



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 25, 2026 – 08:36 PM EDT

PDB ID : 3N9H / pdb_00003n9h
Title : Crystal Structural of mutant Y305A in the copper amine oxidase from
hansenula polymorpha
Authors : Chen, Z.; Datta, S.; DuBois, J.L.; Klinman, J.P.; Mathews, F.S.
Deposited on : 2010-05-30
Resolution : 2.50 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:

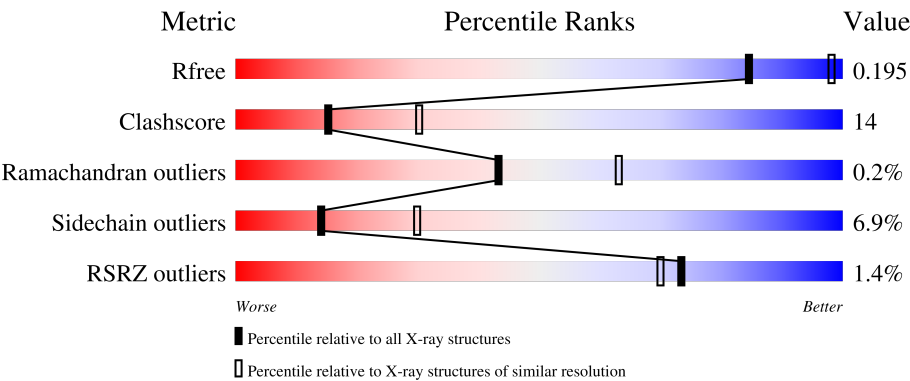
MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (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 2.50 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	5829 (2.50-2.50)
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)
RSRZ outliers	180081	5833 (2.50-2.50)

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	692	% 68%23%5%
1	B	692	% 68%23%5%
1	C	692	% 69%22%5%
1	D	692	2% 69%22%5%
1	E	692	% 69%22%5%

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Mol	Chain	Length	Quality of chain
1	F	692	% 68% 23% • 5%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 34296 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 Peroxisomal primary amine oxidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	655	Total	C	N	O	S	0	2	0
			5203	3309	895	975	24			
1	B	655	Total	C	N	O	S	0	2	0
			5203	3309	895	975	24			
1	C	655	Total	C	N	O	S	0	2	0
			5203	3309	895	975	24			
1	D	655	Total	C	N	O	S	0	2	0
			5203	3309	895	975	24			
1	E	655	Total	C	N	O	S	0	2	0
			5203	3309	895	975	24			
1	F	655	Total	C	N	O	S	0	2	0
			5203	3309	895	975	24			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	305	ALA	TYR	engineered mutation	UNP P12807
B	305	ALA	TYR	engineered mutation	UNP P12807
C	305	ALA	TYR	engineered mutation	UNP P12807
D	305	ALA	TYR	engineered mutation	UNP P12807
E	305	ALA	TYR	engineered mutation	UNP P12807
F	305	ALA	TYR	engineered mutation	UNP P12807

- Molecule 2 is COPPER (II) ION (CCD ID: CU) (formula: Cu).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Cu	0	0
			1	1		
2	B	1	Total	Cu	0	0
			1	1		
2	C	1	Total	Cu	0	0
			1	1		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	D	1	Total 1	Cu 1	0	0
2	E	1	Total 1	Cu 1	0	0
2	F	1	Total 1	Cu 1	0	0

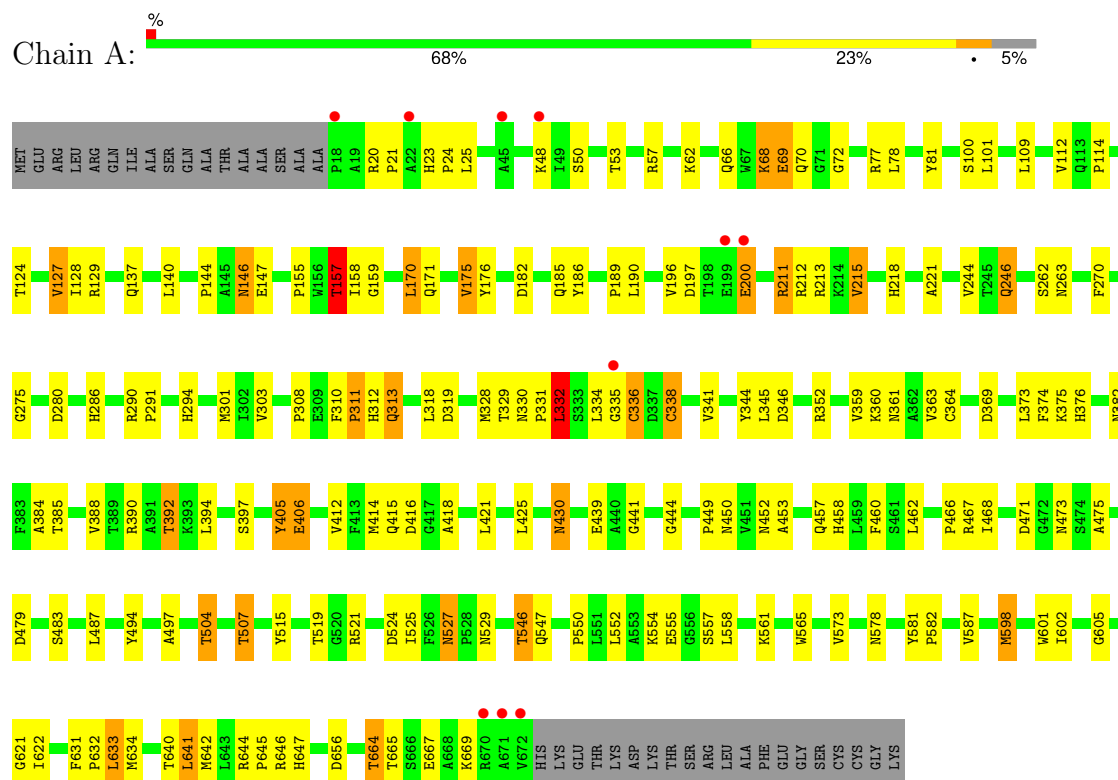
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	507	Total 507	O 507	0	0
3	B	517	Total 517	O 517	0	0
3	C	515	Total 515	O 515	0	0
3	D	509	Total 509	O 509	0	0
3	E	506	Total 506	O 506	0	0
3	F	518	Total 518	O 518	0	0

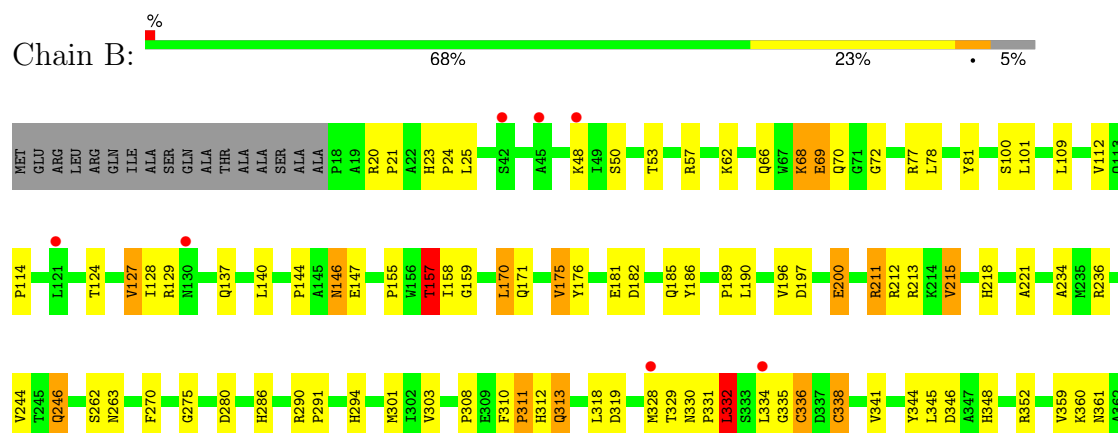
3 Residue-property plots

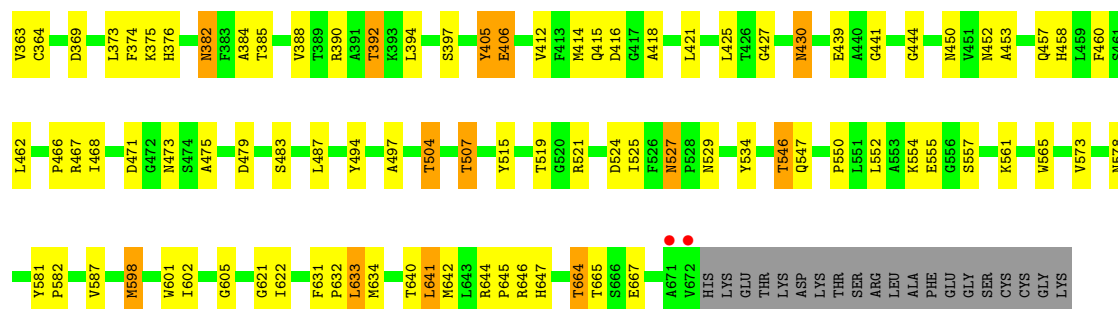
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density.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

