:ARG:CG	2.38	0.53
1:G:25:SER:OG	1:G:58:TYR:O	2.27	0.53
1:D:20:LEU:O	1:D:73:GLY:HA2	2.09	0.53
1:D:55:LEU:HD13	1:D:75:ALA:HB1	1.91	0.53
1:C:108:VAL:HG22	1:C:112:ASN:HA	1.89	0.53
1:D:5:MET:CE	1:D:98:ALA:HB1	2.39	0.53
1:F:31:ASP:OD1	1:F:64:ARG:NH1	2.42	0.53
1:E:69:ILE:HG22	1:E:69:ILE:O	2.08	0.52
1:B:20:LEU:O	1:B:73:GLY:HA2	2.09	0.52
1:G:68:VAL:O	1:G:69:ILE:HG13	2.09	0.52
1:H:108:VAL:HG22	1:H:112:ASN:HA	1.91	0.52
1:C:3:ARG:HH12	1:D:39:LEU:HG	1.73	0.52
1:E:42:GLU:O	1:E:44:VAL:HG23	2.09	0.52
1:H:13:ALA:CB	1:H:69:ILE:HD13	2.34	0.52
1:E:27:THR:HG22	1:E:60:ILE:HB	1.91	0.52
1:A:74:ALA:C	1:A:76:ALA:N	2.66	0.52
1:D:77:HIS:O	1:D:79:VAL:N	2.41	0.52
1:A:2:LEU:HB2	1:C:92:THR:OG1	2.10	0.52
1:G:27:THR:HG22	1:G:60:ILE:HB	1.90	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:31:ASP:OD1	1:A:64:ARG:NH1	2.42	0.52
1:G:44:VAL:N	1:G:57:THR:O	2.32	0.52
1:E:12:ARG:HH12	1:F:21:HIS:CG	2.28	0.52
1:F:12:ARG:NH1	1:G:21:HIS:CA	2.70	0.52
1:F:90:TYR:CE2	1:G:43:GLN:HG3	2.45	0.52
1:G:5:MET:CE	1:H:42:GLU:HG3	2.28	0.52
1:G:11:HIS:CD2	1:G:12:ARG:HG3	2.45	0.52
1:E:12:ARG:HH12	1:F:21:HIS:CD2	2.28	0.52
1:G:30:ALA:HB3	1:G:64:ARG:HG2	1.92	0.52
1:B:19:ASP:OD2	1:B:21:HIS:O	2.27	0.52
1:D:13:ALA:CB	1:D:69:ILE:HD13	2.36	0.52
1:D:25:SER:HB2	1:D:57:THR:OG1	2.10	0.52
1:D:75:ALA:O	1:D:77:HIS:O	2.27	0.52
1:F:11:HIS:HE1	1:G:23:VAL:CB	2.19	0.52
1:G:74:ALA:C	1:G:76:ALA:H	2.18	0.52
1:H:2:LEU:HD23	1:H:94:ASP:HA	1.92	0.52
1:H:12:ARG:NH2	2:H:2003:HOH:O	2.16	0.52
1:H:30:ALA:HB3	1:H:64:ARG:CG	2.39	0.52
1:B:7:LYS:NZ	1:B:42:GLU:OE2	2.41	0.51
1:C:49:ILE:N	1:C:49:ILE:HD12	2.25	0.51
1:H:26:VAL:HA	1:H:70:GLY:O	2.10	0.51
1:F:49:ILE:H	1:F:49:ILE:HD12	1.76	0.51
1:H:9:LYS:HE2	1:H:11:HIS:HB2	1.92	0.51
1:A:25:SER:OG	1:A:26:VAL:N	2.42	0.51
1:A:39:LEU:HG	1:B:3:ARG:HH12	1.71	0.51
1:B:39:LEU:HD12	1:D:5:MET:CE	2.27	0.51
1:F:55:LEU:HD13	1:F:75:ALA:HB1	1.91	0.51
1:H:25:SER:OG	1:H:26:VAL:N	2.43	0.51
1:A:74:ALA:C	1:A:76:ALA:H	2.17	0.51
1:D:2:LEU:HD23	1:D:94:ASP:HA	1.92	0.51
1:D:69:ILE:HG22	1:D:69:ILE:O	2.10	0.51
1:B:39:LEU:CD1	1:D:5:MET:HE1	2.27	0.51
1:E:24:GLY:HA2	1:E:60:ILE:HD12	1.93	0.51
1:F:30:ALA:HB3	1:F:64:ARG:HG2	1.90	0.51
1:G:49:ILE:HD12	1:G:49:ILE:N	2.25	0.51
1:C:25:SER:OG	1:C:26:VAL:N	2.40	0.51
1:G:64:ARG:C	1:G:66:SER:H	2.19	0.51
1:H:109:ASP:C	1:H:111:TYR:N	2.67	0.51
1:E:25:SER:OG	1:E:26:VAL:N	2.44	0.51
1:C:30:ALA:HB3	1:C:64:ARG:HG2	1.92	0.51
1:D:5:MET:HE1	1:D:98:ALA:HB1	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:47:VAL:CG2	1:D:86:ILE:HD12	2.41	0.51
1:E:25:SER:CB	1:E:57:THR:OG1	2.60	0.50
1:G:27:THR:HG22	1:G:60:ILE:CG2	2.42	0.50
1:B:74:ALA:C	1:B:76:ALA:H	2.19	0.50
1:D:90:TYR:O	1:D:91:ALA:HB2	2.12	0.50
1:D:109:ASP:C	1:D:111:TYR:H	2.19	0.50
1:E:108:VAL:HG22	1:E:112:ASN:HA	1.92	0.50
1:G:8:SER:OG	1:G:89:ALA:HB3	2.10	0.50
1:H:3:ARG:CB	1:H:5:MET:HE3	2.41	0.50
