



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2026 – 06:46 AM UTC

PDB ID : 1HRI / pdb_00001hri
Title : STRUCTURE DETERMINATION OF ANTIVIRAL COMPOUND SCH
38057 COMPLEXED WITH HUMAN RHINOVIRUS 14
Authors : Zhang, A.; Nanni, R.G.; Oren, D.A.; Arnold, E.
Deposited on : 1992-10-01
Resolution : 3.00 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)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

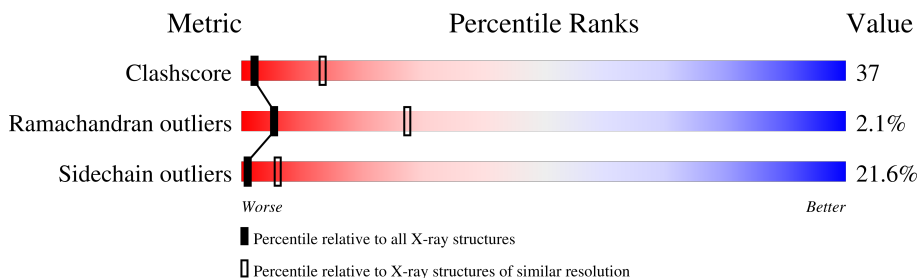
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 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))
Clashscore	190562	2977 (3.00-3.00)
Ramachandran outliers	187476	2877 (3.00-3.00)
Sidechain outliers	187428	2880 (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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	1	289	18% 43% 26% 8% 6%
2	2	262	25% 39% 26% 8% .
3	3	236	25% 37% 30% 8%
4	4	68	15% 22% 12% 10% 41%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 6289 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 HUMAN RHINOVIRUS 14 COAT PROTEIN (SUBUNIT VP1).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	1	273	Total	C	N	O	S	0	0	0
			2170	1373	375	414	8			

- Molecule 2 is a protein called HUMAN RHINOVIRUS 14 COAT PROTEIN (SUBUNIT VP2).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	2	255	Total	C	N	O	S	0	0	0
			1952	1238	330	372	12			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
2	170	LEU	ILE	conflict	UNP P03303

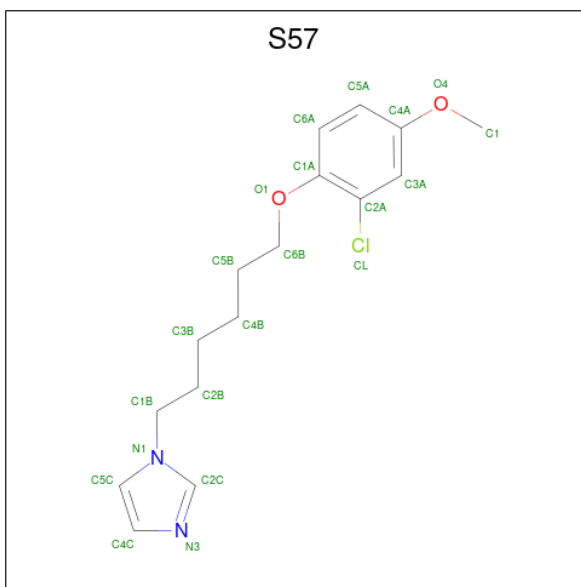
- Molecule 3 is a protein called HUMAN RHINOVIRUS 14 COAT PROTEIN (SUBUNIT VP3).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	3	236	Total	C	N	O	S	0	0	0
			1849	1184	305	353	7			

- Molecule 4 is a protein called HUMAN RHINOVIRUS 14 COAT PROTEIN (SUBUNIT VP4).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	4	40	Total	C	N	O	S	0	0	0
			297	186	47	62	2			

- Molecule 5 is 1-[6-(2-CHLORO-4-METHYXYPHENOXY)-HEXYL]-IMIDAZOLE (CCD ID: S57) (formula: C₁₆H₂₁ClN₂O₂).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	Cl	N	O		
5	1	1	21	16	1	2	2	0	0