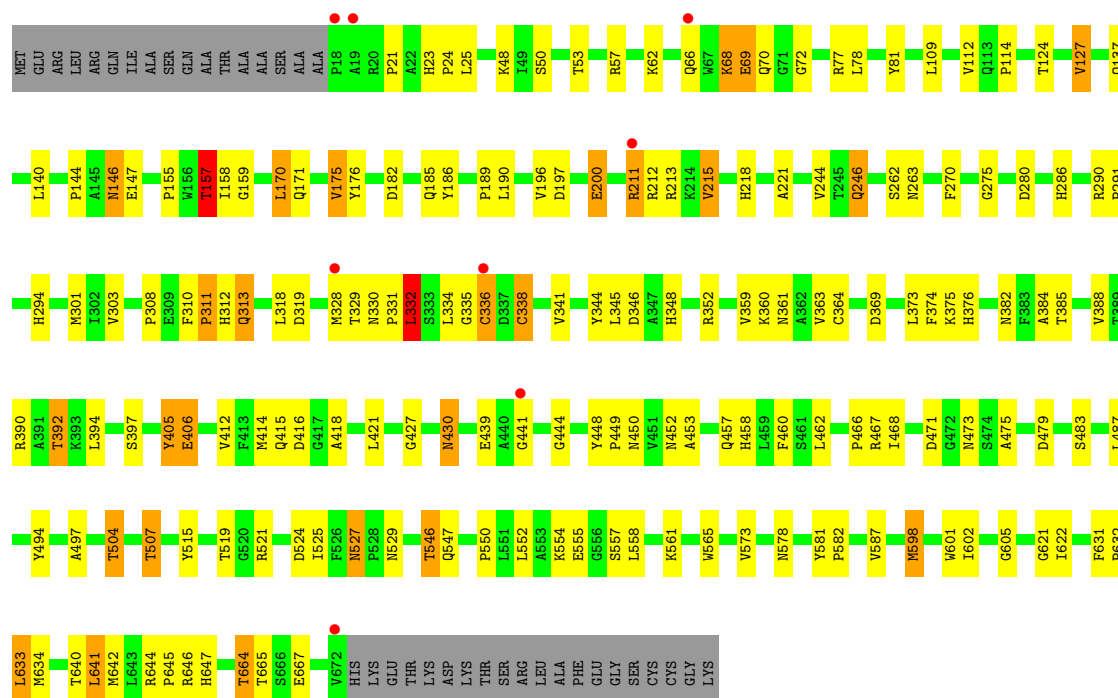


• Molecule 1: Peroxisomal primary amine oxidase

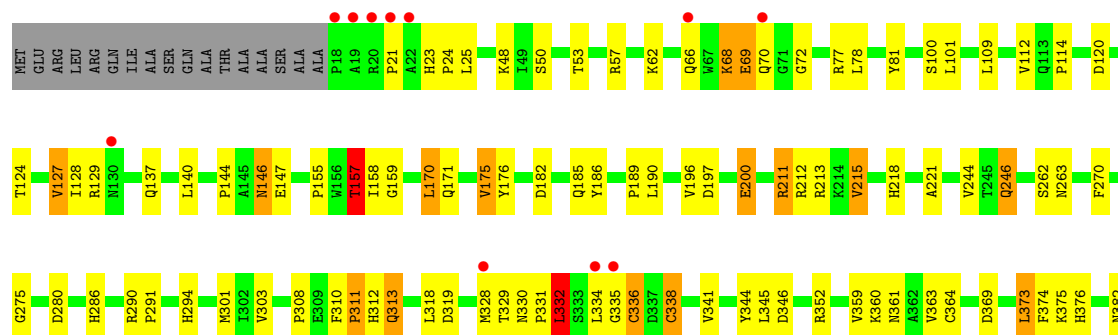


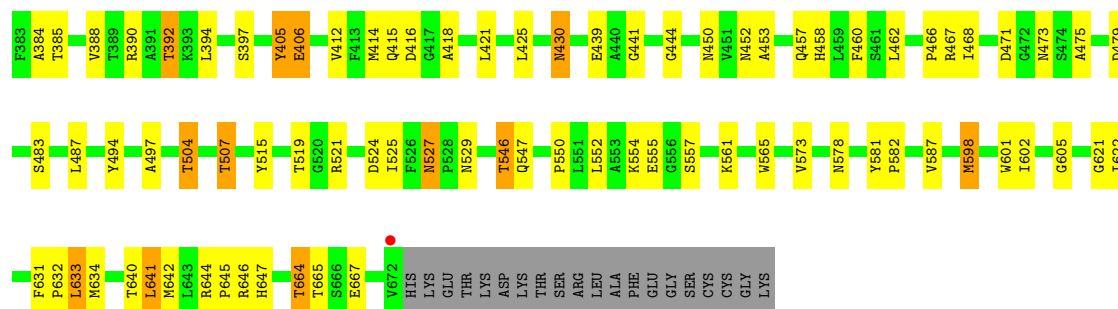


• Molecule 1: Peroxisomal primary amine oxidase

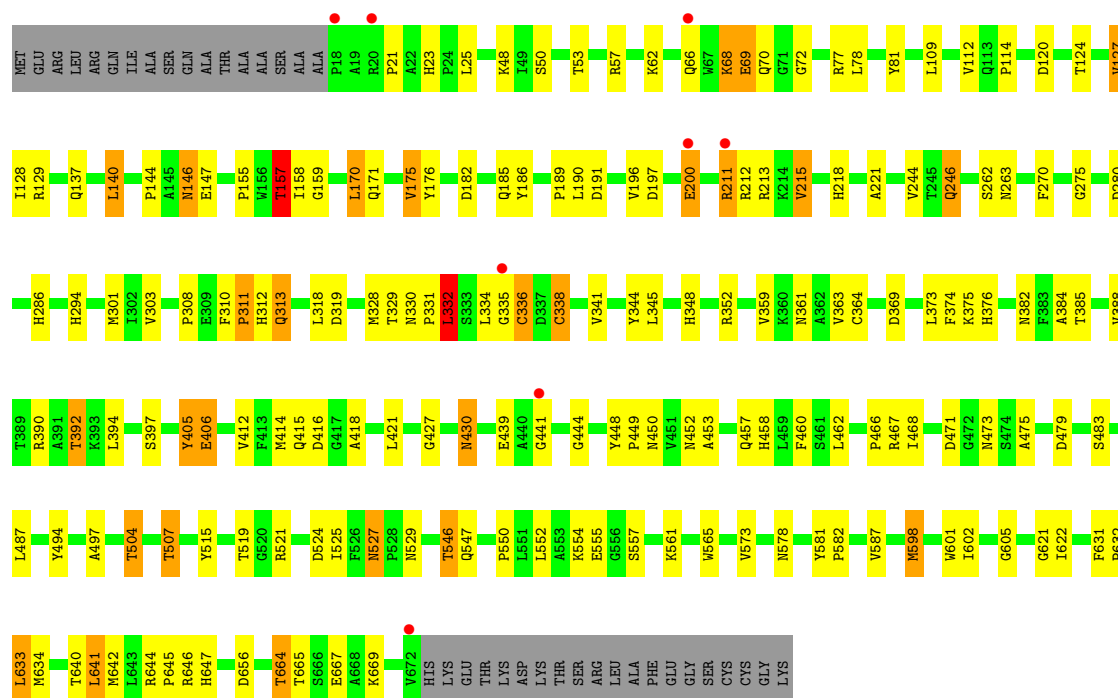


• Molecule 1: Peroxisomal primary amine oxidase

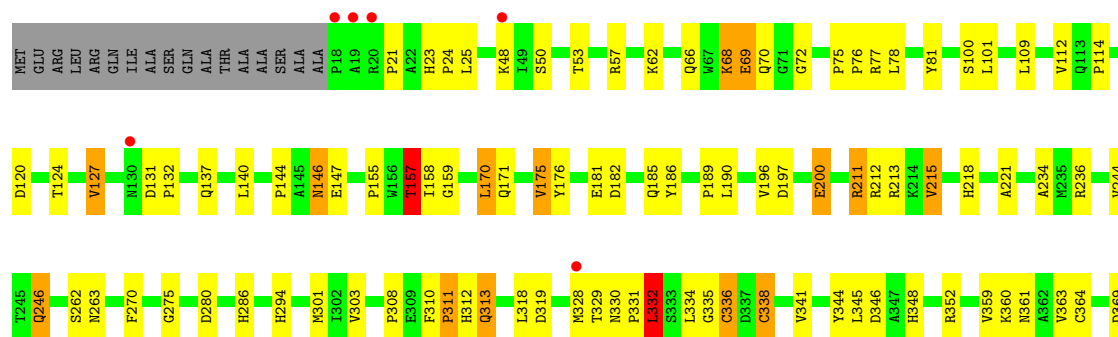


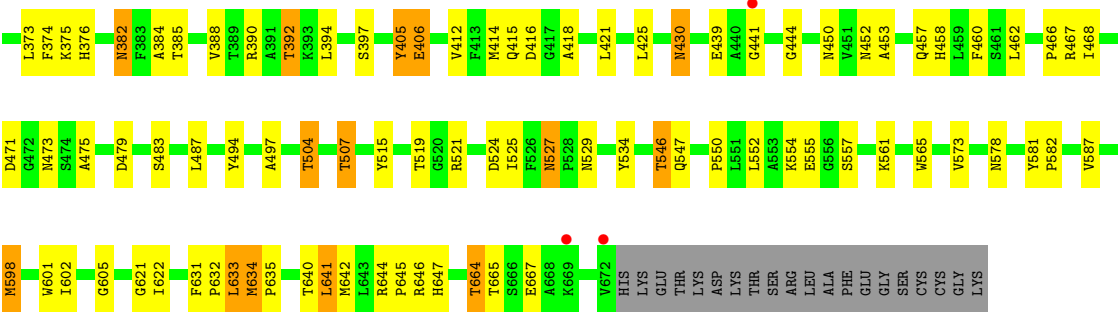


• Molecule 1: Peroxisomal primary amine oxidase



• Molecule 1: Peroxisomal primary amine oxidase





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	138.91Å 147.15Å 233.76Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.10 – 2.50 30.10 – 2.50	Depositor EDS
% Data completeness (in resolution range)	81.0 (30.10-2.50) 81.0 (30.10-2.50)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.41 (at 2.42Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.185 , 0.198 0.182 , 0.195	Depositor DCC
R_{free} test set	13877 reflections (9.99%)	wwPDB-VP
Wilson B-factor (Å ²)	24.8	Xtriage
Anisotropy	0.555	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 38.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	34296	wwPDB-VP
Average B, all atoms (Å ²)	29.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.87% 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](#)

Bond lengths and bond angles in the following residue types are not validated in this section: TPQ, CU

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	0.53	1/5337 (0.0%)	1.08	29/7262 (0.4%)
1	B	0.53	1/5337 (0.0%)	1.08	29/7262 (0.4%)
1	C	0.53	1/5337 (0.0%)	1.08	29/7262 (0.4%)
1	D	0.53	1/5337 (0.0%)	1.08	29/7262 (0.4%)
1	E	0.53	1/5337 (0.0%)	1.08	29/7262 (0.4%)
1	F	0.53	1/5337 (0.0%)	1.08	29/7262 (0.4%)
All	All	0.53	6/32022 (0.0%)	1.08	174/43572 (0.4%)

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	598	MET	SD-CE	-7.31	1.61	1.79
1	D	598	MET	SD-CE	-7.29	1.61	1.79
1	C	598	MET	SD-CE	-7.28	1.61	1.79
1	A	598	MET	SD-CE	-7.27	1.61	1.79
1	B	598	MET	SD-CE	-7.26	1.61	1.79
1	F	598	MET	SD-CE	-7.26	1.61	1.79

All (174) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	157	THR	N-CA-C	-9.56	97.92	110.53
1	B	157	THR	N-CA-C	-9.55	97.93	110.53
1	E	157	THR	N-CA-C	-9.54	97.93	110.53
1	A	157	THR	N-CA-C	-9.54	97.94	110.53
1	C	157	THR	N-CA-C	-9.52	97.97	110.53
1	D	157	THR	N-CA-C	-9.52	97.97	110.53
1	C	158	ILE	N-CA-C	-7.05	103.48	113.07
1	B	158	ILE	N-CA-C	-7.03	103.51	113.07
1	E	158	ILE	N-CA-C	-7.02	103.52	113.07

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	158	ILE	N-CA-C	-7.01	103.53	113.07
1	D	158	ILE	N-CA-C	-7.00	103.55	113.07
1	F	158	ILE	N-CA-C	-7.00	103.55	113.07
1	D	384	ALA	N-CA-C	-7.00	103.73	111.36
1	F	334	LEU	N-CA-C	7.00	119.56	111.02
1	A	384	ALA	N-CA-C	-6.99	103.74	111.36
1	C	384	ALA	N-CA-C	-6.99	103.74	111.36
1	E	334	LEU	N-CA-C	6.98	119.54	111.02
1	F	384	ALA	N-CA-C	-6.97	103.77	111.36
1	A	334	LEU	N-CA-C	6.96	119.52	111.02
1	E	384	ALA	N-CA-C	-6.96	103.77	111.36
1	B	334	LEU	N-CA-C	6.96	119.51	111.02
1	C	334	LEU	N-CA-C	6.96	119.51	111.02
1	B	384	ALA	N-CA-C	-6.95	103.79	111.36
1	D	334	LEU	N-CA-C	6.95	119.50	111.02
1	B	332	LEU	N-CA-C	6.94	121.58	113.18
1	C	332	LEU	N-CA-C	6.94	121.57	113.18
1	A	332	LEU	N-CA-C	6.91	121.55	113.18
1	F	332	LEU	N-CA-C	6.90	121.53	113.18
1	D	332	LEU	N-CA-C	6.90	121.53	113.18
1	E	332	LEU	N-CA-C	6.90	121.53	113.18
1	C	157	THR	CB-CA-C	-6.88	95.58	109.68
1	B	157	THR	CB-CA-C	-6.88	95.58	109.68
1	F	157	THR	CB-CA-C	-6.88	95.59	109.68
1	A	157	THR	CB-CA-C	-6.87	95.59	109.68
1	D	157	THR	CB-CA-C	-6.87	95.59	109.68
1	E	157	THR	CB-CA-C	-6.87	95.59	109.68
1	D	186	TYR	N-CA-C	6.67	120.51	112.38
1	B	186	TYR	N-CA-C	6.64	120.48	112.38
1	A	186	TYR	N-CA-C	6.63	120.47	112.38
1	F	186	TYR	N-CA-C	6.62	120.46	112.38
1	E	186	TYR	N-CA-C	6.62	120.45	112.38
1	C	186	TYR	N-CA-C	6.61	120.44	112.38
1	E	336	CYS	N-CA-C	-6.56	104.58	112.58
1	C	336	CYS	N-CA-C	-6.52	104.62	112.58
1	A	336	CYS	N-CA-C	-6.52	104.63	112.58
1	F	336	CYS	N-CA-C	-6.51	104.64	112.58
1	B	336	CYS	N-CA-C	-6.49	104.66	112.58
1	D	336	CYS	N-CA-C	-6.48	104.67	112.58
1	C	521	ARG	N-CA-C	6.42	119.29	110.24
1	D	521	ARG	N-CA-C	6.39	119.25	110.24
1	A	521	ARG	N-CA-C	6.39	119.25	110.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	521	ARG	N-CA-C	6.38	119.24	110.24
1	F	521	ARG	N-CA-C	6.38	119.24	110.24
1	E	521	ARG	N-CA-C	6.37	119.22	110.24
1	F	331	PRO	N-CA-C	-6.37	100.50	110.50
1	D	331	PRO	N-CA-C	-6.35	100.53	110.50
1	C	331	PRO	N-CA-C	-6.34	100.55	110.50
1	A	331	PRO	N-CA-C	-6.34	100.55	110.50
1	B	331	PRO	N-CA-C	-6.33	100.57	110.50
1	E	331	PRO	N-CA-C	-6.32	100.58	110.50
1	E	175	VAL	N-CA-C	6.26	117.15	108.89
1	C	175	VAL	N-CA-C	6.23	117.12	108.89
1	F	175	VAL	N-CA-C	6.23	117.11	108.89
1	F	634	MET	N-CA-C	5.96	118.53	110.31
1	B	634	MET	N-CA-C	5.95	118.52	110.31
1	C	634	MET	N-CA-C	5.94	118.51	110.31
1	A	634	MET	N-CA-C	5.94	118.51	110.31
1	E	634	MET	N-CA-C	5.94	118.51	110.31
1	D	634	MET	N-CA-C	5.93	118.50	110.31
1	E	397	SER	N-CA-C	5.93	118.70	109.52
1	B	397	SER	N-CA-C	5.92	118.70	109.52
1	A	397	SER	N-CA-C	5.92	118.69	109.52
1	D	397	SER	N-CA-C	5.92	118.69	109.52
1	B	550	PRO	N-CA-C	-5.91	101.81	111.68
1	D	550	PRO	N-CA-C	-5.91	101.81	111.68
1	F	397	SER	N-CA-C	5.90	118.67	109.52
1	A	550	PRO	N-CA-C	-5.90	101.83	111.68
1	C	550	PRO	N-CA-C	-5.90	101.83	111.68
1	E	373	LEU	N-CA-C	-5.89	104.26	112.45
1	A	373	LEU	N-CA-C	-5.89	104.26	112.45
1	C	397	SER	N-CA-C	5.89	118.65	109.52
1	F	373	LEU	N-CA-C	-5.89	104.26	112.45
1	B	373	LEU	N-CA-C	-5.89	104.27	112.45
1	C	373	LEU	N-CA-C	-5.89	104.27	112.45
1	E	550	PRO	N-CA-C	-5.89	101.85	111.68
1	D	373	LEU	N-CA-C	-5.88	104.28	112.45
1	F	550	PRO	N-CA-C	-5.88	101.86	111.68
1	D	175	VAL	N-CA-C	5.82	117.13	109.21
1	A	175	VAL	N-CA-C	5.82	117.12	109.21
1	B	175	VAL	N-CA-C	5.82	117.12	109.21
1	E	246	GLN	CA-C-N	5.81	125.95	119.32
1	E	246	GLN	C-N-CA	5.81	125.95	119.32
1	C	246	GLN	CA-C-N	5.80	125.93	119.32

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	246	GLN	C-N-CA	5.80	125.93	119.32
1	B	246	GLN	CA-C-N	5.78	125.91	119.32
1	B	246	GLN	C-N-CA	5.78	125.91	119.32
1	A	246	GLN	CA-C-N	5.78	125.91	119.32
1	A	246	GLN	C-N-CA	5.78	125.91	119.32
1	D	246	GLN	CA-C-N	5.75	125.88	119.32
1	D	246	GLN	C-N-CA	5.75	125.88	119.32
1	F	246	GLN	CA-C-N	5.75	125.88	119.32
1	F	246	GLN	C-N-CA	5.75	125.88	119.32
1	B	412	VAL	N-CA-C	5.65	116.00	107.75
1	E	412	VAL	N-CA-C	5.65	116.00	107.75
1	D	412	VAL	N-CA-C	5.65	116.00	107.75
1	A	412	VAL	N-CA-C	5.64	115.98	107.75
1	C	412	VAL	N-CA-C	5.63	115.97	107.75
1	F	412	VAL	N-CA-C	5.63	115.97	107.75
1	C	416	ASP	N-CA-C	-5.47	105.82	112.88
1	F	319	ASP	N-CA-C	5.46	117.66	111.11
1	B	430	ASN	N-CA-C	-5.45	100.91	109.25
1	C	430	ASN	N-CA-C	-5.45	100.91	109.25
1	E	430	ASN	N-CA-C	-5.45	100.92	109.25
1	F	430	ASN	N-CA-C	-5.45	100.92	109.25
1	B	319	ASP	N-CA-C	5.45	117.65	111.11
1	A	430	ASN	N-CA-C	-5.44	100.92	109.25
1	D	430	ASN	N-CA-C	-5.44	100.92	109.25
1	E	416	ASP	N-CA-C	-5.44	105.86	112.88
1	F	416	ASP	N-CA-C	-5.44	105.86	112.88
1	E	319	ASP	N-CA-C	5.44	117.63	111.11
1	D	416	ASP	N-CA-C	-5.43	105.87	112.88
1	A	416	ASP	N-CA-C	-5.43	105.88	112.88
1	A	319	ASP	N-CA-C	5.43	117.62	111.11
1	C	319	ASP	N-CA-C	5.41	117.60	111.11
1	B	416	ASP	N-CA-C	-5.39	105.92	112.88
1	D	319	ASP	N-CA-C	5.39	117.58	111.11
1	F	525	ILE	N-CA-C	-5.39	98.72	107.28
1	F	587	VAL	N-CA-C	5.39	120.52	108.88
1	C	587	VAL	N-CA-C	5.38	120.50	108.88
1	E	525	ILE	N-CA-C	-5.38	98.73	107.28
1	A	525	ILE	N-CA-C	-5.37	98.74	107.28
1	A	587	VAL	N-CA-C	5.37	120.48	108.88
1	C	215	VAL	CB-CA-C	-5.37	102.65	111.51
1	C	525	ILE	N-CA-C	-5.37	98.74	107.28
1	D	215	VAL	CB-CA-C	-5.37	102.65	111.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	525	ILE	N-CA-C	-5.37	98.75	107.28
1	E	587	VAL	N-CA-C	5.37	120.47	108.88
1	B	587	VAL	N-CA-C	5.37	120.47	108.88
1	A	215	VAL	CB-CA-C	-5.36	102.67	111.51
1	B	215	VAL	CB-CA-C	-5.36	102.67	111.51
1	B	525	ILE	N-CA-C	-5.36	98.77	107.28
1	D	587	VAL	N-CA-C	5.35	120.43	108.88
1	F	215	VAL	CB-CA-C	-5.34	102.69	111.51
1	E	215	VAL	CB-CA-C	-5.34	102.70	111.51
1	C	57	ARG	N-CA-C	-5.25	97.98	107.75
1	A	57	ARG	N-CA-C	-5.25	97.98	107.75
1	F	57	ARG	N-CA-C	-5.25	97.98	107.75
1	E	57	ARG	N-CA-C	-5.24	98.00	107.75
1	D	57	ARG	N-CA-C	-5.24	98.01	107.75
1	B	57	ARG	N-CA-C	-5.23	98.03	107.75
1	C	196	VAL	N-CA-C	5.22	116.00	108.48
1	A	196	VAL	N-CA-C	5.20	115.97	108.48
1	F	196	VAL	N-CA-C	5.20	115.97	108.48
1	E	196	VAL	N-CA-C	5.19	115.95	108.48
1	B	196	VAL	N-CA-C	5.18	115.94	108.48
1	F	515	TYR	N-CA-C	-5.18	103.20	110.50
1	B	78	LEU	N-CA-C	5.18	118.18	109.95
1	E	78	LEU	N-CA-C	5.17	118.18	109.95
1	A	515	TYR	N-CA-C	-5.17	103.21	110.50
1	B	515	TYR	N-CA-C	-5.17	103.21	110.50
1	C	78	LEU	N-CA-C	5.17	118.17	109.95
1	D	196	VAL	N-CA-C	5.17	115.93	108.48
1	E	515	TYR	N-CA-C	-5.17	103.21	110.50
1	A	78	LEU	N-CA-C	5.17	118.16	109.95
1	F	78	LEU	N-CA-C	5.16	118.16	109.95
1	C	515	TYR	N-CA-C	-5.16	103.23	110.50
1	D	515	TYR	N-CA-C	-5.15	103.23	110.50
1	D	78	LEU	N-CA-C	5.15	118.13	109.95
1	F	170	LEU	N-CA-C	5.11	117.89	109.72
1	A	170	LEU	N-CA-C	5.10	117.88	109.72
1	C	170	LEU	N-CA-C	5.09	117.86	109.72
1	B	170	LEU	N-CA-C	5.09	117.86	109.72
1	E	170	LEU	N-CA-C	5.08	117.85	109.72
1	D	170	LEU	N-CA-C	5.06	117.81	109.72