1:A:20:LEU:O	1:A:73:GLY:HA2	2.11	0.50
1:E:57:THR:OG1	1:E:58:TYR:N	2.44	0.50
1:G:33:MET:O	1:G:38:LEU:N	2.41	0.50
1:G:108:VAL:HG22	1:G:109:ASP:H	1.77	0.50
1:C:12:ARG:HH21	1:D:23:VAL:HG23	1.75	0.50
1:G:108:VAL:CG2	1:G:112:ASN:HA	2.42	0.50
1:B:15:VAL:HG23	1:B:83:ASP:O	2.12	0.50
1:D:27:THR:HA	1:D:60:ILE:O	2.11	0.50
1:F:74:ALA:C	1:F:76:ALA:N	2.68	0.50
1:H:31:ASP:OD1	1:H:64:ARG:NH1	2.43	0.50
1:A:25:SER:HB2	1:A:57:THR:OG1	2.11	0.50
1:B:44:VAL:N	1:B:57:THR:O	2.29	0.50
1:B:49:ILE:HD12	1:B:49:ILE:N	2.27	0.50
1:G:108:VAL:CG2	1:G:113:LYS:N	2.74	0.50
1:B:109:ASP:C	1:B:111:TYR:H	2.19	0.50
1:C:86:ILE:HD13	1:D:23:VAL:HG11	1.93	0.50
1:E:7:LYS:NZ	1:E:42:GLU:OE2	2.44	0.50
1:A:12:ARG:HH22	1:C:21:HIS:HA	1.77	0.50
1:A:64:ARG:C	1:A:66:SER:H	2.19	0.50
1:B:68:VAL:O	1:B:69:ILE:HG13	2.12	0.50
1:C:3:ARG:HB2	1:C:5:MET:HE3	1.94	0.50
1:E:30:ALA:HB3	1:E:64:ARG:HG3	1.93	0.50
1:B:55:LEU:HD13	1:B:75:ALA:HB1	1.92	0.49
1:C:19:ASP:OD2	1:C:21:HIS:O	2.30	0.49
1:C:24:GLY:N	1:C:72:ASN:HB2	2.26	0.49
1:E:13:ALA:CB	1:E:69:ILE:HD13	2.35	0.49
1:G:54:ARG:NE	1:H:55:LEU:HD22	2.26	0.49
1:B:21:HIS:CA	1:D:12:ARG:HH22	2.21	0.49
1:F:5:MET:HG2	1:G:42:GLU:HG3	1.94	0.49
1:F:12:ARG:NH1	1:G:21:HIS:CD2	2.79	0.49
1:B:22:TYR:N	1:D:12:ARG:CZ	2.58	0.49
1:D:27:THR:HG22	1:D:60:ILE:HB	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:44:VAL:HG21	1:D:59:ALA:HB2	1.94	0.49
1:F:5:MET:CE	1:G:39:LEU:HD12	2.30	0.49
1:F:48:ASP:HA	1:F:85:VAL:HG12	1.94	0.49
1:A:26:VAL:HA	1:A:70:GLY:O	2.12	0.49
1:C:25:SER:CB	1:C:57:THR:OG1	2.58	0.49
1:D:48:ASP:HA	1:D:85:VAL:HG12	1.95	0.49
1:D:74:ALA:C	1:D:76:ALA:N	2.67	0.49
1:E:94:ASP:O	1:E:96:ALA:N	2.45	0.49
1:G:7:LYS:NZ	1:G:42:GLU:OE2	2.45	0.49
1:H:55:LEU:HD13	1:H:75:ALA:HB1	1.95	0.49
1:A:49:ILE:HD12	1:A:49:ILE:H	1.78	0.49
1:F:3:ARG:HH11	1:G:39:LEU:HG	1.76	0.49
1:H:30:ALA:HB3	1:H:64:ARG:HG3	1.95	0.49
1:A:90:TYR:OH	1:C:57:THR:HA	2.12	0.49
1:D:109:ASP:C	1:D:111:TYR:N	2.70	0.49
1:B:27:THR:HG22	1:B:60:ILE:HB	1.94	0.49
1:G:109:ASP:C	1:G:111:TYR:H	2.18	0.49
1:H:24:GLY:HA2	1:H:60:ILE:HD12	1.94	0.49
1:A:2:LEU:HD23	1:A:94:ASP:HA	1.95	0.49
1:B:109:ASP:OD1	1:B:110:ALA:N	2.46	0.49
1:G:49:ILE:HD12	1:G:49:ILE:H	1.78	0.49
1:H:20:LEU:HD13	1:H:76:ALA:HB3	1.93	0.49
1:H:108:VAL:CG2	1:H:113:LYS:N	2.75	0.49
1:E:11:HIS:HE1	1:F:23:VAL:CG2	2.24	0.48
1:E:33:MET:O	1:E:38:LEU:N	2.45	0.48
1:G:90:TYR:CE2	1:H:43:GLN:HG3	2.47	0.48
1:G:101:TYR:O	1:G:103:PRO:HD3	2.13	0.48
1:A:86:ILE:HD11	1:C:23:VAL:HG21	1.95	0.48
1:E:4:THR:HA	1:E:92:THR:HA	1.95	0.48
1:B:8:SER:OG	1:B:89:ALA:HB3	2.11	0.48
1:B:33:MET:O	1:B:38:LEU:N	2.46	0.48
1:D:47:VAL:HG23	1:D:86:ILE:HD12	1.95	0.48
1:F:64:ARG:O	1:F:66:SER:N	2.46	0.48
1:G:13:ALA:CB	1:G:69:ILE:HD13	2.35	0.48
1:G:23:VAL:CG1	1:G:24:GLY:N	2.75	0.48
1:G:69:ILE:HG22	1:G:69:ILE:O	2.13	0.48
1:G:86:ILE:HD13	1:H:23:VAL:HG21	1.95	0.48