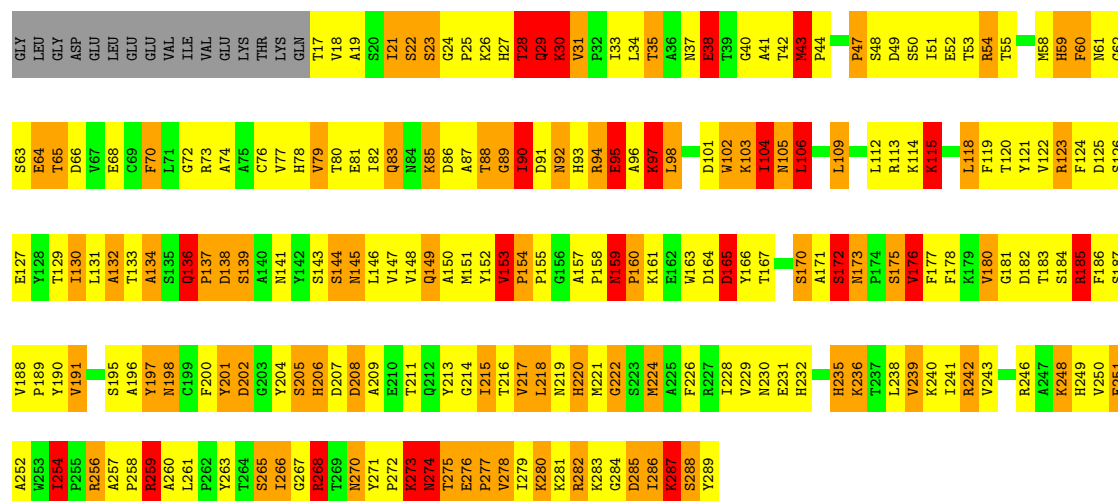
3 Residue-property plots

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. 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. 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.

Note EDS was not executed.

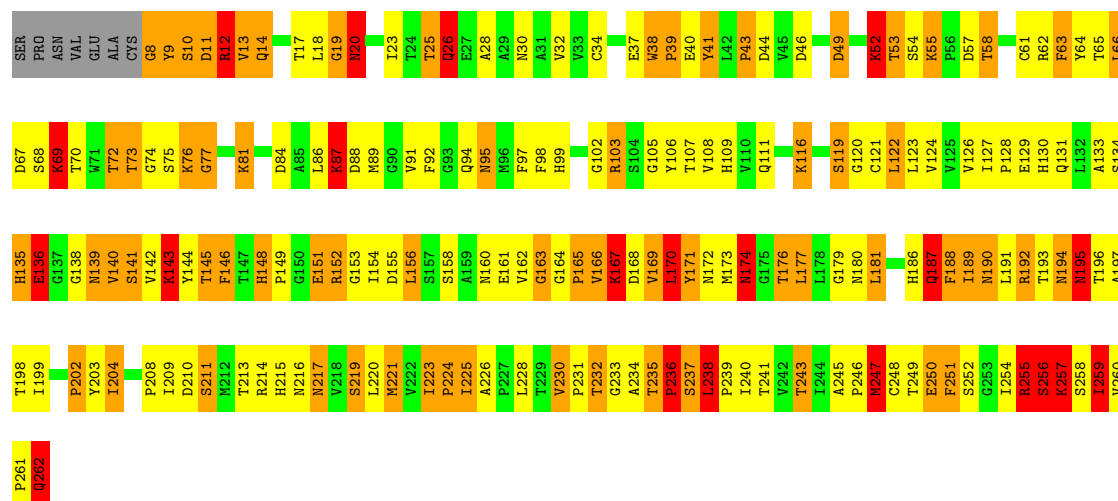
• Molecule 1: HUMAN RHINOVIRUS 14 COAT PROTEIN (SUBUNIT VP1)

Chain 1: 

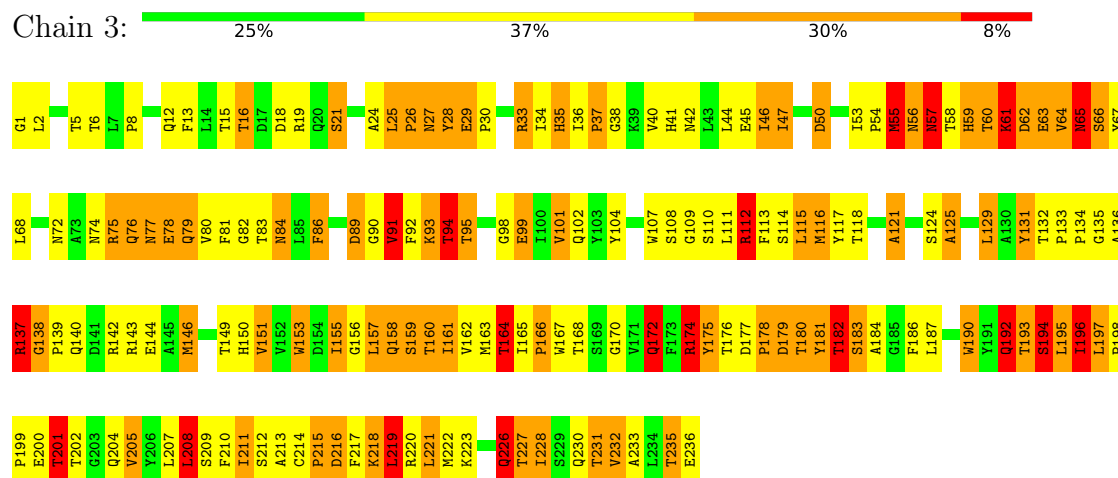


• Molecule 2: HUMAN RHINOVIRUS 14 COAT PROTEIN (SUBUNIT VP2)