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	5203	0	5044	154	3
1	B	5203	0	5044	159	1
1	C	5203	0	5044	156	0
1	D	5203	0	5044	154	2
1	E	5203	0	5044	155	1
1	F	5203	0	5044	158	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
2	E	1	0	0	0	0
2	F	1	0	0	0	0
3	A	507	0	0	14	0
3	B	517	0	0	18	0
3	C	515	0	0	15	0
3	D	509	0	0	15	1
3	E	506	0	0	14	0
3	F	518	0	0	18	0
All	All	34296	0	30264	833	4

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 14.

All (833) 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:546:THR:HG21	1:D:546:THR:CG2	1.40	1.50
1:E:546:THR:HG21	1:F:546:THR:CG2	1.41	1.50
1:A:546:THR:HG21	1:B:546:THR:CG2	1.42	1.49
1:C:546:THR:CG2	1:D:546:THR:HG21	1.40	1.48
1:A:546:THR:CG2	1:B:546:THR:HG21	1.41	1.48
1:E:546:THR:CG2	1:F:546:THR:HG21	1.40	1.46
1:D:211:ARG:H	1:D:211:ARG:HD3	1.09	1.15
1:A:211:ARG:H	1:A:211:ARG:HD3	1.09	1.13
1:C:546:THR:CG2	1:D:546:THR:CG2	2.11	1.13