1:A:13:ALA:CB	1:A:69:ILE:HD13	2.40	0.48
1:G:69:ILE:HD12	1:G:112:ASN:ND2	2.29	0.48
1:H:24:GLY:HA2	1:H:60:ILE:CD1	2.43	0.48
1:B:4:THR:O	1:B:5:MET:HG2	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:71:ILE:CD1	1:D:79:VAL:HG12	2.43	0.48
1:H:27:THR:HG22	1:H:60:ILE:HB	1.96	0.48
1:B:109:ASP:C	1:B:111:TYR:N	2.72	0.48
1:H:108:VAL:HG22	1:H:109:ASP:H	1.77	0.48
1:C:15:VAL:HG11	1:C:71:ILE:HD12	1.96	0.48
1:C:49:ILE:HD12	1:C:49:ILE:H	1.78	0.48
1:F:26:VAL:HA	1:F:70:GLY:O	2.13	0.48
1:H:27:THR:HA	1:H:60:ILE:O	2.13	0.48
1:B:71:ILE:HD13	1:B:79:VAL:HB	1.96	0.48
1:G:10:ILE:HD12	1:G:87:LEU:HD12	1.96	0.48
1:G:109:ASP:C	1:G:111:TYR:N	2.71	0.48
1:C:11:HIS:CD2	1:C:12:ARG:HG3	2.48	0.47
1:D:30:ALA:HB3	1:D:64:ARG:HG3	1.94	0.47
1:D:108:VAL:CG2	1:D:113:LYS:H	2.23	0.47
1:B:39:LEU:CG	1:D:3:ARG:NH1	2.65	0.47
1:D:71:ILE:HD13	1:D:79:VAL:HB	1.96	0.47
1:G:11:HIS:CE1	1:H:23:VAL:HG23	2.41	0.47
1:A:109:ASP:C	1:A:111:TYR:H	2.20	0.47
1:C:24:GLY:HA2	1:C:60:ILE:HD12	1.97	0.47
1:G:74:ALA:C	1:G:76:ALA:N	2.70	0.47
1:B:69:ILE:HD12	1:B:112:ASN:ND2	2.30	0.47
1:C:74:ALA:C	1:C:76:ALA:N	2.71	0.47
1:D:23:VAL:CG1	1:D:24:GLY:N	2.78	0.47
1:F:12:ARG:NH1	1:G:22:TYR:H	2.12	0.47
1:A:23:VAL:CG1	1:A:24:GLY:N	2.77	0.47
1:A:44:VAL:HG21	1:A:59:ALA:HB2	1.95	0.47
1:D:8:SER:OG	1:D:89:ALA:HB3	2.14	0.47
1:E:31:ASP:OD1	1:E:64:ARG:NH1	2.46	0.47
1:C:3:ARG:HD2	1:C:5:MET:CE	2.45	0.47
1:D:88:ILE:CD1	2:D:2002:HOH:O	2.62	0.47
1:F:20:LEU:O	1:F:73:GLY:HA2	2.14	0.47
1:A:66:SER:CB	1:A:68:VAL:HG23	2.44	0.47
1:A:86:ILE:HD13	1:C:23:VAL:HG21	1.95	0.47
1:B:23:VAL:CG1	1:B:24:GLY:N	2.77	0.47
1:B:108:VAL:HG22	1:B:109:ASP:H	1.80	0.47
1:D:23:VAL:HG12	1:D:24:GLY:N	2.30	0.47
1:E:68:VAL:C	1:E:69:ILE:HG13	2.38	0.47
1:E:71:ILE:HD13	1:E:79:VAL:CG1	2.45	0.47
1:E:74:ALA:C	1:E:76:ALA:H	2.23	0.47
1:F:17:CYS:SG	1:F:18:ALA:N	2.87	0.47
1:F:77:HIS:O	1:F:79:VAL:N	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:108:VAL:CG2	1:B:112:ASN:HA	2.44	0.47
1:H:49:ILE:HD13	1:H:84:LEU:O	2.14	0.47
1:F:55:LEU:HD13	1:F:75:ALA:CB	2.45	0.47
1:C:55:LEU:HD13	1:C:75:ALA:CB	2.44	0.47
1:D:71:ILE:HD13	1:D:79:VAL:CG1	2.45	0.47
1:F:109:ASP:OD1	1:F:110:ALA:N	2.48	0.47
1:G:4:THR:HA	1:G:92:THR:HA	1.96	0.47
1:H:3:ARG:HD2	1:H:5:MET:HE1	1.95	0.47
1:H:55:LEU:HD21	1:H:78:LEU:HD13	1.97	0.47
1:A:24:GLY:HA3	1:A:60:ILE:HD12	1.96	0.46
1:C:27:THR:HG22	1:C:60:ILE:HB	1.97	0.46
1:E:26:VAL:HA	1:E:70:GLY:O	2.15	0.46
1:G:24:GLY:HA3	1:G:60:ILE:HD12	1.96	0.46
1:C:109:ASP:C	1:C:111:TYR:H	2.23	0.46
1:E:11:HIS:CD2	1:E:12:ARG:HG3	2.50	0.46
1:E:71:ILE:CD1	1:E:79:VAL:HG12	2.46	0.46
1:H:75:ALA:O	1:H:77:HIS:O	2.33	0.46
1:C:12:ARG:CZ	1:D:22:TYR:N	2.76	0.46
1:C:49:ILE:HD11	1:C:86:ILE:CG1	2.42	0.46
1:D:31:ASP:OD1	1:D:64:ARG:NH1	2.49	0.46
1:H:49:ILE:HD12	1:H:49:ILE:N	2.29	0.46
1:A:108:VAL:HG22	1:A:109:ASP:H	1.81	0.46
1:B:4:THR:HA	1:B:92:THR:HA	1.97	0.46