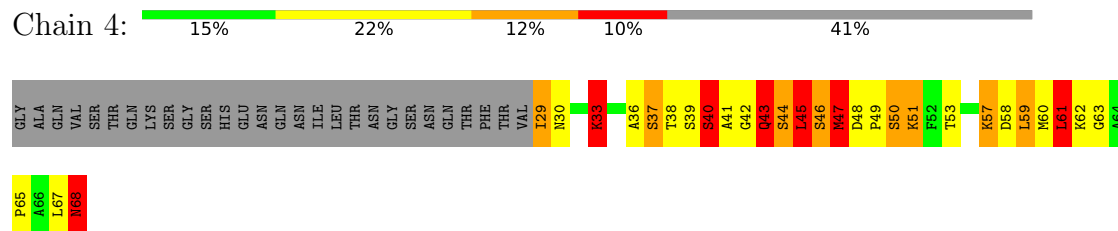
Chain 2: 



• Molecule 3: HUMAN RHINOVIRUS 14 COAT PROTEIN (SUBUNIT VP3)



• Molecule 4: HUMAN RHINOVIRUS 14 COAT PROTEIN (SUBUNIT VP4)



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 21 3	Depositor
Cell constants a, b, c, α , β , γ	445.10Å 445.10Å 445.10Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	(Not available) – 3.00	Depositor
% Data completeness (in resolution range)	(Not available) ((Not available)-3.00)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program		Depositor
R, R_{free}	(Not available) , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	6289	wwPDB-VP
Average B, all atoms (Å ²)	0.0	wwPDB-VP

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: S57

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	1	2.12	76/2228 (3.4%)	2.59	188/3031 (6.2%)
2	2	2.40	96/2001 (4.8%)	2.77	193/2735 (7.1%)
3	3	2.22	75/1898 (4.0%)	2.70	181/2597 (7.0%)
4	4	2.64	14/302 (4.6%)	3.14	33/406 (8.1%)
All	All	2.27	261/6429 (4.1%)	2.71	595/8769 (6.8%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	1	0	2
2	2	0	2
All	All	0	4