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:211:ARG:H	1:C:211:ARG:HD3	1.09	1.12
1:F:211:ARG:H	1:F:211:ARG:HD3	1.09	1.12
1:E:211:ARG:H	1:E:211:ARG:HD3	1.09	1.12
1:E:546:THR:CG2	1:F:546:THR:CG2	2.11	1.10
1:B:211:ARG:HD3	1:B:211:ARG:H	1.09	1.08
1:E:494:TYR:CD1	1:F:313:GLN:HG2	1.88	1.07
1:A:546:THR:CG2	1:B:546:THR:CG2	2.13	1.05
1:E:313:GLN:HG2	1:F:494:TYR:CD1	1.93	1.03
1:A:311:PRO:HA	1:A:313:GLN:HE22	1.24	1.02
1:A:494:TYR:CD1	1:B:313:GLN:HG2	1.94	1.02
1:E:311:PRO:HA	1:E:313:GLN:HE22	1.24	1.02
1:D:311:PRO:HA	1:D:313:GLN:HE22	1.24	1.02
1:B:311:PRO:HA	1:B:313:GLN:HE22	1.24	1.01
1:C:313:GLN:HG2	1:D:494:TYR:CD1	1.96	1.01
1:C:311:PRO:HA	1:C:313:GLN:HE22	1.24	1.00
1:C:494:TYR:CD1	1:D:313:GLN:HG2	1.95	1.00
1:F:311:PRO:HA	1:F:313:GLN:HE22	1.24	1.00
1:A:23:HIS:HD2	1:A:25:LEU:H	1.07	0.98
1:A:313:GLN:HG2	1:B:494:TYR:CD1	1.98	0.98
1:E:23:HIS:HD2	1:E:25:LEU:H	1.07	0.98
1:B:23:HIS:HD2	1:B:25:LEU:H	1.07	0.97
1:F:23:HIS:HD2	1:F:25:LEU:H	1.07	0.95
1:D:23:HIS:HD2	1:D:25:LEU:H	1.07	0.94
1:E:546:THR:HG21	1:F:546:THR:HG21	0.98	0.91
1:C:23:HIS:HD2	1:C:25:LEU:H	1.07	0.91
1:F:211:ARG:H	1:F:211:ARG:CD	1.86	0.88
1:D:211:ARG:H	1:D:211:ARG:CD	1.86	0.88
1:B:211:ARG:H	1:B:211:ARG:CD	1.86	0.87
1:E:546:THR:HG23	1:F:546:THR:HG21	1.55	0.87
1:E:211:ARG:H	1:E:211:ARG:CD	1.86	0.87
1:A:211:ARG:H	1:A:211:ARG:CD	1.86	0.86
1:C:664:THR:HG22	1:C:667:GLU:H	1.40	0.86
1:F:664:THR:HG22	1:F:667:GLU:H	1.40	0.86
1:A:664:THR:HG22	1:A:667:GLU:H	1.40	0.86
1:E:664:THR:HG22	1:E:667:GLU:H	1.40	0.85
1:B:664:THR:HG22	1:B:667:GLU:H	1.40	0.85
1:C:211:ARG:H	1:C:211:ARG:CD	1.86	0.85
1:D:664:THR:HG22	1:D:667:GLU:H	1.40	0.85
1:B:328[B]:MET:HE2	3:B:1510:HOH:O	1.77	0.84
1:C:546:THR:HG21	1:D:546:THR:HG23	1.57	0.84
1:C:546:THR:HG23	1:D:546:THR:HG21	1.56	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:328[B]:MET:HE2	3:D:1510:HOH:O	1.77	0.84
1:F:328[B]:MET:HE2	3:F:1510:HOH:O	1.77	0.84
1:F:598:MET:HE2	1:F:602:ILE:HG13	1.60	0.84
1:C:328[B]:MET:HE2	3:C:1510:HOH:O	1.77	0.84
1:D:598:MET:HE2	1:D:602:ILE:HG13	1.60	0.83
1:E:328[B]:MET:HE2	3:E:1510:HOH:O	1.77	0.83
1:A:328[B]:MET:HE2	3:A:1510:HOH:O	1.77	0.83
1:B:598:MET:HE2	1:B:602:ILE:HG13	1.60	0.82
1:D:507:THR:HG21	3:D:1235:HOH:O	1.80	0.82
1:A:598:MET:HE2	1:A:602:ILE:HG13	1.60	0.82
1:C:507:THR:HG21	3:C:1235:HOH:O	1.80	0.82
1:C:137:GLN:OE1	1:C:212:ARG:NH2	2.13	0.81
1:E:598:MET:HE2	1:E:602:ILE:HG13	1.60	0.81
1:F:211:ARG:HD3	1:F:211:ARG:N	1.93	0.81
1:C:598:MET:HE2	1:C:602:ILE:HG13	1.60	0.81
1:B:507:THR:HG21	3:B:1235:HOH:O	1.80	0.81
1:E:137:GLN:OE1	1:E:212:ARG:NH2	2.13	0.81
1:F:507:THR:HG21	3:F:1235:HOH:O	1.80	0.81
1:A:137:GLN:OE1	1:A:212:ARG:NH2	2.13	0.80
1:E:507:THR:HG21	3:E:1235:HOH:O	1.80	0.80
1:A:311:PRO:HA	1:A:313:GLN:NE2	1.96	0.80
1:E:311:PRO:HA	1:E:313:GLN:NE2	1.96	0.80
1:B:311:PRO:HA	1:B:313:GLN:NE2	1.96	0.80
1:C:211:ARG:HD3	1:C:211:ARG:N	1.93	0.80
1:D:137:GLN:OE1	1:D:212:ARG:NH2	2.13	0.80
1:F:137:GLN:OE1	1:F:212:ARG:NH2	2.13	0.80
1:B:137:GLN:OE1	1:B:212:ARG:NH2	2.13	0.80
1:B:211:ARG:HD3	1:B:211:ARG:N	1.93	0.80
1:E:211:ARG:HD3	1:E:211:ARG:N	1.93	0.80
1:A:507:THR:HG21	3:A:1235:HOH:O	1.80	0.80
1:D:311:PRO:HA	1:D:313:GLN:NE2	1.96	0.79
1:C:546:THR:HG21	1:D:546:THR:HG21	0.97	0.79
1:A:546:THR:HG21	1:B:546:THR:HG23	1.59	0.79
1:F:311:PRO:HA	1:F:313:GLN:NE2	1.96	0.79
1:A:211:ARG:HD3	1:A:211:ARG:N	1.93	0.79
1:A:546:THR:HG23	1:B:546:THR:HG21	1.57	0.79
1:E:546:THR:HG21	1:F:546:THR:HG23	1.58	0.79
1:C:311:PRO:HA	1:C:313:GLN:NE2	1.96	0.79
1:A:546:THR:HG21	1:B:546:THR:HG21	0.97	0.77
1:E:338:CYS:HG	1:E:364:CYS:HG	0.78	0.76
1:D:527:ASN:HD22	1:D:529:ASN:H	1.34	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:546:THR:HG23	1:B:546:THR:CG2	2.14	0.76
1:E:527:ASN:HD22	1:E:529:ASN:H	1.34	0.76
1:B:527:ASN:HD22	1:B:529:ASN:H	1.34	0.76
1:E:546:THR:CG2	1:F:546:THR:HG23	2.13	0.76
1:C:157:THR:HB	1:C:159:GLY:H	1.51	0.75
1:D:211:ARG:HD3	1:D:211:ARG:N	1.93	0.75
1:A:527:ASN:HD22	1:A:529:ASN:H	1.34	0.75
1:C:546:THR:CG2	1:D:546:THR:HG23	2.13	0.75
1:F:527:ASN:HD22	1:F:529:ASN:H	1.34	0.75
1:A:546:THR:CG2	1:B:546:THR:HG23	2.15	0.75
1:B:157:THR:HB	1:B:159:GLY:H	1.51	0.75
1:E:157:THR:HB	1:E:159:GLY:H	1.51	0.75
1:E:546:THR:HG23	1:F:546:THR:CG2	2.11	0.75
1:F:157:THR:HB	1:F:159:GLY:H	1.51	0.75
1:D:23:HIS:CD2	1:D:25:LEU:H	2.00	0.75
1:A:157:THR:HB	1:A:159:GLY:H	1.51	0.74
1:D:157:THR:HB	1:D:159:GLY:H	1.51	0.74
1:A:468:ILE:H	1:A:473:ASN:HD21	1.36	0.74
1:F:468:ILE:H	1:F:473:ASN:HD21	1.36	0.74
1:B:23:HIS:CD2	1:B:25:LEU:H	2.00	0.73
1:C:527:ASN:HD22	1:C:529:ASN:H	1.34	0.73
1:D:468:ILE:H	1:D:473:ASN:HD21	1.36	0.73
1:F:23:HIS:CD2	1:F:25:LEU:H	2.00	0.73
1:E:23:HIS:CD2	1:E:25:LEU:H	2.00	0.73
1:C:23:HIS:CD2	1:C:25:LEU:H	2.00	0.73
1:B:468:ILE:H	1:B:473:ASN:HD21	1.36	0.72
1:E:468:ILE:H	1:E:473:ASN:HD21	1.36	0.72
1:C:439:GLU:C	1:C:441:GLY:H	1.99	0.70
1:C:546:THR:HG23	1:D:546:THR:CG2	2.12	0.70
1:A:439:GLU:C	1:A:441:GLY:H	1.99	0.70
1:D:439:GLU:C	1:D:441:GLY:H	1.99	0.70
1:E:527:ASN:ND2	1:E:529:ASN:H	1.89	0.70
1:B:527:ASN:ND2	1:B:529:ASN:H	1.89	0.70
1:D:70:GLN:HG3	3:D:1501:HOH:O	1.92	0.70
1:F:70:GLN:HG3	3:F:1501:HOH:O	1.92	0.70
1:C:527:ASN:ND2	1:C:529:ASN:H	1.89	0.69
1:B:70:GLN:HG3	3:B:1501:HOH:O	1.92	0.69
1:C:70:GLN:HG3	3:C:1501:HOH:O	1.92	0.69
1:C:468:ILE:H	1:C:473:ASN:HD21	1.36	0.69
1:F:21:PRO:HG3	1:F:77:ARG:CZ	2.23	0.69
1:E:21:PRO:HG3	1:E:77:ARG:CZ	2.23	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:527:ASN:HD22	1:A:527:ASN:C	2.01	0.69
1:B:21:PRO:HG3	1:B:77:ARG:CZ	2.23	0.69
1:E:439:GLU:C	1:E:441:GLY:H	1.99	0.69
1:E:527:ASN:HD22	1:E:527:ASN:C	2.01	0.69
1:F:439:GLU:C	1:F:441:GLY:H	1.99	0.69
1:F:527:ASN:ND2	1:F:529:ASN:H	1.89	0.69
1:D:21:PRO:HG3	1:D:77:ARG:CZ	2.23	0.69
1:A:527:ASN:ND2	1:A:529:ASN:H	1.89	0.69
1:A:21:PRO:HG3	1:A:77:ARG:CZ	2.23	0.68
1:D:527:ASN:ND2	1:D:529:ASN:H	1.89	0.68
1:A:70:GLN:HG3	3:A:1501:HOH:O	1.92	0.68
1:A:406:GLU:OE2	1:B:376:HIS:ND1	2.27	0.68
1:D:527:ASN:HD22	1:D:527:ASN:C	2.01	0.68
1:D:439:GLU:HG3	1:D:441:GLY:H	1.59	0.68
1:E:70:GLN:HG3	3:E:1501:HOH:O	1.92	0.68
1:C:21:PRO:HG3	1:C:77:ARG:CZ	2.23	0.68
1:C:527:ASN:HD22	1:C:527:ASN:C	2.01	0.68
1:E:439:GLU:HG3	1:E:441:GLY:H	1.59	0.68
1:A:439:GLU:HG3	1:A:441:GLY:H	1.59	0.68
1:B:527:ASN:HD22	1:B:527:ASN:C	2.01	0.68
1:B:439:GLU:C	1:B:441:GLY:H	1.99	0.68
1:B:439:GLU:HG3	1:B:441:GLY:H	1.59	0.68
1:E:494:TYR:CE1	1:F:313:GLN:HG2	2.28	0.68
1:F:439:GLU:HG3	1:F:441:GLY:H	1.59	0.67
1:F:527:ASN:HD22	1:F:527:ASN:C	2.01	0.67
1:A:23:HIS:CD2	1:A:25:LEU:H	2.00	0.66
1:E:286:HIS:HD2	3:F:1371:HOH:O	1.77	0.66
1:A:457:GLN:HE22	1:A:552:LEU:H	1.43	0.66
1:A:286:HIS:HD2	3:B:1371:HOH:O	1.77	0.66
1:C:439:GLU:HG3	1:C:441:GLY:H	1.59	0.66
1:E:573:VAL:HG11	1:E:598:MET:HE1	1.78	0.66
1:A:507:THR:HG23	1:A:605:GLY:O	1.96	0.66
1:A:246:GLN:HB2	1:A:341:VAL:HG21	1.78	0.66
1:C:457:GLN:HE22	1:C:552:LEU:H	1.43	0.66
1:E:507:THR:HG23	1:E:605:GLY:O	1.96	0.66
1:B:507:THR:HG23	1:B:605:GLY:O	1.96	0.65
1:F:573:VAL:HG11	1:F:598:MET:HE1	1.78	0.65
1:A:494:TYR:CE1	1:B:313:GLN:HG2	2.31	0.65
1:D:507:THR:HG23	1:D:605:GLY:O	1.96	0.65
1:E:457:GLN:HE22	1:E:552:LEU:H	1.43	0.65
1:F:246:GLN:HB2	1:F:341:VAL:HG21	1.78	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:457:GLN:HE22	1:B:552:LEU:H	1.43	0.65
1:F:457:GLN:HE22	1:F:552:LEU:H	1.43	0.65
1:D:573:VAL:HG11	1:D:598:MET:HE1	1.78	0.65
1:C:507:THR:HG23	1:C:605:GLY:O	1.96	0.65
1:E:308:PRO:HB3	1:F:497:ALA:HB2	1.77	0.65
1:B:573:VAL:HG11	1:B:598:MET:HE1	1.78	0.64
1:F:507:THR:HG23	1:F:605:GLY:O	1.96	0.64
1:C:573:VAL:HG11	1:C:598:MET:HE1	1.78	0.64
1:A:573:VAL:HG11	1:A:598:MET:HE1	1.78	0.64
1:C:246:GLN:HB2	1:C:341:VAL:HG21	1.78	0.64
1:E:406:GLU:OE2	1:F:376:HIS:ND1	2.29	0.64
1:E:313:GLN:HG2	1:F:494:TYR:CE1	2.33	0.64
1:B:246:GLN:HB2	1:B:341:VAL:HG21	1.78	0.64
1:D:457:GLN:HE22	1:D:552:LEU:H	1.43	0.64
1:F:338:CYS:HG	1:F:364:CYS:HG	0.77	0.64
1:D:246:GLN:HB2	1:D:341:VAL:HG21	1.78	0.63
1:D:338:CYS:HG	1:D:364:CYS:CB	2.11	0.63
1:E:246:GLN:HB2	1:E:341:VAL:HG21	1.78	0.63
1:C:313:GLN:HG2	1:D:494:TYR:CE1	2.33	0.63
1:A:308:PRO:HB3	1:B:497:ALA:HB2	1.81	0.63
1:E:546:THR:HG21	1:F:546:THR:HG22	1.71	0.62
1:F:504:THR:HG21	3:F:1434:HOH:O	2.00	0.62
1:C:504:THR:HG21	3:C:1434:HOH:O	2.00	0.62
1:C:494:TYR:CE1	1:D:313:GLN:HG2	2.33	0.62
1:E:504:THR:HG21	3:E:1434:HOH:O	2.00	0.62
1:A:313:GLN:HG2	1:B:494:TYR:CE1	2.35	0.62
3:C:1371:HOH:O	1:D:286:HIS:HD2	1.83	0.62
1:B:664:THR:CG2	1:B:667:GLU:HG3	2.31	0.61
1:C:497:ALA:HB2	1:D:308:PRO:HB3	1.82	0.61
1:F:664:THR:CG2	1:F:667:GLU:HG3	2.31	0.61
1:B:504:THR:HG21	3:B:1434:HOH:O	2.00	0.61
1:E:664:THR:CG2	1:E:667:GLU:HG3	2.31	0.61
1:D:664:THR:CG2	1:D:667:GLU:HG3	2.31	0.61
1:E:497:ALA:HB2	1:F:308:PRO:HB3	1.82	0.61
1:C:664:THR:CG2	1:C:667:GLU:HG3	2.31	0.61
1:D:504:THR:HG21	3:D:1434:HOH:O	2.00	0.61
1:C:308:PRO:HB3	1:D:497:ALA:HB2	1.83	0.60
1:A:504:THR:HG21	3:A:1434:HOH:O	2.00	0.60
1:E:338:CYS:CB	1:E:364:CYS:HG	2.15	0.60
1:A:664:THR:CG2	1:A:667:GLU:HG3	2.31	0.60
1:C:376:HIS:ND1	1:D:406:GLU:OE2	2.33	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:211:ARG:CD	1:F:211:ARG:N	2.60	0.59
1:C:527:ASN:HD21	1:C:529:ASN:HB2	1.68	0.59
1:E:527:ASN:HD21	1:E:529:ASN:HB2	1.68	0.59
1:F:338:CYS:CB	1:F:364:CYS:HG	2.15	0.59
1:E:414:MET:HE3	1:E:418:ALA:HB3	1.85	0.58
1:C:286:HIS:HD2	3:D:1371:HOH:O	1.85	0.58
1:A:439:GLU:C	1:A:441:GLY:N	2.62	0.58
1:C:414:MET:HE3	1:C:418:ALA:HB3	1.86	0.58
1:F:631:PHE:CG	1:F:632:PRO:HA	2.39	0.58
1:B:527:ASN:HD21	1:B:529:ASN:HB2	1.68	0.58
1:B:631:PHE:CG	1:B:632:PRO:HA	2.39	0.58
3:E:1371:HOH:O	1:F:286:HIS:HD2	1.86	0.58
1:F:527:ASN:HD21	1:F:529:ASN:HB2	1.68	0.58
1:C:631:PHE:CG	1:C:632:PRO:HA	2.39	0.58
1:E:631:PHE:CG	1:E:632:PRO:HA	2.39	0.58
1:E:146:ASN:C	1:E:146:ASN:HD22	2.12	0.58
1:A:414:MET:HE3	1:A:418:ALA:HB3	1.85	0.58
1:A:527:ASN:HD21	1:A:529:ASN:HB2	1.68	0.58
1:A:631:PHE:CG	1:A:632:PRO:HA	2.39	0.58
1:B:392:THR:HG22	3:B:1004:HOH:O	2.03	0.58
1:D:631:PHE:CG	1:D:632:PRO:HA	2.39	0.58
1:A:146:ASN:C	1:A:146:ASN:HD22	2.11	0.57
1:F:414:MET:HE3	1:F:418:ALA:HB3	1.85	0.57
1:B:146:ASN:HD22	1:B:146:ASN:C	2.11	0.57
1:B:467:ARG:HD2	1:B:471:ASP:OD1	2.05	0.57
1:F:146:ASN:C	1:F:146:ASN:HD22	2.11	0.57
1:B:414:MET:HE3	1:B:418:ALA:HB3	1.86	0.57
1:C:392:THR:HG22	3:C:1004:HOH:O	2.04	0.57
1:F:467:ARG:HD2	1:F:471:ASP:OD1	2.05	0.57
1:D:414:MET:HE3	1:D:418:ALA:HB3	1.85	0.57
1:D:527:ASN:HD21	1:D:529:ASN:HB2	1.68	0.57
1:A:664:THR:HG22	1:A:667:GLU:HG3	1.87	0.57
1:E:664:THR:HG22	1:E:667:GLU:HG3	1.87	0.57
1:C:546:THR:HG22	1:D:546:THR:HG21	1.71	0.57
1:D:62:LYS:HE2	1:D:66[A]:GLN:OE1	2.05	0.57
1:F:573:VAL:CG1	1:F:598:MET:HE1	2.35	0.57
1:A:467:ARG:HD2	1:A:471:ASP:OD1	2.04	0.56
1:B:62:LYS:HE2	1:B:66[A]:GLN:OE1	2.05	0.56
1:E:467:ARG:HD2	1:E:471:ASP:OD1	2.04	0.56
1:C:146:ASN:C	1:C:146:ASN:HD22	2.11	0.56
1:C:338:CYS:HG	1:C:364:CYS:CB	2.14	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:554:LYS:NZ	1:B:483:SER:O	2.38	0.56
1:C:467:ARG:HD2	1:C:471:ASP:OD1	2.05	0.56
1:D:146:ASN:C	1:D:146:ASN:HD22	2.11	0.56
1:D:573:VAL:CG1	1:D:598:MET:HE1	2.35	0.56
1:F:62:LYS:HE2	1:F:66[A]:GLN:OE1	2.05	0.56
1:D:439:GLU:C	1:D:441:GLY:N	2.62	0.56
1:F:664:THR:HG22	1:F:667:GLU:HG3	1.87	0.56
1:A:62:LYS:HE2	1:A:66[A]:GLN:OE1	2.05	0.56
1:B:664:THR:HG22	1:B:667:GLU:HG3	1.87	0.56
1:C:573:VAL:CG1	1:C:598:MET:HE1	2.35	0.56
1:F:392:THR:HG22	3:F:1004:HOH:O	2.06	0.56
1:C:375:LYS:HG3	1:C:388:VAL:HG22	1.88	0.56
1:D:392:THR:HG22	3:D:1004:HOH:O	2.06	0.56
1:D:467:ARG:HD2	1:D:471:ASP:OD1	2.05	0.56
1:E:211:ARG:CD	1:E:211:ARG:N	2.60	0.56
1:C:182:ASP:OD1	1:D:664:THR:HG23	2.05	0.56
1:E:62:LYS:HE2	1:E:66[A]:GLN:OE1	2.05	0.56
1:E:375:LYS:HG3	1:E:388:VAL:HG22	1.88	0.56
1:A:546:THR:HG21	1:B:546:THR:HG22	1.72	0.56
1:E:573:VAL:CG1	1:E:598:MET:HE1	2.35	0.56
1:A:573:VAL:CG1	1:A:598:MET:HE1	2.35	0.55
1:C:62:LYS:HE2	1:C:66[A]:GLN:OE1	2.05	0.55
1:A:497:ALA:HB2	1:B:308:PRO:HB3	1.87	0.55
1:C:664:THR:HG22	1:C:667:GLU:HG3	1.87	0.55
1:D:375:LYS:HG3	1:D:388:VAL:HG22	1.88	0.55
1:B:573:VAL:CG1	1:B:598:MET:HE1	2.35	0.55
1:D:664:THR:HG22	1:D:667:GLU:HG3	1.87	0.55