1:C:27:THR:HG22	1:C:60:ILE:CG2	2.46	0.46
1:C:74:ALA:C	1:C:76:ALA:H	2.22	0.46
1:C:109:ASP:C	1:C:111:TYR:N	2.73	0.46
1:E:44:VAL:N	1:E:57:THR:O	2.29	0.46
1:E:109:ASP:C	1:E:111:TYR:H	2.24	0.46
1:B:13:ALA:CB	1:B:69:ILE:HD13	2.34	0.46
1:C:55:LEU:CD1	1:C:75:ALA:HB1	2.46	0.46
1:G:31:ASP:OD1	1:G:64:ARG:NH1	2.47	0.46
1:H:57:THR:OG1	1:H:58:TYR:N	2.49	0.46
1:B:57:THR:OG1	1:B:58:TYR:N	2.49	0.46
1:B:64:ARG:O	1:B:66:SER:N	2.47	0.46
1:F:6:LEU:HD22	1:G:58:TYR:CD2	2.50	0.46
1:G:49:ILE:HD11	1:G:86:ILE:CG1	2.44	0.46
1:A:49:ILE:HD12	1:A:49:ILE:N	2.30	0.46
1:D:55:LEU:HD21	1:D:78:LEU:HD13	1.97	0.46
1:E:94:ASP:C	1:E:96:ALA:N	2.71	0.46
1:G:20:LEU:HD11	1:G:77:HIS:NE2	2.31	0.46
1:A:75:ALA:HB2	1:B:54:ARG:NH2	2.31	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:23:VAL:HG12	1:A:24:GLY:N	2.30	0.46
1:B:65:GLY:C	1:B:67:GLY:N	2.74	0.46
1:B:71:ILE:HD13	1:B:79:VAL:CG1	2.46	0.46
1:C:4:THR:HA	1:C:92:THR:HA	1.98	0.46
1:F:55:LEU:CD1	1:F:75:ALA:HB1	2.46	0.46
1:A:108:VAL:CG2	1:A:112:ASN:HA	2.46	0.46
1:F:69:ILE:HD12	1:F:112:ASN:ND2	2.31	0.46
1:A:71:ILE:HD13	1:A:79:VAL:HB	1.98	0.45
1:B:47:VAL:HG21	1:B:86:ILE:HD12	1.98	0.45
1:E:20:LEU:HD11	1:E:77:HIS:NE2	2.31	0.45
1:F:49:ILE:HD12	1:F:49:ILE:N	2.31	0.45
1:G:57:THR:OG1	1:G:58:TYR:N	2.48	0.45
1:H:109:ASP:OD1	1:H:110:ALA:N	2.49	0.45
1:B:27:THR:HG22	1:B:60:ILE:CG2	2.47	0.45
1:B:74:ALA:C	1:B:76:ALA:N	2.70	0.45
1:D:55:LEU:HD13	1:D:75:ALA:CB	2.46	0.45
1:F:12:ARG:HH22	1:G:21:HIS:CA	2.18	0.45
1:B:25:SER:CB	1:B:57:THR:OG1	2.64	0.45
1:B:42:GLU:O	1:B:44:VAL:HG23	2.17	0.45
1:B:57:THR:HA	1:D:90:TYR:OH	2.16	0.45
1:D:47:VAL:HG23	1:D:47:VAL:O	2.16	0.45
1:D:108:VAL:HG22	1:D:112:ASN:HA	1.97	0.45
1:E:71:ILE:CD1	1:E:79:VAL:CG1	2.94	0.45
1:F:33:MET:O	1:F:38:LEU:N	2.49	0.45
1:H:71:ILE:HD13	1:H:79:VAL:CG1	2.47	0.45
1:D:25:SER:OG	1:D:26:VAL:N	2.50	0.45
1:A:20:LEU:HD13	1:A:76:ALA:HB3	1.97	0.45
1:D:108:VAL:CG2	1:D:113:LYS:N	2.79	0.45
1:G:30:ALA:HB3	1:G:64:ARG:HG3	1.99	0.45
1:H:7:LYS:NZ	1:H:42:GLU:OE2	2.49	0.45
1:H:68:VAL:C	1:H:69:ILE:HG13	2.41	0.45
1:B:24:GLY:H	1:B:72:ASN:HB2	1.81	0.45
1:C:13:ALA:CB	1:C:69:ILE:HD13	2.39	0.45
1:C:94:ASP:O	1:C:96:ALA:N	2.50	0.45
1:D:7:LYS:NZ	1:D:42:GLU:OE2	2.49	0.45
1:F:68:VAL:C	1:F:69:ILE:HG13	2.42	0.45
1:A:49:ILE:HD11	1:A:86:ILE:CG1	2.47	0.45
1:B:24:GLY:N	1:B:72:ASN:HB2	2.32	0.45
1:C:12:ARG:NH2	1:D:22:TYR:H	2.13	0.45
1:D:4:THR:HA	1:D:92:THR:HA	1.99	0.45
1:E:55:LEU:CD1	1:E:75:ALA:HB1	2.47	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:109:ASP:OD1	1:E:110:ALA:N	2.50	0.45
1:F:12:ARG:CZ	1:G:22:TYR:N	2.80	0.45
1:F:108:VAL:CG2	1:F:113:LYS:N	2.79	0.45
1:G:23:VAL:HG12	1:G:24:GLY:N	2.30	0.45
1:H:20:LEU:O	1:H:73:GLY:HA2	2.16	0.45
1:A:30:ALA:HB3	1:A:64:ARG:HG3	1.98	0.45
1:B:71:ILE:CD1	1:B:79:VAL:HG12	2.46	0.45
1:E:24:GLY:H	1:E:72:ASN:HB2	1.81	0.45
1:F:25:SER:OG	1:F:58:TYR:O	2.31	0.45