1:E:157:THR:HB	1:E:159:GLY:N	2.21	0.55
1:A:182:ASP:OD1	1:B:664:THR:HG23	2.06	0.55
3:A:1371:HOH:O	1:B:286:HIS:HD2	1.89	0.55
1:C:664:THR:HG23	1:D:182:ASP:OD1	2.06	0.55
1:F:375:LYS:HG3	1:F:388:VAL:HG22	1.88	0.55
1:B:598:MET:HE2	1:B:602:ILE:CG1	2.35	0.55
1:B:631:PHE:CD1	1:B:632:PRO:HA	2.42	0.55
1:F:598:MET:HE2	1:F:602:ILE:CG1	2.35	0.55
1:C:631:PHE:CD1	1:C:632:PRO:HA	2.42	0.54
1:D:631:PHE:CD1	1:D:632:PRO:HA	2.42	0.54
1:F:631:PHE:CD1	1:F:632:PRO:HA	2.42	0.54
1:A:375:LYS:HG3	1:A:388:VAL:HG22	1.88	0.54
1:A:631:PHE:CD1	1:A:632:PRO:HA	2.42	0.54
1:B:439:GLU:C	1:B:441:GLY:N	2.62	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:631:PHE:CD1	1:E:632:PRO:HA	2.42	0.54
1:A:310:PHE:HA	1:A:313:GLN:NE2	2.23	0.54
1:E:554:LYS:NZ	1:F:483:SER:O	2.41	0.54
1:F:479:ASP:HB3	1:F:519:THR:HB	1.90	0.54
1:A:338:CYS:HG	1:A:364:CYS:HG	0.66	0.54
1:D:310:PHE:HA	1:D:313:GLN:NE2	2.23	0.54
1:B:157:THR:HB	1:B:159:GLY:N	2.21	0.54
1:B:310:PHE:HA	1:B:313:GLN:NE2	2.23	0.54
1:B:479:ASP:HB3	1:B:519:THR:HB	1.90	0.54
1:E:479:ASP:HB3	1:E:519:THR:HB	1.90	0.54
1:A:468:ILE:N	1:A:473:ASN:HD21	2.05	0.54
1:D:479:ASP:HB3	1:D:519:THR:HB	1.90	0.54
1:D:598:MET:HE2	1:D:602:ILE:CG1	2.35	0.54
1:E:310:PHE:HA	1:E:313:GLN:NE2	2.23	0.54
1:F:157:THR:HB	1:F:159:GLY:N	2.21	0.54
1:C:211:ARG:CD	1:C:211:ARG:N	2.60	0.54
1:C:310:PHE:HA	1:C:313:GLN:NE2	2.23	0.53
1:E:376:HIS:ND1	1:F:406:GLU:OE2	2.40	0.53
1:A:211:ARG:CD	1:A:211:ARG:N	2.60	0.53
1:C:330:ASN:O	1:C:332:LEU:HD13	2.08	0.53
1:E:439:GLU:C	1:E:441:GLY:N	2.62	0.53
1:B:375:LYS:HG3	1:B:388:VAL:HG22	1.88	0.53
1:D:557:SER:O	1:D:561:LYS:HG3	2.09	0.53
1:F:155:PRO:HB2	1:F:171:GLN:OE1	2.09	0.53
1:A:376:HIS:ND1	1:B:406:GLU:OE2	2.42	0.53
1:E:330:ASN:O	1:E:332:LEU:HD13	2.08	0.53
1:A:330:ASN:O	1:A:332:LEU:HD13	2.08	0.53
1:A:392:THR:HG22	3:A:1004:HOH:O	2.08	0.53
1:A:664:THR:HG23	1:B:182:ASP:OD1	2.08	0.53
1:C:155:PRO:HB2	1:C:171:GLN:OE1	2.09	0.53
1:C:406:GLU:OE2	1:D:376:HIS:ND1	2.36	0.53
1:C:479:ASP:HB3	1:C:519:THR:HB	1.90	0.53
1:D:468:ILE:N	1:D:473:ASN:HD21	2.05	0.53
1:E:155:PRO:HB2	1:E:171:GLN:OE1	2.09	0.53
1:F:310:PHE:HA	1:F:313:GLN:NE2	2.23	0.53
1:F:330:ASN:O	1:F:332:LEU:HD13	2.08	0.53
1:A:406:GLU:HG3	1:B:375:LYS:O	2.09	0.53
1:A:557:SER:O	1:A:561:LYS:HG3	2.09	0.53
1:B:330:ASN:O	1:B:332:LEU:HD13	2.08	0.53
1:C:557:SER:O	1:C:561:LYS:HG3	2.09	0.53
1:D:155:PRO:HB2	1:D:171:GLN:OE1	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:557:SER:O	1:F:561:LYS:HG3	2.09	0.53
1:A:155:PRO:HB2	1:A:171:GLN:OE1	2.09	0.53
1:E:457:GLN:NE2	1:E:552:LEU:H	2.07	0.53
1:C:483:SER:O	1:D:554:LYS:NZ	2.42	0.53
1:B:557:SER:O	1:B:561:LYS:HG3	2.09	0.52
1:E:392:THR:HG22	3:E:1004:HOH:O	2.09	0.52
1:C:157:THR:HB	1:C:159:GLY:N	2.21	0.52
1:C:468:ILE:N	1:C:473:ASN:HD21	2.05	0.52
1:A:457:GLN:NE2	1:A:552:LEU:H	2.07	0.52
1:A:479:ASP:HB3	1:A:519:THR:HB	1.90	0.52
1:B:155:PRO:HB2	1:B:171:GLN:OE1	2.09	0.52
1:D:157:THR:HB	1:D:159:GLY:N	2.21	0.52
1:E:557:SER:O	1:E:561:LYS:HG3	2.09	0.52
1:F:439:GLU:HG3	1:F:441:GLY:N	2.25	0.52
1:C:312:HIS:HD2	3:C:1289:HOH:O	1.93	0.52
1:D:457:GLN:NE2	1:D:552:LEU:H	2.07	0.52
1:E:439:GLU:HG3	1:E:441:GLY:N	2.25	0.52
1:A:312:HIS:HD2	3:A:1289:HOH:O	1.93	0.52
1:B:468:ILE:N	1:B:473:ASN:HD21	2.05	0.52
1:D:69:GLU:CD	1:D:467:ARG:HH22	2.18	0.52
1:F:439:GLU:C	1:F:441:GLY:N	2.62	0.52
1:B:69:GLU:CD	1:B:467:ARG:HH22	2.18	0.52
1:C:69:GLU:CD	1:C:467:ARG:HH22	2.18	0.52
1:E:312:HIS:HD2	3:E:1289:HOH:O	1.93	0.52
1:E:444:GLY:HA3	1:E:452:ASN:HD21	1.75	0.52
1:A:664:THR:HG23	1:B:182:ASP:CG	2.34	0.52
1:B:312:HIS:HD2	3:B:1289:HOH:O	1.93	0.52
1:D:330:ASN:O	1:D:332:LEU:HD13	2.08	0.52
1:E:182:ASP:OD1	1:F:664:THR:HG23	2.10	0.52
1:D:547:GLN:NE2	1:D:640:THR:H	2.08	0.52
1:C:439:GLU:C	1:C:441:GLY:N	2.62	0.52
1:A:69:GLU:CD	1:A:467:ARG:HH22	2.18	0.52
1:F:69:GLU:CD	1:F:467:ARG:HH22	2.18	0.52
1:E:468:ILE:H	1:E:473:ASN:ND2	2.08	0.51
1:D:335:GLY:O	1:D:336:CYS:HB2	2.11	0.51
1:E:69:GLU:CD	1:E:467:ARG:HH22	2.18	0.51
1:E:547:GLN:NE2	1:E:640:THR:H	2.08	0.51
1:F:444:GLY:HA3	1:F:452:ASN:HD21	1.75	0.51
1:F:547:GLN:NE2	1:F:640:THR:H	2.08	0.51
1:B:444:GLY:HA3	1:B:452:ASN:HD21	1.75	0.51
1:B:547:GLN:NE2	1:B:640:THR:H	2.08	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:468:ILE:N	1:E:473:ASN:HD21	2.05	0.51
1:E:546:THR:HG22	1:F:546:THR:HG21	1.71	0.51
1:B:457:GLN:NE2	1:B:552:LEU:H	2.07	0.51
1:D:439:GLU:HG3	1:D:441:GLY:N	2.25	0.51
1:A:157:THR:HB	1:A:159:GLY:N	2.21	0.51
1:A:439:GLU:HG3	1:A:441:GLY:N	2.25	0.51
1:A:547:GLN:NE2	1:A:640:THR:H	2.08	0.51
1:C:457:GLN:NE2	1:C:552:LEU:H	2.07	0.51
1:D:312:HIS:HD2	3:D:1289:HOH:O	1.93	0.51
1:E:598:MET:HE2	1:E:602:ILE:CG1	2.35	0.51
1:A:598:MET:HE2	1:A:602:ILE:CG1	2.35	0.51
3:A:1008:HOH:O	1:B:375:LYS:HE2	2.11	0.51
1:C:335:GLY:O	1:C:336:CYS:HB2	2.11	0.51
1:C:444:GLY:HA3	1:C:452:ASN:HD21	1.75	0.51
1:D:444:GLY:HA3	1:D:452:ASN:HD21	1.75	0.51
1:E:335:GLY:O	1:E:336:CYS:HB2	2.11	0.51
1:A:335:GLY:O	1:A:336:CYS:HB2	2.11	0.51
1:B:335:GLY:O	1:B:336:CYS:HB2	2.11	0.51
1:A:444:GLY:HA3	1:A:452:ASN:HD21	1.75	0.51
1:C:332:LEU:HD23	1:C:364:CYS:HB3	1.93	0.51
1:C:598:MET:HE2	1:C:602:ILE:CG1	2.35	0.51
1:F:312:HIS:HD2	3:F:1289:HOH:O	1.93	0.51
1:F:332:LEU:HD23	1:F:364:CYS:HB3	1.93	0.51
1:C:439:GLU:HG3	1:C:441:GLY:N	2.25	0.51
1:D:468:ILE:H	1:D:473:ASN:ND2	2.08	0.51
1:E:332:LEU:HD23	1:E:364:CYS:HB3	1.93	0.51
1:A:176:TYR:HB3	1:A:185:GLN:HB2	1.93	0.50
1:C:23:HIS:HD2	1:C:25:LEU:N	1.92	0.50
1:E:176:TYR:HB3	1:E:185:GLN:HB2	1.93	0.50
1:F:468:ILE:N	1:F:473:ASN:HD21	2.05	0.50
1:C:547:GLN:NE2	1:C:640:THR:H	2.08	0.50
1:F:335:GLY:O	1:F:336:CYS:HB2	2.10	0.50
1:B:332:LEU:HD23	1:B:364:CYS:HB3	1.93	0.50
1:B:338:CYS:CB	1:B:364:CYS:HG	2.21	0.50
1:B:439:GLU:HG3	1:B:441:GLY:N	2.25	0.50
1:A:332:LEU:HD23	1:A:364:CYS:HB3	1.93	0.50
1:B:338:CYS:HG	1:B:364:CYS:HG	0.66	0.50
1:C:176:TYR:HB3	1:C:185:GLN:HB2	1.93	0.50
1:D:332:LEU:HD23	1:D:364:CYS:HB3	1.93	0.50
3:C:1008:HOH:O	1:D:375:LYS:HE2	2.11	0.49
1:E:494:TYR:CG	1:F:313:GLN:HG2	2.42	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:23:HIS:HD2	1:B:25:LEU:N	1.92	0.49
1:D:176:TYR:HB3	1:D:185:GLN:HB2	1.93	0.49
1:E:146:ASN:C	1:E:146:ASN:ND2	2.71	0.49
1:F:176:TYR:HB3	1:F:185:GLN:HB2	1.93	0.49
1:F:262:SER:O	1:F:263:ASN:HB2	2.13	0.49
1:A:146:ASN:C	1:A:146:ASN:ND2	2.70	0.49
1:E:406:GLU:HG3	1:F:375:LYS:O	2.12	0.49
1:F:457:GLN:NE2	1:F:552:LEU:H	2.07	0.49
1:B:146:ASN:C	1:B:146:ASN:ND2	2.70	0.49
1:B:176:TYR:HB3	1:B:185:GLN:HB2	1.93	0.49
1:C:146:ASN:C	1:C:146:ASN:ND2	2.71	0.49
1:C:468:ILE:H	1:C:473:ASN:ND2	2.08	0.49
1:A:338:CYS:CB	1:A:364:CYS:HG	2.21	0.49
1:A:449:PRO:HD3	1:B:534:TYR:CE1	2.48	0.49
1:B:211:ARG:CD	1:B:211:ARG:N	2.60	0.49
1:C:375:LYS:HE2	3:D:1008:HOH:O	2.12	0.49
1:B:262:SER:O	1:B:263:ASN:HB2	2.13	0.49
1:E:23:HIS:HD2	1:E:25:LEU:N	1.92	0.49
1:B:598:MET:HE3	1:B:598:MET:HA	1.95	0.49
1:A:598:MET:HE3	1:A:598:MET:HA	1.95	0.48
1:F:146:ASN:C	1:F:146:ASN:ND2	2.70	0.48
1:D:598:MET:HA	1:D:598:MET:HE3	1.95	0.48
1:D:262:SER:O	1:D:263:ASN:HB2	2.13	0.48
1:D:405:TPQ:H3	3:D:1053:HOH:O	2.13	0.48
1:E:262:SER:O	1:E:263:ASN:HB2	2.13	0.48
1:E:664:THR:HG23	1:F:182:ASP:OD1	2.13	0.48
1:C:262:SER:O	1:C:263:ASN:HB2	2.13	0.48
1:F:468:ILE:H	1:F:473:ASN:ND2	2.08	0.48
1:F:405:TPQ:H3	3:F:1053:HOH:O	2.13	0.48
1:A:144:PRO:HB2	1:A:146:ASN:ND2	2.29	0.48
1:C:182:ASP:CG	1:D:664:THR:HG23	2.38	0.48
1:D:23:HIS:HD2	1:D:25:LEU:N	1.92	0.48
1:E:144:PRO:HB2	1:E:146:ASN:ND2	2.29	0.48
1:E:405:TPQ:H3	3:E:1053:HOH:O	2.13	0.48
1:C:144:PRO:HB2	1:C:146:ASN:ND2	2.29	0.48
1:C:554:LYS:NZ	1:D:483:SER:O	2.45	0.48
1:E:301:MET:O	1:E:318:LEU:HA	2.14	0.48
1:D:301:MET:O	1:D:318:LEU:HA	2.14	0.48
1:F:144:PRO:HB2	1:F:146:ASN:ND2	2.29	0.48
1:F:301:MET:O	1:F:318:LEU:HA	2.14	0.48
1:E:598:MET:HE3	1:E:598:MET:HA	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:262:SER:O	1:A:263:ASN:HB2	2.13	0.48
1:A:330:ASN:HD22	1:B:375:LYS:NZ	2.11	0.48
1:A:405:TPQ:H3	3:A:1053:HOH:O	2.13	0.48
1:D:211:ARG:CD	1:D:211:ARG:N	2.60	0.48
1:B:405:TPQ:H3	3:B:1053:HOH:O	2.13	0.47
1:C:405:TPQ:H3	3:C:1053:HOH:O	2.13	0.47
1:F:23:HIS:HD2	1:F:25:LEU:N	1.92	0.47
1:A:330:ASN:HD22	1:B:375:LYS:HZ3	1.62	0.47
1:A:656:ASP:O	1:B:236:ARG:HG3	2.14	0.47
1:C:598:MET:HE3	1:C:598:MET:HA	1.95	0.47
1:F:598:MET:HE3	1:F:598:MET:HA	1.95	0.47
1:A:633:LEU:HD13	1:B:374:PHE:CD1	2.49	0.47
1:E:581:TYR:HA	1:E:582:PRO:HD2	1.77	0.47
1:B:301:MET:O	1:B:318:LEU:HA	2.14	0.47
1:C:301:MET:O	1:C:318:LEU:HA	2.14	0.47
1:D:144:PRO:HB2	1:D:146:ASN:ND2	2.29	0.47
3:E:1008:HOH:O	1:F:375:LYS:HE2	2.14	0.47
1:B:468:ILE:H	1:B:473:ASN:ND2	2.08	0.47
1:B:144:PRO:HB2	1:B:146:ASN:ND2	2.29	0.47
1:C:244:VAL:HG22	1:D:244:VAL:HG22	1.96	0.47
1:C:546:THR:HG21	1:D:546:THR:HG22	1.71	0.47
1:D:527:ASN:ND2	1:D:527:ASN:C	2.73	0.47
1:A:197:ASP:CG	1:A:200:GLU:HB2	2.40	0.46
1:A:301:MET:O	1:A:318:LEU:HA	2.14	0.46
1:A:527:ASN:HD21	1:A:529:ASN:HD22	1.64	0.46
1:B:197:ASP:CG	1:B:200:GLU:HB2	2.40	0.46
1:B:527:ASN:HD21	1:B:529:ASN:HD22	1.63	0.46
1:D:527:ASN:HD21	1:D:529:ASN:HD22	1.64	0.46
1:E:197:ASP:CG	1:E:200:GLU:HB2	2.40	0.46
1:E:527:ASN:HD21	1:E:529:ASN:HD22	1.64	0.46
1:F:527:ASN:HD21	1:F:529:ASN:HD22	1.64	0.46
1:C:581:TYR:HA	1:C:582:PRO:HD2	1.77	0.46
1:A:468:ILE:H	1:A:473:ASN:ND2	2.08	0.46
1:A:527:ASN:C	1:A:527:ASN:ND2	2.73	0.46
1:C:439:GLU:HG3	1:C:441:GLY:HA2	1.98	0.46
1:C:527:ASN:ND2	1:C:527:ASN:C	2.73	0.46
1:F:439:GLU:HG3	1:F:441:GLY:HA2	1.98	0.46
1:F:527:ASN:ND2	1:F:527:ASN:C	2.73	0.46
1:B:185:GLN:HG2	3:B:1266:HOH:O	2.16	0.46
1:B:439:GLU:HG3	1:B:441:GLY:HA2	1.98	0.46
1:E:656:ASP:O	1:F:236:ARG:HG3	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:68:LYS:HE2	1:F:280:ASP:OD2	2.16	0.46
1:A:375:LYS:HE2	3:B:1008:HOH:O	2.14	0.46
1:D:197:ASP:CG	1:D:200:GLU:HB2	2.40	0.46
1:E:664:THR:HG23	1:F:182:ASP:CG	2.40	0.46
1:F:197:ASP:CG	1:F:200:GLU:HB2	2.40	0.46
1:A:244:VAL:HG22	1:B:244:VAL:HG22	1.97	0.46
1:C:197:ASP:CG	1:C:200:GLU:HB2	2.40	0.46
1:C:344:TYR:CD1	1:C:361:ASN:HB3	2.51	0.46
1:C:374:PHE:CD1	1:D:633:LEU:HD13	2.51	0.46
1:C:375:LYS:O	1:D:406:GLU:HG3	2.15	0.46
1:A:185:GLN:HG2	3:A:1266:HOH:O	2.16	0.46
1:D:185:GLN:HG2	3:D:1266:HOH:O	2.16	0.46
1:A:406:GLU:CD	1:B:376:HIS:HA	2.40	0.46
1:A:642:MET:HE3	1:A:644:ARG:CD	2.46	0.46
1:B:344:TYR:CD1	1:B:361:ASN:HB3	2.51	0.46
1:C:68:LYS:HE2	1:C:280:ASP:OD2	2.16	0.46
1:E:449:PRO:HD3	1:F:534:TYR:CE1	2.52	0.46
1:F:344:TYR:CD1	1:F:361:ASN:HB3	2.51	0.46
1:F:642:MET:HE3	1:F:644:ARG:CD	2.46	0.46
1:B:642:MET:HE3	1:B:644:ARG:CD	2.46	0.45
1:C:185:GLN:HG2	3:C:1266:HOH:O	2.16	0.45
1:C:633:LEU:HD13	1:D:374:PHE:CD1	2.51	0.45
1:A:23:HIS:HD2	1:A:25:LEU:N	1.92	0.45
1:A:344:TYR:CD1	1:A:361:ASN:HB3	2.51	0.45
1:D:146:ASN:C	1:D:146:ASN:ND2	2.70	0.45
1:F:185:GLN:HG2	3:F:1266:HOH:O	2.16	0.45
1:C:642:MET:HE3	1:C:644:ARG:CD	2.46	0.45
1:E:68:LYS:HE2	1:E:280:ASP:OD2	2.16	0.45
1:D:642:MET:HE3	1:D:644:ARG:CD	2.46	0.45
1:E:633:LEU:HD13	1:F:374:PHE:CD1	2.51	0.45
1:D:218:HIS:CE1	1:D:450:ASN:ND2	2.85	0.45
1:D:344:TYR:CD1	1:D:361:ASN:HB3	2.51	0.45
1:C:218:HIS:CE1	1:C:450:ASN:ND2	2.85	0.45
1:C:452:ASN:C	1:C:452:ASN:HD22	2.25	0.45
1:E:344:TYR:CD1	1:E:361:ASN:HB3	2.51	0.45
1:B:50:SER:HB2	1:B:352:ARG:CG	2.47	0.45
1:C:527:ASN:HD21	1:C:529:ASN:HD22	1.64	0.45
1:C:664:THR:HG23	1:D:182:ASP:CG	2.41	0.45
1:F:218:HIS:CE1	1:F:450:ASN:ND2	2.85	0.45
1:B:68:LYS:HE2	1:B:280:ASP:OD2	2.16	0.45
1:B:218:HIS:CE1	1:B:450:ASN:ND2	2.85	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:439:GLU:HG3	1:E:441:GLY:HA2	1.98	0.45
1:E:642:MET:HE3	1:E:644:ARG:CD	2.46	0.45
1:F:50:SER:HB2	1:F:352:ARG:CG	2.47	0.45
1:A:642:MET:HE3	1:A:644:ARG:HD2	1.99	0.45
1:B:392:THR:CG2	3:B:1004:HOH:O	2.61	0.45
1:D:50:SER:HB2	1:D:352:ARG:CG	2.47	0.45
1:A:68:LYS:HE2	1:A:280:ASP:OD2	2.16	0.44
1:A:494:TYR:CG	1:B:313:GLN:HG2	2.46	0.44
1:E:218:HIS:CE1	1:E:450:ASN:ND2	2.85	0.44
1:B:452:ASN:C	1:B:452:ASN:HD22	2.25	0.44
1:D:439:GLU:HG3	1:D:441:GLY:HA2	1.98	0.44
1:D:452:ASN:HD22	1:D:452:ASN:C	2.25	0.44
1:E:330:ASN:HD22	1:F:375:LYS:NZ	2.14	0.44
1:E:669:LYS:NZ	1:F:181:GLU:OE1	2.39	0.44
1:F:392:THR:CG2	3:F:1004:HOH:O	2.64	0.44
1:F:452:ASN:C	1:F:452:ASN:HD22	2.25	0.44
1:C:50:SER:HB2	1:C:352:ARG:CG	2.47	0.44
1:C:330:ASN:HD22	1:D:375:LYS:NZ	2.16	0.44
1:D:68:LYS:HE2	1:D:280:ASP:OD2	2.16	0.44
1:A:218:HIS:CE1	1:A:450:ASN:ND2	2.85	0.44
1:A:439:GLU:HG3	1:A:441:GLY:HA2	1.98	0.44
1:B:527:ASN:ND2	1:B:527:ASN:C	2.73	0.44
1:C:146:ASN:HD22	1:C:147:GLU:N	2.16	0.44
1:C:642:MET:HE3	1:C:644:ARG:HD2	1.99	0.44
1:D:581:TYR:HA	1:D:582:PRO:HD2	1.77	0.44
1:E:50:SER:HB2	1:E:352:ARG:CG	2.47	0.44
1:E:565:TRP:CD1	1:E:582:PRO:HB2	2.53	0.44
1:F:458:HIS:O	1:F:621:GLY:HA3	2.18	0.44
1:A:146:ASN:HD22	1:A:147:GLU:N	2.16	0.44
1:D:146:ASN:HD22	1:D:147:GLU:N	2.16	0.44
1:D:565:TRP:CD1	1:D:582:PRO:HB2	2.53	0.44
1:E:185:GLN:HG2	3:E:1266:HOH:O	2.16	0.44
1:A:50:SER:HB2	1:A:352:ARG:CG	2.47	0.44
1:A:565:TRP:CD1	1:A:582:PRO:HB2	2.53	0.44
1:B:452:ASN:HD22	1:B:453:ALA:N	2.16	0.44
1:A:452:ASN:C	1:A:452:ASN:HD22	2.25	0.44
1:C:311:PRO:CA	1:C:313:GLN:NE2	2.75	0.44
1:D:458:HIS:O	1:D:621:GLY:HA3	2.18	0.44
1:E:452:ASN:C	1:E:452:ASN:HD22	2.25	0.44
1:F:146:ASN:ND2	1:F:147:GLU:HG3	2.33	0.44
1:F:565:TRP:CD1	1:F:582:PRO:HB2	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:546:THR:HG22	1:B:546:THR:HG21	1.73	0.44
1:D:120:ASP:OD2	1:D:352:ARG:NH2	2.43	0.44
1:E:301:MET:HE3	1:E:460:PHE:CE2	2.53	0.44
1:E:452:ASN:HD22	1:E:453:ALA:N	2.16	0.44
1:F:452:ASN:HD22	1:F:453:ALA:N	2.16	0.44
1:F:642:MET:HE3	1:F:644:ARG:HD2	1.99	0.44
1:A:146:ASN:ND2	1:A:147:GLU:HG3	2.33	0.43
1:A:392:THR:HG23	1:A:415:GLN:OE1	2.18	0.43
1:A:452:ASN:HD22	1:A:453:ALA:N	2.16	0.43
1:B:234:ALA:HB1	3:B:1231:HOH:O	2.17	0.43
1:B:301:MET:HE3	1:B:460:PHE:CE2	2.53	0.43
1:C:458:HIS:O	1:C:621:GLY:HA3	2.18	0.43
1:D:452:ASN:HD22	1:D:453:ALA:N	2.16	0.43
1:E:157:THR:CB	1:E:159:GLY:H	2.27	0.43
1:E:375:LYS:HE2	3:F:1008:HOH:O	2.18	0.43
1:B:294:HIS:HD2	3:B:1287:HOH:O	2.01	0.43
1:C:146:ASN:ND2	1:C:147:GLU:HG3	2.33	0.43
1:C:375:LYS:NZ	1:D:330:ASN:HD22	2.15	0.43
1:E:146:ASN:ND2	1:E:147:GLU:HG3	2.33	0.43
1:E:642:MET:HE3	1:E:644:ARG:HD2	1.99	0.43
1:F:392:THR:HG23	1:F:415:GLN:OE1	2.18	0.43
1:A:669:LYS:NZ	1:B:181:GLU:OE1	2.35	0.43
1:D:301:MET:HE3	1:D:460:PHE:CE2	2.53	0.43
1:D:369:ASP:OD1	1:D:390:ARG:NH1	2.52	0.43
1:E:392:THR:HG23	1:E:415:GLN:OE1	2.18	0.43
1:F:146:ASN:HD22	1:F:147:GLU:N	2.16	0.43
1:F:382:ASN:ND2	3:F:1071:HOH:O	2.50	0.43
1:F:581:TYR:HA	1:F:582:PRO:HD2	1.77	0.43
1:A:23:HIS:HA	1:A:24:PRO:HD3	1.91	0.43
1:A:369:ASP:OD1	1:A:390:ARG:NH1	2.52	0.43
1:B:146:ASN:ND2	1:B:147:GLU:HG3	2.33	0.43
1:B:290:ARG:HA	1:B:291:PRO:HD3	1.90	0.43
1:B:458:HIS:O	1:B:621:GLY:HA3	2.18	0.43
1:C:303:VAL:HA	1:C:457:GLN:O	2.19	0.43
1:C:369:ASP:OD1	1:C:390:ARG:NH1	2.52	0.43
1:D:642:MET:HE3	1:D:644:ARG:HD2	1.99	0.43
1:E:303:VAL:HA	1:E:457:GLN:O	2.19	0.43
1:E:483:SER:O	1:F:554:LYS:NZ	2.51	0.43
1:E:573:VAL:HG11	1:E:598:MET:CE	2.47	0.43
1:A:301:MET:HE3	1:A:460:PHE:CE2	2.53	0.43
1:A:303:VAL:HA	1:A:457:GLN:O	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:642:MET:HE3	1:B:644:ARG:HD2	1.99	0.43
1:C:301:MET:HE3	1:C:460:PHE:CE2	2.53	0.43
1:C:406:GLU:HG3	1:D:375:LYS:O	2.18	0.43
1:C:573:VAL:HG11	1:C:598:MET:CE	2.47	0.43
1:F:221:ALA:HA	3:F:1210:HOH:O	2.19	0.43
1:F:634:MET:HA	1:F:635:PRO:HD3	1.83	0.43
1:A:458:HIS:O	1:A:621:GLY:HA3	2.18	0.43
1:B:146:ASN:HD22	1:B:147:GLU:N	2.16	0.43
1:B:303:VAL:HA	1:B:457:GLN:O	2.19	0.43
1:C:66[B]:GLN:HE21	1:C:72:GLY:HA3	1.84	0.43
1:C:392:THR:CG2	3:C:1004:HOH:O	2.63	0.43
1:D:146:ASN:ND2	1:D:147:GLU:HG3	2.33	0.43
1:D:392:THR:HG23	1:D:415:GLN:OE1	2.18	0.43
1:F:301:MET:HE3	1:F:460:PHE:CE2	2.53	0.43
1:F:369:ASP:OD1	1:F:390:ARG:NH1	2.52	0.43
1:C:452:ASN:HD22	1:C:453:ALA:N	2.16	0.43
1:D:221:ALA:HA	3:D:1210:HOH:O	2.19	0.43
1:E:244:VAL:HG22	1:F:244:VAL:HG22	2.00	0.43
1:E:294:HIS:HD2	3:E:1287:HOH:O	2.01	0.43
1:F:66[B]:GLN:HE21	1:F:72:GLY:HA3	1.84	0.43
1:D:373:LEU:HD12	1:D:373:LEU:HA	1.88	0.43
1:E:66[B]:GLN:HE21	1:E:72:GLY:HA3	1.84	0.43
1:E:140:LEU:HD12	1:E:140:LEU:HA	1.86	0.43
1:A:176:TYR:CE1	1:A:189:PRO:HB3	2.54	0.43
1:B:565:TRP:CD1	1:B:582:PRO:HB2	2.53	0.43
1:E:146:ASN:HD22	1:E:147:GLU:N	2.16	0.43
1:E:458:HIS:O	1:E:621:GLY:HA3	2.18	0.43
1:A:294:HIS:HD2	3:A:1287:HOH:O	2.01	0.43
1:B:66[B]:GLN:HE21	1:B:72:GLY:HA3	1.84	0.43
1:B:581:TYR:HA	1:B:582:PRO:HD2	1.77	0.43
1:C:385:THR:OG1	1:C:665:THR:HA	2.19	0.43
1:D:66[B]:GLN:HE21	1:D:72:GLY:HA3	1.84	0.43
1:D:294:HIS:HD2	3:D:1287:HOH:O	2.01	0.43
1:F:303:VAL:HA	1:F:457:GLN:O	2.19	0.43
1:A:385:THR:OG1	1:A:665:THR:HA	2.19	0.42
1:C:23:HIS:HA	1:C:24:PRO:HD3	1.91	0.42
1:C:221:ALA:HA	3:C:1210:HOH:O	2.19	0.42
1:F:294:HIS:HD2	3:F:1287:HOH:O	2.01	0.42
1:F:311:PRO:CA	1:F:313:GLN:NE2	2.75	0.42
1:B:439:GLU:HG3	1:B:441:GLY:CA	2.50	0.42
1:B:573:VAL:HG11	1:B:598:MET:CE	2.47	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:598:MET:HE3	1:B:601:TRP:HB2	2.02	0.42
1:C:646:ARG:O	1:C:647:HIS:HB2	2.20	0.42
1:A:270:PHE:HA	1:A:275:GLY:O	2.20	0.42
1:A:311:PRO:CA	1:A:313:GLN:NE2	2.75	0.42
1:A:598:MET:HE3	1:A:601:TRP:HB2	2.02	0.42
1:B:392:THR:HG23	1:B:415:GLN:OE1	2.18	0.42
1:C:310:PHE:HA	1:C:313:GLN:HE21	1.85	0.42
1:C:439:GLU:HG3	1:C:441:GLY:CA	2.50	0.42
1:E:310:PHE:HA	1:E:313:GLN:HE21	1.85	0.42
1:A:439:GLU:HG3	1:A:441:GLY:CA	2.50	0.42
1:C:157:THR:CB	1:C:159:GLY:H	2.27	0.42
1:C:176:TYR:CE1	1:C:189:PRO:HB3	2.54	0.42
1:C:565:TRP:CD1	1:C:582:PRO:HB2	2.53	0.42
1:D:176:TYR:CE1	1:D:189:PRO:HB3	2.54	0.42
1:E:53:THR:O	1:E:81:TYR:HA	2.20	0.42
1:F:53:THR:O	1:F:81:TYR:HA	2.20	0.42
1:B:646:ARG:O	1:B:647:HIS:HB2	2.20	0.42
1:C:392:THR:HG23	1:C:415:GLN:OE1	2.18	0.42
1:D:128:ILE:HG13	1:D:129:ARG:N	2.35	0.42
1:D:303:VAL:HA	1:D:457:GLN:O	2.19	0.42
1:E:176:TYR:CE1	1:E:189:PRO:HB3	2.54	0.42
1:E:221:ALA:HA	3:E:1210:HOH:O	2.19	0.42
1:E:369:ASP:OD1	1:E:390:ARG:NH1	2.52	0.42
1:F:176:TYR:CE1	1:F:189:PRO:HB3	2.54	0.42
1:A:374:PHE:CD1	1:B:633:LEU:HD13	2.54	0.42
1:D:53:THR:O	1:D:81:TYR:HA	2.20	0.42
1:D:270:PHE:HA	1:D:275:GLY:O	2.20	0.42
1:E:646:ARG:O	1:E:647:HIS:HB2	2.20	0.42
1:B:128:ILE:HG13	1:B:129:ARG:N	2.35	0.42
1:B:385:THR:OG1	1:B:665:THR:HA	2.19	0.42
1:D:385:THR:OG1	1:D:665:THR:HA	2.19	0.42
1:D:439:GLU:HG3	1:D:441:GLY:CA	2.49	0.42
1:E:385:THR:OG1	1:E:665:THR:HA	2.19	0.42
1:F:124:THR:O	1:F:127:VAL:HG13	2.20	0.42
1:A:66[B]:GLN:HE21	1:A:72:GLY:HA3	1.84	0.42
1:A:581:TYR:HA	1:A:582:PRO:HD2	1.77	0.42
1:B:645:PRO:O	1:B:646:ARG:HD2	2.20	0.42
1:C:598:MET:HE3	1:C:601:TRP:HB2	2.02	0.42
1:E:120:ASP:OD2	1:E:352:ARG:NH2	2.43	0.42
1:A:175:VAL:HG11	1:A:190:LEU:HD12	2.02	0.42
1:A:345:LEU:HB2	1:A:363:VAL:HB	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:425:LEU:HB3	3:A:1499:HOH:O	2.20	0.42
1:B:369:ASP:OD1	1:B:390:ARG:NH1	2.52	0.42
1:C:175:VAL:HG11	1:C:190:LEU:HD12	2.02	0.42
1:D:573:VAL:HG11	1:D:598:MET:CE	2.47	0.42
1:E:345:LEU:HB2	1:E:363:VAL:HB	2.02	0.42
1:A:128:ILE:HG13	1:A:129:ARG:N	2.35	0.42
1:B:176:TYR:CE1	1:B:189:PRO:HB3	2.54	0.42
1:B:221:ALA:HA	3:B:1210:HOH:O	2.19	0.42
1:B:270:PHE:HA	1:B:275:GLY:O	2.20	0.42
1:C:558:LEU:HD23	1:C:558:LEU:HA	1.88	0.42
1:D:124:THR:O	1:D:127:VAL:HG13	2.20	0.42
1:D:646:ARG:O	1:D:647:HIS:HB2	2.20	0.42
1:E:330:ASN:HD22	1:F:375:LYS:HZ3	1.68	0.42
1:F:100:SER:O	1:F:101:LEU:C	2.63	0.42
1:F:385:THR:OG1	1:F:665:THR:HA	2.19	0.42
1:A:221:ALA:HA	3:A:1210:HOH:O	2.19	0.41
1:B:53:THR:O	1:B:81:TYR:HA	2.20	0.41
1:E:312:HIS:HE1	3:E:1060:HOH:O	2.03	0.41
1:F:439:GLU:HG3	1:F:441:GLY:CA	2.50	0.41
1:A:53:THR:O	1:A:81:TYR:HA	2.20	0.41
1:A:475:ALA:HA	1:A:524:ASP:O	2.21	0.41
1:A:483:SER:O	1:B:554:LYS:NZ	2.53	0.41
1:B:425:LEU:HB3	3:B:1499:HOH:O	2.20	0.41
1:C:290:ARG:HA	1:C:291:PRO:HD3	1.90	0.41
1:D:475:ALA:HA	1:D:524:ASP:O	2.21	0.41
1:D:645:PRO:O	1:D:646:ARG:HD2	2.20	0.41
1:F:573:VAL:HG11	1:F:598:MET:CE	2.47	0.41
1:A:124:THR:O	1:A:127:VAL:HG13	2.20	0.41
1:A:646:ARG:O	1:A:647:HIS:HB2	2.20	0.41
1:B:310:PHE:HA	1:B:313:GLN:HE21	1.85	0.41
1:C:124:THR:O	1:C:127:VAL:HG13	2.20	0.41
1:C:294:HIS:HD2	3:C:1287:HOH:O	2.01	0.41
1:D:100:SER:O	1:D:101:LEU:C	2.63	0.41
1:D:598:MET:HE3	1:D:601:TRP:HB2	2.02	0.41
1:E:475:ALA:HA	1:E:524:ASP:O	2.21	0.41
1:E:645:PRO:O	1:E:646:ARG:HD2	2.20	0.41
1:F:375:LYS:HG2	1:F:376:HIS:N	2.35	0.41
1:F:425:LEU:HB3	3:F:1499:HOH:O	2.20	0.41
1:A:558:LEU:HD23	1:A:558:LEU:HA	1.88	0.41
1:C:346:ASP:OD2	1:C:360:LYS:HE3	2.21	0.41
1:C:475:ALA:HA	1:C:524:ASP:O	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:290:ARG:HA	1:D:291:PRO:HD3	1.90	0.41
1:D:345:LEU:HB2	1:D:363:VAL:HB	2.02	0.41
1:E:439:GLU:HG3	1:E:441:GLY:CA	2.50	0.41
1:C:270:PHE:HA	1:C:275:GLY:O	2.20	0.41
1:C:312:HIS:HE1	3:C:1060:HOH:O	2.03	0.41
1:C:345:LEU:HB2	1:C:363:VAL:HB	2.02	0.41
1:D:641:LEU:C	1:D:641:LEU:CD2	2.94	0.41
1:E:270:PHE:HA	1:E:275:GLY:O	2.20	0.41
1:E:311:PRO:CA	1:E:313:GLN:NE2	2.75	0.41
1:E:406:GLU:CD	1:F:376:HIS:HA	2.44	0.41
1:E:565:TRP:CD1	1:E:565:TRP:H	2.39	0.41
1:F:120:ASP:OD2	1:F:352:ARG:NH2	2.43	0.41
1:F:270:PHE:HA	1:F:275:GLY:O	2.20	0.41
1:A:641:LEU:C	1:A:641:LEU:CD2	2.94	0.41
1:A:645:PRO:O	1:A:646:ARG:HD2	2.20	0.41
1:B:100:SER:O	1:B:101:LEU:C	2.63	0.41
1:B:382:ASN:ND2	3:B:1071:HOH:O	2.48	0.41
1:C:375:LYS:HG2	1:C:376:HIS:N	2.35	0.41
1:F:345:LEU:HB2	1:F:363:VAL:HB	2.02	0.41
1:A:100:SER:O	1:A:101:LEU:C	2.63	0.41
1:A:565:TRP:CD1	1:A:565:TRP:H	2.39	0.41
1:E:124:THR:O	1:E:127:VAL:HG13	2.20	0.41
1:E:375:LYS:HG2	1:E:376:HIS:N	2.35	0.41
1:F:157:THR:CB	1:F:159:GLY:H	2.27	0.41
1:F:641:LEU:C	1:F:641:LEU:CD2	2.94	0.41
1:B:124:THR:O	1:B:127:VAL:HG13	2.20	0.41
1:B:312:HIS:HE1	3:B:1060:HOH:O	2.03	0.41
1:C:348:HIS:HD2	3:C:1460:HOH:O	2.04	0.41
1:E:641:LEU:C	1:E:641:LEU:CD2	2.94	0.41
1:F:175:VAL:HG11	1:F:190:LEU:HD12	2.02	0.41
1:F:475:ALA:HA	1:F:524:ASP:O	2.20	0.41
1:F:645:PRO:O	1:F:646:ARG:HD2	2.20	0.41
1:A:346:ASP:OD2	1:A:360:LYS:HE3	2.21	0.41
1:A:573:VAL:HG11	1:A:598:MET:CE	2.47	0.41
1:B:157:THR:CB	1:B:159:GLY:H	2.27	0.41
1:B:175:VAL:HG11	1:B:190:LEU:HD12	2.02	0.41
1:C:53:THR:O	1:C:81:TYR:HA	2.20	0.41
1:C:448:TYR:O	1:C:449:PRO:C	2.64	0.41
1:C:565:TRP:CD1	1:C:565:TRP:H	2.39	0.41
1:C:641:LEU:C	1:C:641:LEU:CD2	2.94	0.41
1:D:310:PHE:HA	1:D:313:GLN:HE21	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:374:PHE:CD1	1:F:633:LEU:HD13	2.55	0.41
1:F:312:HIS:HE1	3:F:1060:HOH:O	2.03	0.41
1:F:646:ARG:O	1:F:647:HIS:HB2	2.20	0.41
1:A:312:HIS:HE1	3:A:1060:HOH:O	2.03	0.41
1:B:345:LEU:HB2	1:B:363:VAL:HB	2.02	0.41
1:B:475:ALA:HA	1:B:524:ASP:O	2.20	0.41
1:C:375:LYS:HZ3	1:D:330:ASN:HD22	1.69	0.41
1:C:645:PRO:O	1:C:646:ARG:HD2	2.20	0.41
1:F:131:ASP:HA	1:F:132:PRO:HD3	1.97	0.41
1:B:70:GLN:HA	1:B:70:GLN:NE2	2.36	0.40
1:B:641:LEU:C	1:B:641:LEU:CD2	2.94	0.40
1:D:392:THR:CG2	3:D:1004:HOH:O	2.65	0.40
1:E:50:SER:HB2	1:E:352:ARG:HG3	2.03	0.40
1:E:175:VAL:HG11	1:E:190:LEU:HD12	2.02	0.40
1:E:406:GLU:HG2	1:E:427:GLY:CA	2.51	0.40
1:F:23:HIS:HA	1:F:24:PRO:HD3	1.91	0.40
1:F:234:ALA:HB1	3:F:1231:HOH:O	2.21	0.40
1:A:182:ASP:CG	1:B:664:THR:HG23	2.47	0.40
1:B:375:LYS:HG2	1:B:376:HIS:N	2.35	0.40
1:B:406:GLU:HG2	1:B:427:GLY:CA	2.52	0.40
1:C:406:GLU:HG2	1:C:427:GLY:CA	2.51	0.40
1:D:23:HIS:CD2	1:D:24:PRO:HD2	2.57	0.40
1:E:598:MET:HE3	1:E:601:TRP:HB2	2.02	0.40
1:F:348:HIS:HD2	3:F:1460:HOH:O	2.04	0.40
1:F:598:MET:HE3	1:F:601:TRP:HB2	2.02	0.40
1:A:23:HIS:CD2	1:A:24:PRO:HD2	2.57	0.40
1:D:312:HIS:HE1	3:D:1060:HOH:O	2.03	0.40
1:E:448:TYR:O	1:E:449:PRO:C	2.64	0.40
1:B:23:HIS:CD2	1:B:24:PRO:HD2	2.57	0.40
1:B:346:ASP:OD2	1:B:360:LYS:HE3	2.21	0.40
1:C:376:HIS:HA	1:D:406:GLU:CD	2.46	0.40
1:D:23:HIS:HA	1:D:24:PRO:HD3	1.91	0.40
1:D:50:SER:HB2	1:D:352:ARG:HG3	2.03	0.40
1:D:175:VAL:HG11	1:D:190:LEU:HD12	2.02	0.40
1:D:346:ASP:OD2	1:D:360:LYS:HE3	2.21	0.40
1:D:425:LEU:HB3	3:D:1499:HOH:O	2.20	0.40
1:E:191:ASP:OD1	1:E:212:ARG:NH1	2.55	0.40
1:F:75:PRO:HA	1:F:76:PRO:HD3	1.97	0.40
1:F:346:ASP:OD2	1:F:360:LYS:HE3	2.21	0.40
1:A:290:ARG:HA	1:A:291:PRO:HD3	1.90	0.40
1:B:348:HIS:HD2	3:B:1460:HOH:O	2.04	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:70:GLN:HA	1:C:70:GLN:NE2	2.36	0.40
1:C:313:GLN:HG2	1:D:494:TYR:CG	2.52	0.40
1:E:128:ILE:HG13	1:E:129:ARG:N	2.35	0.40
1:E:348:HIS:HD2	3:E:1460:HOH:O	2.04	0.40