1:E:49:ILE:HD12	1:E:49:ILE:H	1.82	0.45
1:A:42:GLU:O	1:A:44:VAL:HG23	2.17	0.44
1:A:109:ASP:C	1:A:111:TYR:N	2.72	0.44
1:E:3:ARG:NH1	1:F:39:LEU:CG	2.65	0.44
1:E:48:ASP:OD1	1:E:83:ASP:OD2	2.35	0.44
1:E:109:ASP:C	1:E:111:TYR:N	2.74	0.44
1:F:108:VAL:HG22	1:F:112:ASN:HA	1.97	0.44
1:A:29:ASP:O	1:A:30:ALA:C	2.60	0.44
1:C:68:VAL:C	1:C:69:ILE:HG13	2.42	0.44
1:D:65:GLY:C	1:D:67:GLY:N	2.76	0.44
1:E:24:GLY:HA2	1:E:60:ILE:CD1	2.47	0.44
1:E:48:ASP:HA	1:E:85:VAL:HG12	1.99	0.44
1:H:24:GLY:H	1:H:72:ASN:HB2	1.83	0.44
1:H:24:GLY:N	1:H:72:ASN:HB2	2.33	0.44
1:A:101:TYR:O	1:A:103:PRO:HD3	2.17	0.44
1:B:17:CYS:SG	1:B:18:ALA:N	2.90	0.44
1:E:28:ILE:N	1:E:60:ILE:O	2.48	0.44
1:F:29:ASP:O	1:F:30:ALA:C	2.60	0.44
1:H:15:VAL:HG11	1:H:71:ILE:HD12	1.99	0.44
1:B:25:SER:OG	1:B:26:VAL:N	2.48	0.44
1:A:19:ASP:OD2	1:A:21:HIS:O	2.35	0.44
1:B:49:ILE:HD12	1:B:49:ILE:H	1.82	0.44
1:D:3:ARG:HD2	1:D:5:MET:HE3	1.94	0.44
1:D:55:LEU:CD1	1:D:75:ALA:HB1	2.48	0.44
1:A:69:ILE:HD12	1:A:112:ASN:ND2	2.33	0.44
1:B:23:VAL:HG12	1:B:24:GLY:N	2.32	0.44
1:E:12:ARG:NH2	1:F:21:HIS:HA	2.33	0.44
1:E:66:SER:OG	1:E:68:VAL:HG23	2.18	0.44
1:F:47:VAL:O	1:F:47:VAL:HG23	2.18	0.44
1:H:4:THR:HA	1:H:92:THR:HA	1.98	0.44
1:C:24:GLY:HA2	1:C:60:ILE:CD1	2.48	0.44
1:H:108:VAL:CG2	1:H:112:ASN:HA	2.48	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:73:GLY:O	1:A:74:ALA:HB3	2.18	0.43
1:B:39:LEU:O	1:B:40:GLU:C	2.60	0.43
1:F:3:ARG:HH12	1:G:39:LEU:HG	1.77	0.43
1:B:55:LEU:HD13	1:B:75:ALA:CB	2.48	0.43
1:E:23:VAL:CG1	1:E:24:GLY:N	2.80	0.43
1:F:23:VAL:CG1	1:F:24:GLY:N	2.81	0.43
1:G:68:VAL:C	1:G:69:ILE:HG13	2.44	0.43
1:A:1:MET:CB	1:C:93:MET:HE3	2.49	0.43
1:A:57:THR:HA	1:B:90:TYR:OH	2.18	0.43
1:B:46:ILE:O	1:B:54:ARG:HA	2.18	0.43
1:F:24:GLY:N	1:F:72:ASN:HB2	2.33	0.43
1:D:65:GLY:C	1:D:67:GLY:H	2.26	0.43
1:E:74:ALA:C	1:E:76:ALA:N	2.71	0.43
1:G:93:MET:HG3	2:G:2001:HOH:O	2.18	0.43
1:H:77:HIS:O	1:H:79:VAL:N	2.47	0.43
1:A:7:LYS:NZ	1:A:42:GLU:OE2	2.50	0.43
1:C:47:VAL:HG23	1:C:47:VAL:O	2.18	0.43
1:F:27:THR:HG22	1:F:60:ILE:CG2	2.48	0.43
1:F:108:VAL:HG22	1:F:109:ASP:H	1.84	0.43
1:H:94:ASP:C	1:H:96:ALA:N	2.77	0.43
1:A:65:GLY:C	1:A:67:GLY:N	2.74	0.43
1:C:109:ASP:OD1	1:C:110:ALA:N	2.51	0.43
1:F:42:GLU:O	1:F:44:VAL:HG23	2.19	0.43
1:F:94:ASP:C	1:F:96:ALA:N	2.77	0.43
1:H:74:ALA:C	1:H:76:ALA:N	2.76	0.43
1:B:65:GLY:C	1:B:67:GLY:H	2.26	0.43
1:D:27:THR:HG22	1:D:60:ILE:CG2	2.48	0.43
1:G:109:ASP:OD1	1:G:110:ALA:N	2.52	0.43
1:H:94:ASP:O	1:H:96:ALA:N	2.51	0.43
1:D:108:VAL:HG22	1:D:109:ASP:H	1.83	0.43
1:F:5:MET:HG2	1:G:42:GLU:HA	2.01	0.43
1:A:21:HIS:C	1:B:12:ARG:HH22	2.27	0.42
1:A:42:GLU:HG3	1:B:5:MET:HG2	2.01	0.42
1:A:71:ILE:CD1	1:A:79:VAL:HG12	2.49	0.42
1:C:57:THR:OG1	1:C:58:TYR:N	2.52	0.42
1:E:23:VAL:HB	1:H:9:LYS:HZ1	1.84	0.42
1:E:55:LEU:HD13	1:E:75:ALA:CB	2.48	0.42
1:E:101:TYR:O	1:E:103:PRO:HD3	2.19	0.42