All (4) 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:20:ARG:CZ	1:E:70:GLN:OE1[4_455]	2.02	0.18
1:A:20:ARG:CZ	1:D:70:GLN:OE1[4_555]	2.10	0.10
1:A:66[B]:GLN:OE1	3:D:1255:HOH:O[4_555]	2.18	0.02
1:A:20:ARG:NH1	1:D:70:GLN:OE1[4_555]	2.19	0.01

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	654/692 (94%)	619 (95%)	34 (5%)	1 (0%)	43	63
1	B	654/692 (94%)	619 (95%)	34 (5%)	1 (0%)	43	63
1	C	654/692 (94%)	619 (95%)	34 (5%)	1 (0%)	43	63
1	D	654/692 (94%)	619 (95%)	34 (5%)	1 (0%)	43	63
1	E	654/692 (94%)	619 (95%)	34 (5%)	1 (0%)	43	63
1	F	654/692 (94%)	619 (95%)	34 (5%)	1 (0%)	43	63
All	All	3924/4152 (94%)	3714 (95%)	204 (5%)	6 (0%)	43	63

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	200	GLU

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Mol	Chain	Res	Type
1	B	200	GLU
1	C	200	GLU
1	D	200	GLU
1	E	200	GLU
1	F	200	GLU

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	566/592 (96%)	527 (93%)	39 (7%)	14	30
1	B	566/592 (96%)	527 (93%)	39 (7%)	14	30
1	C	566/592 (96%)	527 (93%)	39 (7%)	14	30
1	D	566/592 (96%)	527 (93%)	39 (7%)	14	30
1	E	566/592 (96%)	527 (93%)	39 (7%)	14	30
1	F	566/592 (96%)	527 (93%)	39 (7%)	14	30
All	All	3396/3552 (96%)	3162 (93%)	234 (7%)	14	30

All (234) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	48	LYS
1	A	68	LYS
1	A	69	GLU
1	A	109	LEU
1	A	112	VAL
1	A	114	PRO
1	A	127	VAL
1	A	140	LEU
1	A	146	ASN
1	A	157	THR
1	A	170	LEU
1	A	211	ARG
1	A	213	ARG

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Mol	Chain	Res	Type
1	A	215	VAL
1	A	311	PRO
1	A	313	GLN
1	A	329	THR
1	A	332	LEU
1	A	338	CYS
1	A	359	VAL
1	A	382	ASN
1	A	392	THR
1	A	394	LEU
1	A	406	GLU
1	A	421	LEU
1	A	430	ASN
1	A	462	LEU
1	A	466	PRO
1	A	487	LEU
1	A	504	THR
1	A	507	THR
1	A	527	ASN
1	A	546	THR
1	A	555	GLU
1	A	578	ASN
1	A	622	ILE
1	A	633	LEU
1	A	641	LEU
1	A	664	THR
1	B	48	LYS
1	B	68	LYS
1	B	69	GLU
1	B	109	LEU
1	B	112	VAL
1	B	114	PRO
1	B	127	VAL
1	B	140	LEU
1	B	146	ASN
1	B	157	THR
1	B	170	LEU
1	B	211	ARG
1	B	213	ARG
1	B	215	VAL
1	B	311	PRO
1	B	313	GLN

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Mol	Chain	Res	Type
1	B	329	THR
1	B	332	LEU
1	B	338	CYS
1	B	359	VAL
1	B	382	ASN
1	B	392	THR
1	B	394	LEU
1	B	406	GLU
1	B	421	LEU
1	B	430	ASN
1	B	462	LEU
1	B	466	PRO
1	B	487	LEU
1	B	504	THR
1	B	507	THR
1	B	527	ASN
1	B	546	THR
1	B	555	GLU
1	B	578	ASN
1	B	622	ILE
1	B	633	LEU
1	B	641	LEU
1	B	664	THR
1	C	48	LYS
1	C	68	LYS
1	C	69	GLU
1	C	109	LEU
1	C	112	VAL
1	C	114	PRO
1	C	127	VAL
1	C	140	LEU
1	C	146	ASN
1	C	157	THR
1	C	170	LEU
1	C	211	ARG
1	C	213	ARG
1	C	215	VAL
1	C	311	PRO
1	C	313	GLN
1	C	329	THR
1	C	332	LEU
1	C	338	CYS

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Mol	Chain	Res	Type
1	C	359	VAL
1	C	382	ASN
1	C	392	THR
1	C	394	LEU
1	C	406	GLU
1	C	421	LEU
1	C	430	ASN
1	C	462	LEU
1	C	466	PRO
1	C	487	LEU
1	C	504	THR
1	C	507	THR
1	C	527	ASN
1	C	546	THR
1	C	555	GLU
1	C	578	ASN
1	C	622	ILE
1	C	633	LEU
1	C	641	LEU
1	C	664	THR
1	D	48	LYS
1	D	68	LYS
1	D	69	GLU
1	D	109	LEU
1	D	112	VAL
1	D	114	PRO
1	D	127	VAL
1	D	140	LEU
1	D	146	ASN
1	D	157	THR
1	D	170	LEU
1	D	211	ARG
1	D	213	ARG
1	D	215	VAL
1	D	311	PRO
1	D	313	GLN
1	D	329	THR
1	D	332	LEU
1	D	338	CYS
1	D	359	VAL
1	D	382	ASN
1	D	392	THR

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Mol	Chain	Res	Type
1	D	394	LEU
1	D	406	GLU
1	D	421	LEU
1	D	430	ASN
1	D	462	LEU
1	D	466	PRO
1	D	487	LEU
1	D	504	THR
1	D	507	THR
1	D	527	ASN
1	D	546	THR
1	D	555	GLU
1	D	578	ASN
1	D	622	ILE
1	D	633	LEU
1	D	641	LEU
1	D	664	THR
1	E	48	LYS
1	E	68	LYS
1	E	69	GLU
1	E	109	LEU
1	E	112	VAL
1	E	114	PRO
1	E	127	VAL
1	E	140	LEU
1	E	146	ASN
1	E	157	THR
1	E	170	LEU
1	E	211	ARG
1	E	213	ARG
1	E	215	VAL
1	E	311	PRO
1	E	313	GLN
1	E	329	THR
1	E	332	LEU
1	E	338	CYS
1	E	359	VAL
1	E	382	ASN
1	E	392	THR
1	E	394	LEU
1	E	406	GLU
1	E	421	LEU

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Mol	Chain	Res	Type
1	E	430	ASN
1	E	462	LEU
1	E	466	PRO
1	E	487	LEU
1	E	504	THR
1	E	507	THR
1	E	527	ASN
1	E	546	THR
1	E	555	GLU
1	E	578	ASN
1	E	622	ILE
1	E	633	LEU
1	E	641	LEU
1	E	664	THR
1	F	48	LYS
1	F	68	LYS
1	F	69	GLU
1	F	109	LEU
1	F	112	VAL
1	F	114	PRO
1	F	127	VAL
1	F	140	LEU
1	F	146	ASN
1	F	157	THR
1	F	170	LEU
1	F	211	ARG
1	F	213	ARG
1	F	215	VAL
1	F	311	PRO
1	F	313	GLN
1	F	329	THR
1	F	332	LEU
1	F	338	CYS
1	F	359	VAL
1	F	382	ASN
1	F	392	THR
1	F	394	LEU
1	F	406	GLU
1	F	421	LEU
1	F	430	ASN
1	F	462	LEU
1	F	466	PRO

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Mol	Chain	Res	Type
1	F	487	LEU
1	F	504	THR
1	F	507	THR
1	F	527	ASN
1	F	546	THR
1	F	555	GLU
1	F	578	ASN
1	F	622	ILE
1	F	633	LEU
1	F	641	LEU
1	F	664	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (120) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	23	HIS
1	A	70	GLN
1	A	130	ASN
1	A	146	ASN
1	A	218	HIS
1	A	288	ASN
1	A	294	HIS
1	A	312	HIS
1	A	313	GLN
1	A	330	ASN
1	A	361	ASN
1	A	450	ASN
1	A	452	ASN
1	A	457	GLN
1	A	473	ASN
1	A	527	ASN
1	A	529	ASN
1	A	547	GLN
1	A	611	ASN
1	A	658	GLN
1	B	23	HIS
1	B	70	GLN
1	B	130	ASN
1	B	146	ASN
1	B	218	HIS
1	B	288	ASN
1	B	294	HIS

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Mol	Chain	Res	Type
1	B	312	HIS
1	B	313	GLN
1	B	330	ASN
1	B	361	ASN
1	B	450	ASN
1	B	452	ASN
1	B	457	GLN
1	B	473	ASN
1	B	527	ASN
1	B	529	ASN
1	B	547	GLN
1	B	611	ASN
1	C	23	HIS
1	C	70	GLN
1	C	146	ASN
1	C	218	HIS
1	C	288	ASN
1	C	294	HIS
1	C	312	HIS
1	C	313	GLN
1	C	330	ASN
1	C	361	ASN
1	C	450	ASN
1	C	452	ASN
1	C	457	GLN
1	C	473	ASN
1	C	527	ASN
1	C	529	ASN
1	C	547	GLN
1	C	611	ASN
1	C	658	GLN
1	D	23	HIS
1	D	70	GLN
1	D	130	ASN
1	D	146	ASN
1	D	218	HIS
1	D	288	ASN
1	D	294	HIS
1	D	312	HIS
1	D	313	GLN
1	D	330	ASN
1	D	361	ASN

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Mol	Chain	Res	Type
1	D	450	ASN
1	D	452	ASN
1	D	457	GLN
1	D	473	ASN
1	D	527	ASN
1	D	529	ASN
1	D	547	GLN
1	D	578	ASN
1	D	611	ASN
1	D	658	GLN
1	E	23	HIS
1	E	70	GLN
1	E	130	ASN
1	E	146	ASN
1	E	218	HIS
1	E	288	ASN
1	E	294	HIS
1	E	312	HIS
1	E	313	GLN
1	E	330	ASN
1	E	361	ASN
1	E	450	ASN
1	E	452	ASN
1	E	457	GLN
1	E	473	ASN
1	E	527	ASN
1	E	529	ASN
1	E	547	GLN
1	E	578	ASN
1	E	611	ASN
1	E	658	GLN
1	F	23	HIS
1	F	70	GLN
1	F	130	ASN
1	F	146	ASN
1	F	218	HIS
1	F	288	ASN
1	F	294	HIS
1	F	312	HIS
1	F	313	GLN
1	F	330	ASN
1	F	361	ASN

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Mol	Chain	Res	Type
1	F	450	ASN
1	F	452	ASN
1	F	457	GLN
1	F	473	ASN
1	F	527	ASN
1	F	529	ASN
1	F	547	GLN
1	F	578	ASN
1	F	611	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

6 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	TPQ	C	405	1	13,14,15	2.28	5 (38%)	13,19,21	1.27	1 (7%)
1	TPQ	B	405	1	13,14,15	2.28	5 (38%)	13,19,21	1.26	1 (7%)
1	TPQ	D	405	1	13,14,15	2.27	5 (38%)	13,19,21	1.27	1 (7%)
1	TPQ	E	405	1	13,14,15	2.27	5 (38%)	13,19,21	1.28	1 (7%)
1	TPQ	F	405	1	13,14,15	2.28	5 (38%)	13,19,21	1.28	1 (7%)
1	TPQ	A	405	1	13,14,15	2.27	5 (38%)	13,19,21	1.27	1 (7%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	TPQ	C	405	1	-	4/5/22/24	0/1/1/1
1	TPQ	B	405	1	-	4/5/22/24	0/1/1/1
1	TPQ	D	405	1	-	4/5/22/24	0/1/1/1
1	TPQ	E	405	1	-	4/5/22/24	0/1/1/1
1	TPQ	F	405	1	-	4/5/22/24	0/1/1/1
1	TPQ	A	405	1	-	4/5/22/24	0/1/1/1

All (30) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	F	405	TPQ	C1-C2	-4.79	1.42	1.49
1	C	405	TPQ	C1-C2	-4.77	1.42	1.49
1	D	405	TPQ	C1-C2	-4.74	1.42	1.49
1	A	405	TPQ	C1-C2	-4.74	1.42	1.49
1	E	405	TPQ	C1-C2	-4.72	1.42	1.49
1	B	405	TPQ	C1-C2	-4.72	1.42	1.49
1	B	405	TPQ	C3-C4	4.03	1.43	1.36
1	E	405	TPQ	C3-C4	4.03	1.43	1.36
1	F	405	TPQ	C3-C4	4.01	1.43	1.36
1	D	405	TPQ	C3-C4	4.01	1.43	1.36
1	A	405	TPQ	C3-C4	4.00	1.43	1.36
1	C	405	TPQ	C3-C4	4.00	1.43	1.36
1	C	405	TPQ	O5-C5	3.14	1.32	1.24
1	B	405	TPQ	O5-C5	3.12	1.32	1.24
1	E	405	TPQ	O5-C5	3.12	1.32	1.24
1	A	405	TPQ	O5-C5	3.12	1.32	1.24
1	F	405	TPQ	O5-C5	3.12	1.32	1.24
1	D	405	TPQ	O5-C5	3.11	1.32	1.24
1	E	405	TPQ	C6-C1	3.09	1.42	1.34
1	B	405	TPQ	C6-C1	3.09	1.42	1.34
1	F	405	TPQ	C6-C1	3.08	1.42	1.34
1	C	405	TPQ	C6-C1	3.08	1.42	1.34
1	A	405	TPQ	C6-C1	3.08	1.42	1.34
1	D	405	TPQ	C6-C1	3.07	1.42	1.34
1	E	405	TPQ	O4-C4	2.15	1.39	1.33
1	A	405	TPQ	O4-C4	2.15	1.39	1.33
1	D	405	TPQ	O4-C4	2.15	1.39	1.33
1	B	405	TPQ	O4-C4	2.14	1.39	1.33
1	C	405	TPQ	O4-C4	2.14	1.39	1.33
1	F	405	TPQ	O4-C4	2.12	1.39	1.33

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	405	TPQ	C6-C1-C2	2.36	120.33	118.66
1	F	405	TPQ	C6-C1-C2	2.35	120.33	118.66
1	A	405	TPQ	C6-C1-C2	2.33	120.31	118.66
1	C	405	TPQ	C6-C1-C2	2.32	120.31	118.66
1	D	405	TPQ	C6-C1-C2	2.32	120.31	118.66
1	B	405	TPQ	C6-C1-C2	2.30	120.30	118.66

There are no chirality outliers.

All (24) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	405	TPQ	N-CA-CB-C1
1	A	405	TPQ	C-CA-CB-C1
1	B	405	TPQ	N-CA-CB-C1
1	B	405	TPQ	C-CA-CB-C1
1	C	405	TPQ	N-CA-CB-C1
1	C	405	TPQ	C-CA-CB-C1
1	D	405	TPQ	N-CA-CB-C1
1	D	405	TPQ	C-CA-CB-C1
1	E	405	TPQ	N-CA-CB-C1
1	E	405	TPQ	C-CA-CB-C1
1	F	405	TPQ	N-CA-CB-C1
1	F	405	TPQ	C-CA-CB-C1
1	A	405	TPQ	C2-C1-CB-CA
1	B	405	TPQ	C2-C1-CB-CA
1	C	405	TPQ	C2-C1-CB-CA
1	D	405	TPQ	C2-C1-CB-CA
1	E	405	TPQ	C2-C1-CB-CA
1	F	405	TPQ	C2-C1-CB-CA
1	A	405	TPQ	C6-C1-CB-CA
1	B	405	TPQ	C6-C1-CB-CA
1	C	405	TPQ	C6-C1-CB-CA
1	D	405	TPQ	C6-C1-CB-CA
1	E	405	TPQ	C6-C1-CB-CA
1	F	405	TPQ	C6-C1-CB-CA

There are no ring outliers.

6 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	C	405	TPQ	1	0
1	B	405	TPQ	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	D	405	TPQ	1	0
1	E	405	TPQ	1	0
1	F	405	TPQ	1	0
1	A	405	TPQ	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 6 ligands modelled in this entry, 6 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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	654/692 (94%)	-0.28	10 (1%) 72 68	16, 26, 46, 81	2 (0%)
1	B	654/692 (94%)	-0.30	9 (1%) 73 70	16, 26, 46, 81	2 (0%)
1	C	654/692 (94%)	-0.26	8 (1%) 76 73	16, 26, 46, 81	2 (0%)
1	D	654/692 (94%)	-0.34	12 (1%) 67 64	16, 26, 46, 81	2 (0%)
1	E	654/692 (94%)	-0.31	8 (1%) 76 73	16, 26, 46, 81	2 (0%)
1	F	654/692 (94%)	-0.35	9 (1%) 73 70	16, 26, 46, 81	2 (0%)
All	All	3924/4152 (94%)	-0.31	56 (1%) 73 70	16, 26, 46, 81	12 (0%)

All (56) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	672	VAL	6.1
1	D	18	PRO	5.3
1	D	19	ALA	4.9
1	B	672	VAL	4.8
1	C	672	VAL	4.8
1	D	130	ASN	4.7
1	A	18	PRO	4.4
1	D	20	ARG	4.3
1	D	21	PRO	4.2
1	E	672	VAL	4.1
1	D	672	VAL	4.1
1	F	672	VAL	4.1
1	C	18	PRO	3.6
1	F	19	ALA	3.4
1	D	22	ALA	3.3
1	A	335	GLY	3.3
1	F	18	PRO	3.2
1	B	48	LYS	3.2
1	A	45	ALA	3.0

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Mol	Chain	Res	Type	RSRZ
1	D	66[A]	GLN	3.0
1	B	45	ALA	2.9
1	A	671	ALA	2.8
1	C	66[A]	GLN	2.8
1	C	441	GLY	2.8
1	E	211	ARG	2.8
1	B	334	LEU	2.6
1	B	328[A]	MET	2.6
1	F	441	GLY	2.6
1	B	121	LEU	2.6
1	C	328[A]	MET	2.5
1	D	335	GLY	2.5
1	E	18	PRO	2.5
1	B	130	ASN	2.5
1	C	19	ALA	2.5
1	F	130	ASN	2.5
1	F	669	LYS	2.4
1	D	334	LEU	2.4
1	E	66[A]	GLN	2.4
1	D	70	GLN	2.3
1	F	20	ARG	2.3
1	E	200	GLU	2.3
1	B	42	SER	2.3
1	E	20	ARG	2.3
1	A	199	GLU	2.2
1	A	200	GLU	2.2
1	C	211	ARG	2.1
1	F	48	LYS	2.1
1	E	441	GLY	2.1
1	E	335	GLY	2.1
1	A	22	ALA	2.1
1	A	670	ARG	2.1
1	C	336	CYS	2.1
1	A	48	LYS	2.0
1	D	328[A]	MET	2.0
1	B	671	ALA	2.0
1	F	328[A]	MET	2.0

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

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum,

median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
1	TPQ	C	405	14/15	0.87	0.11	32,47,55,57	0
1	TPQ	B	405	14/15	0.89	0.13	32,47,55,57	0
1	TPQ	A	405	14/15	0.89	0.14	32,47,55,57	0
1	TPQ	D	405	14/15	0.92	0.11	32,47,55,57	0
1	TPQ	E	405	14/15	0.92	0.15	32,47,55,57	0
1	TPQ	F	405	14/15	0.92	0.12	32,47,55,57	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	CU	B	701	1/1	0.99	0.04	31,31,31,31	0
2	CU	C	701	1/1	0.99	0.03	31,31,31,31	0
2	CU	D	701	1/1	0.99	0.02	31,31,31,31	0
2	CU	E	701	1/1	0.99	0.03	31,31,31,31	0
2	CU	A	701	1/1	1.00	0.02	31,31,31,31	0
2	CU	F	701	1/1	1.00	0.02	31,31,31,31	0

6.5 Other polymers [i](#)

There are no such residues in this entry.