1:C:8:SER:OG	1:C:89:ALA:HB3	2.19	0.42
1:E:20:LEU:O	1:H:12:ARG:NH2	2.52	0.42
1:E:20:LEU:HD13	1:E:76:ALA:HB3	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:24:GLY:H	1:F:72:ASN:HB2	1.84	0.42
1:H:30:ALA:HB3	1:H:64:ARG:HG2	2.01	0.42
1:A:44:VAL:N	1:A:57:THR:O	2.35	0.42
1:D:11:HIS:CD2	1:D:12:ARG:HG3	2.53	0.42
1:D:39:LEU:O	1:D:40:GLU:C	2.61	0.42
1:G:49:ILE:HD13	1:G:84:LEU:O	2.19	0.42
1:A:55:LEU:HD21	1:A:78:LEU:HD13	2.00	0.42
1:C:90:TYR:O	1:C:91:ALA:CB	2.67	0.42
1:C:94:ASP:C	1:C:96:ALA:N	2.78	0.42
1:F:9:LYS:HE2	1:F:11:HIS:HB2	2.00	0.42
1:G:2:LEU:HD23	1:G:94:ASP:HA	2.00	0.42
1:H:108:VAL:CG2	1:H:113:LYS:H	2.22	0.42
1:B:74:ALA:HB3	2:D:2001:HOH:O	2.19	0.42
1:C:1:MET:SD	1:D:93:MET:HE3	2.59	0.42
1:B:21:HIS:C	1:D:12:ARG:HH22	2.28	0.42
1:B:23:VAL:CG2	1:D:86:ILE:CD1	2.74	0.42
1:C:30:ALA:HB3	1:C:64:ARG:HG3	2.00	0.42
1:D:71:ILE:CD1	1:D:79:VAL:CG1	2.98	0.42
1:E:94:ASP:C	1:E:96:ALA:H	2.27	0.42
1:B:108:VAL:HG22	1:B:109:ASP:N	2.35	0.42
1:D:49:ILE:HD12	1:D:49:ILE:N	2.34	0.42
1:E:2:LEU:HD23	1:E:94:ASP:HA	2.01	0.42
1:F:49:ILE:O	1:G:77:HIS:NE2	2.52	0.42
1:H:49:ILE:HB	1:H:84:LEU:O	2.19	0.42
1:A:4:THR:HA	1:A:92:THR:HA	2.01	0.42
1:B:101:TYR:O	1:B:103:PRO:HD3	2.20	0.42
1:H:49:ILE:HD11	1:H:86:ILE:CG1	2.46	0.42
1:H:66:SER:OG	1:H:68:VAL:HG23	2.20	0.42
1:H:80:HIS:O	1:H:83:ASP:CG	2.63	0.42
1:B:28:ILE:N	1:B:60:ILE:O	2.51	0.42
1:F:98:ALA:HB1	1:G:39:LEU:CD1	2.49	0.42
1:G:90:TYR:HH	1:H:57:THR:HA	1.82	0.42
1:H:69:ILE:O	1:H:69:ILE:HG22	2.19	0.42
1:A:69:ILE:O	1:A:69:ILE:HG22	2.19	0.41
1:A:71:ILE:HD13	1:A:79:VAL:CG1	2.50	0.41
1:D:90:TYR:OH	2:D:2002:HOH:O	2.21	0.41
1:E:24:GLY:N	1:E:72:ASN:HB2	2.35	0.41
1:E:49:ILE:HD12	1:E:49:ILE:N	2.35	0.41
1:F:5:MET:HE1	1:G:39:LEU:CD1	2.34	0.41
1:G:28:ILE:N	1:G:60:ILE:O	2.51	0.41
1:H:108:VAL:HG22	1:H:109:ASP:N	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:3:ARG:NH2	1:G:37:ASP:OD2	2.52	0.41
1:G:24:GLY:HA2	1:G:60:ILE:CD1	2.50	0.41
1:H:74:ALA:C	1:H:76:ALA:H	2.27	0.41
1:D:49:ILE:HD11	1:D:86:ILE:CG1	2.48	0.41
1:D:95:ASP:O	1:D:98:ALA:HB3	2.20	0.41
1:G:3:ARG:HD3	1:H:42:GLU:CD	2.45	0.41
1:G:55:LEU:HD11	1:G:79:VAL:HG23	2.02	0.41
1:A:23:VAL:H	1:B:11:HIS:HE1	1.69	0.41
1:C:31:ASP:OD1	1:C:64:ARG:NH1	2.53	0.41
1:D:24:GLY:N	1:D:72:ASN:HB2	2.36	0.41
1:E:39:LEU:O	1:E:40:GLU:C	2.62	0.41
1:F:30:ALA:HB3	1:F:64:ARG:HG3	2.02	0.41
1:G:66:SER:CB	1:G:68:VAL:HG23	2.50	0.41
1:H:10:ILE:HD12	1:H:87:LEU:HD12	2.03	0.41
1:B:64:ARG:C	1:B:66:SER:N	2.77	0.41
1:B:71:ILE:CD1	1:B:79:VAL:CG1	2.98	0.41
1:D:33:MET:O	1:D:38:LEU:N	2.53	0.41
1:D:49:ILE:HD12	1:D:49:ILE:H	1.86	0.41
1:F:53:ALA:O	1:F:54:ARG:CG	2.69	0.41
1:G:15:VAL:HG11	1:G:71:ILE:HD12	2.02	0.41
1:A:3:ARG:CB	1:A:5:MET:HE3	2.49	0.41
1:A:48:ASP:O	1:A:52:GLY:N	2.54	0.41
1:B:75:ALA:HB2	1:D:54:ARG:NH2	2.35	0.41
1:E:65:GLY:C	1:E:67:GLY:N	2.77	0.41
1:F:57:THR:OG1	1:F:58:TYR:N	2.54	0.41
1:F:76:ALA:HA	2:F:2003:HOH:O	2.21	0.41
1:G:47:VAL:O	1:G:47:VAL:HG23	2.19	0.41
1:A:24:GLY:O	1:A:25:SER:C	2.63	0.41
1:A:93:MET:HE1	1:A:101:TYR:CE1	2.55	0.41
1:B:25:SER:O	1:B:72:ASN:N	2.38	0.41
1:B:71:ILE:HG22	1:B:75:ALA:HB3	2.01	0.41
1:E:71:ILE:HD13	1:E:79:VAL:CB	2.50	0.41
1:F:10:ILE:HD12	1:F:87:LEU:HD12	2.02	0.41
1:F:86:ILE:HD11	1:G:23:VAL:CG2	2.50	0.41
1:G:11:HIS:CE1	1:H:23:VAL:CG2	3.03	0.41
1:G:25:SER:OG	1:G:26:VAL:N	2.53	0.41
1:A:23:VAL:HB	1:B:11:HIS:CE1	2.55	0.41
1:A:68:VAL:C	1:A:69:ILE:HG13	2.45	0.41
1:B:47:VAL:O	1:B:47:VAL:HG23	2.20	0.41
1:B:95:ASP:O	1:B:98:ALA:HB3	2.21	0.41
1:D:42:GLU:O	1:D:44:VAL:HG23	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:3:ARG:HH11	1:H:39:LEU:HG	1.66	0.41
1:G:29:ASP:O	1:G:30:ALA:C	2.62	0.41
1:A:11:HIS:CD2	1:A:12:ARG:HG3	2.56	0.41
1:A:65:GLY:C	1:A:67:GLY:H	2.28	0.41
1:B:94:ASP:C	1:B:96:ALA:N	2.75	0.41
1:F:24:GLY:HA2	1:F:60:ILE:CD1	2.51	0.41
1:B:20:LEU:HD11	1:B:77:HIS:NE2	2.36	0.40
1:B:55:LEU:CD1	1:B:75:ALA:HB1	2.51	0.40
1:C:55:LEU:HD21	1:C:78:LEU:HD13	2.02	0.40
1:F:75:ALA:O	1:F:77:HIS:O	2.38	0.40
1:F:76:ALA:HB1	2:F:2003:HOH:O	2.21	0.40
1:F:94:ASP:O	1:F:96:ALA:N	2.55	0.40
1:H:69:ILE:HD12	1:H:112:ASN:ND2	2.36	0.40
1:C:46:ILE:HA	1:C:86:ILE:O	2.21	0.40
1:E:58:TYR:HB3	1:H:6:LEU:HB2	2.04	0.40
1:G:94:ASP:HB3	1:G:97:ARG:HG2	2.03	0.40
1:H:65:GLY:C	1:H:67:GLY:N	2.76	0.40
1:H:71:ILE:HD13	1:H:79:VAL:HB	2.02	0.40
1:A:33:MET:O	1:A:38:LEU:N	2.50	0.40
1:F:48:ASP:OD2	1:F:48:ASP:C	2.64	0.40
1:F:49:ILE:HD11	1:F:86:ILE:CG1	2.47	0.40
1:B:80:HIS:O	1:B:83:ASP:HB2	2.20	0.40
1:E:49:ILE:HD11	1:E:86:ILE:CG1	2.47	0.40
1:G:28:ILE:HG22	1:G:29:ASP:N	2.36	0.40
1:G:90:TYR:O	1:G:91:ALA:CB	2.70	0.40
1:H:71:ILE:CD1	1:H:79:VAL:HG12	2.51	0.40
1:B:25:SER:OG	1:B:58:TYR:O	2.40	0.40
1:B:33:MET:SD	1:B:61:THR:HA	2.61	0.40
1:D:24:GLY:O	1:D:25:SER:C	2.64	0.40
1:F:2:LEU:HD23	1:F:94:ASP:HA	2.02	0.40
1:F:66:SER:CB	1:F:68:VAL:HG23	2.52	0.40

All (2) 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:B:99:ARG:NH2	1:E:95:ASP:OD2[3_564]	1.87	0.33
1:B:99:ARG:NE	1:E:99:ARG:NH2[3_564]	2.03	0.17

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	112/139 (81%)	88 (79%)	16 (14%)	8 (7%)	1	4
1	B	112/139 (81%)	84 (75%)	19 (17%)	9 (8%)	1	3
1	C	112/139 (81%)	85 (76%)	17 (15%)	10 (9%)	0	3
1	D	112/139 (81%)	87 (78%)	15 (13%)	10 (9%)	0	3
1	E	112/139 (81%)	88 (79%)	15 (13%)	9 (8%)	1	3
1	F	112/139 (81%)	86 (77%)	16 (14%)	10 (9%)	0	3
1	G	112/139 (81%)	87 (78%)	18 (16%)	7 (6%)	1	6
1	H	112/139 (81%)	86 (77%)	17 (15%)	9 (8%)	1	3
All	All	896/1112 (81%)	691 (77%)	133 (15%)	72 (8%)	1	3

All (72) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	73	GLY
1	D	73	GLY
1	F	73	GLY
1	A	69	ILE
1	A	73	GLY
1	A	91	ALA
1	B	73	GLY
1	B	91	ALA
1	C	91	ALA
1	C	95	ASP
1	D	69	ILE
1	E	22	TYR
1	E	69	ILE
1	E	73	GLY
1	E	91	ALA
1	E	95	ASP
1	F	69	ILE

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Mol	Chain	Res	Type
1	F	91	ALA
1	G	73	GLY
1	G	91	ALA
1	H	69	ILE
1	H	73	GLY
1	H	91	ALA
1	A	22	TYR
1	A	113	LYS
1	B	22	TYR
1	B	37	ASP
1	B	78	LEU
1	B	113	LYS
1	C	22	TYR
1	C	69	ILE
1	C	78	LEU
1	C	113	LYS
1	D	22	TYR
1	D	37	ASP
1	D	91	ALA
1	D	95	ASP
1	D	113	LYS
1	E	113	LYS
1	F	22	TYR
1	F	95	ASP
1	F	113	LYS
1	G	22	TYR
1	G	69	ILE
1	G	113	LYS
1	H	22	TYR
1	H	37	ASP
1	H	95	ASP
1	H	113	LYS
1	A	78	LEU
1	E	78	LEU
1	F	78	LEU
1	G	37	ASP
1	A	37	ASP
1	B	65	GLY
1	B	69	ILE
1	C	37	ASP
1	D	78	LEU
1	E	37	ASP

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Mol	Chain	Res	Type
1	F	37	ASP
1	F	65	GLY
1	A	24	GLY
1	C	65	GLY
1	H	65	GLY
1	D	24	GLY
1	F	24	GLY
1	B	24	GLY
1	E	65	GLY
1	H	24	GLY
1	C	24	GLY
1	G	24	GLY
1	D	65	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	89/109 (82%)	86 (97%)	3 (3%)	32	66
1	B	89/109 (82%)	87 (98%)	2 (2%)	45	74
1	C	89/109 (82%)	87 (98%)	2 (2%)	45	74
1	D	89/109 (82%)	86 (97%)	3 (3%)	32	66
1	E	89/109 (82%)	86 (97%)	3 (3%)	32	66
1	F	89/109 (82%)	86 (97%)	3 (3%)	32	66
1	G	89/109 (82%)	87 (98%)	2 (2%)	45	74
1	H	89/109 (82%)	86 (97%)	3 (3%)	32	66
All	All	712/872 (82%)	691 (97%)	21 (3%)	37	70

All (21) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	4	THR
1	A	12	ARG

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Mol	Chain	Res	Type
1	A	108	VAL
1	B	4	THR
1	B	12	ARG
1	C	4	THR
1	C	12	ARG
1	D	4	THR
1	D	12	ARG
1	D	108	VAL
1	E	4	THR
1	E	12	ARG
1	E	108	VAL
1	F	4	THR
1	F	12	ARG
1	F	108	VAL
1	G	4	THR
1	G	12	ARG
1	H	4	THR
1	H	12	ARG
1	H	108	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (21) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	11	HIS
1	A	80	HIS
1	B	11	HIS
1	B	80	HIS
1	C	11	HIS
1	C	21	HIS
1	D	11	HIS
1	D	80	HIS
1	E	11	HIS
1	E	21	HIS
1	E	80	HIS
1	F	11	HIS
1	F	21	HIS
1	F	80	HIS
1	G	11	HIS
1	G	21	HIS
1	G	72	ASN
1	G	80	HIS
1	H	11	HIS

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Mol	Chain	Res	Type
1	H	21	HIS
1	H	80	HIS

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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	114/139 (82%)	-1.11	0 100 100	22, 33, 56, 63	0
1	B	114/139 (82%)	-1.00	0 100 100	25, 36, 49, 67	0
1	C	114/139 (82%)	-0.94	0 100 100	21, 34, 53, 68	0
1	D	114/139 (82%)	-0.89	0 100 100	24, 34, 51, 68	0
1	E	114/139 (82%)	-1.00	1 (0%) 81 61	23, 35, 51, 62	0
1	F	114/139 (82%)	-1.08	0 100 100	22, 34, 52, 66	0
1	G	114/139 (82%)	-0.97	0 100 100	25, 34, 50, 72	0
1	H	114/139 (82%)	-0.95	0 100 100	25, 35, 51, 61	0
All	All	912/1112 (82%)	-0.99	1 (0%) 92 86	21, 34, 52, 72	0

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	22	TYR	3.1

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 oligosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers ⓘ

There are no such residues in this entry.