All (261) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1	285	ASP	CA-CB	17.77	1.79	1.53
4	4	41	ALA	C-O	13.33	1.41	1.24
3	3	57	ASN	CA-CB	12.78	1.75	1.53
4	4	42	GLY	N-CA	12.59	1.63	1.45
2	2	194	ASN	CA-CB	11.51	1.71	1.53
1	1	283	LYS	N-CA	10.88	1.61	1.46
1	1	144	SER	N-CA	10.33	1.58	1.45
3	3	164	THR	C-O	10.22	1.36	1.24
4	4	45	LEU	C-N	9.39	1.46	1.33
2	2	187	GLN	N-CA	9.31	1.57	1.45
2	2	256	SER	C-O	9.29	1.36	1.24
1	1	52	GLU	C-O	9.14	1.35	1.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1	282	ARG	CD-NE	9.12	1.59	1.46
2	2	152	ARG	CD-NE	8.88	1.58	1.46
2	2	102	GLY	N-CA	8.88	1.54	1.45
2	2	168	ASP	C-O	8.82	1.34	1.24
2	2	174	ASN	C-O	8.43	1.30	1.23
3	3	50	ASP	CA-CB	-8.28	1.40	1.53
3	3	232	VAL	N-CA	8.17	1.55	1.46
1	1	95	GLU	C-N	-8.10	1.22	1.33
1	1	73	ARG	C-O	8.02	1.33	1.23
2	2	77	GLY	N-CA	7.83	1.53	1.45
3	3	138	GLY	N-CA	7.83	1.55	1.44
2	2	236	PRO	C-O	7.80	1.34	1.24
2	2	161	GLU	CA-CB	-7.78	1.42	1.53
1	1	285	ASP	N-CA	-7.77	1.34	1.45
2	2	135	HIS	CE1-NE2	-7.66	1.24	1.32
3	3	1	GLY	N-CA	7.65	1.57	1.45
2	2	12	ARG	NE-CZ	7.59	1.41	1.33
1	1	72	GLY	C-O	7.53	1.34	1.23
2	2	52	LYS	N-CA	7.53	1.55	1.46
3	3	215	PRO	C-N	-7.47	1.23	1.33
1	1	143	SER	C-O	7.47	1.33	1.24
1	1	94	ARG	CD-NE	7.42	1.56	1.46
1	1	288	SER	C-O	7.37	1.32	1.23
2	2	11	ASP	CA-CB	7.36	1.66	1.53
1	1	28	THR	CA-CB	7.34	1.64	1.53
2	2	120	GLY	N-CA	7.22	1.53	1.45
1	1	132	ALA	C-O	7.20	1.32	1.24
3	3	77	ASN	C-O	7.17	1.33	1.24
3	3	60	THR	CA-CB	7.16	1.65	1.54
2	2	260	VAL	N-CA	7.15	1.55	1.46
4	4	40	SER	CB-OG	7.05	1.56	1.42
2	2	108	VAL	C-O	7.01	1.32	1.24
2	2	219	SER	CA-CB	-7.01	1.41	1.53
1	1	30	LYS	C-O	7.00	1.32	1.23
2	2	9	TYR	C-O	6.99	1.32	1.23
1	1	276	GLU	C-O	6.97	1.30	1.24
2	2	58	THR	C-O	6.97	1.32	1.24
2	2	74	GLY	C-O	6.94	1.31	1.23
1	1	182	ASP	C-N	-6.91	1.23	1.33
1	1	202	ASP	CA-CB	-6.86	1.42	1.53
4	4	49	PRO	C-N	-6.85	1.24	1.34
1	1	91	ASP	N-CA	6.84	1.55	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1	133	THR	N-CA	6.84	1.54	1.45
1	1	288	SER	CA-CB	6.84	1.65	1.53
3	3	86	PHE	CA-CB	-6.84	1.42	1.52
1	1	23	SER	N-CA	6.81	1.54	1.45
2	2	223	ILE	CA-CB	6.80	1.59	1.54
3	3	6	THR	N-CA	6.76	1.54	1.45
2	2	243	THR	C-O	6.74	1.32	1.24
2	2	193	THR	C-N	-6.73	1.23	1.33
2	2	152	ARG	CZ-NH2	6.73	1.42	1.33
2	2	194	ASN	N-CA	-6.72	1.37	1.45
3	3	216	ASP	CA-CB	6.72	1.64	1.53
2	2	197	ALA	C-O	6.71	1.31	1.23
1	1	73	ARG	N-CA	6.67	1.53	1.45
1	1	165	ASP	CA-CB	6.67	1.64	1.53
2	2	256	SER	CB-OG	6.67	1.55	1.42
2	2	10	SER	C-N	-6.66	1.25	1.33
1	1	251	GLU	CA-CB	-6.62	1.42	1.53
1	1	280	LYS	C-O	6.62	1.31	1.24
2	2	39	PRO	C-O	6.58	1.31	1.23
3	3	57	ASN	N-CA	-6.57	1.37	1.46
1	1	134	ALA	CA-CB	-6.56	1.42	1.53
2	2	109	HIS	CE1-NE2	-6.54	1.26	1.32
2	2	9	TYR	N-CA	6.54	1.53	1.46
1	1	85	LYS	C-O	6.54	1.31	1.23
3	3	156	GLY	C-O	-6.51	1.18	1.24
2	2	190	ASN	CA-CB	-6.50	1.44	1.53
2	2	52	LYS	CE-NZ	6.50	1.68	1.49
4	4	62	LYS	C-O	6.50	1.31	1.24
4	4	44	SER	CB-OG	6.49	1.55	1.42
2	2	262	GLN	CD-OE1	6.46	1.35	1.23
1	1	79	VAL	C-N	-6.44	1.24	1.33
3	3	57	ASN	C-N	-6.43	1.25	1.33
2	2	30	ASN	N-CA	6.43	1.54	1.46
2	2	217	ASN	C-O	6.43	1.32	1.24
4	4	62	LYS	N-CA	6.42	1.54	1.46
1	1	231	GLU	CA-CB	-6.41	1.44	1.53
3	3	205	VAL	N-CA	6.35	1.53	1.46
1	1	22	SER	C-N	-6.33	1.25	1.33
1	1	95	GLU	CB-CG	6.33	1.71	1.52
2	2	8	GLY	N-CA	6.30	1.55	1.45
1	1	94	ARG	NE-CZ	6.29	1.40	1.33
4	4	63	GLY	N-CA	6.29	1.54	1.45

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1	148	VAL	C-N	-6.29	1.25	1.33
3	3	165	ILE	N-CA	6.28	1.54	1.46
1	1	218	LEU	C-N	-6.24	1.25	1.33
3	3	5	THR	C-O	6.24	1.31	1.24
3	3	118	THR	CB-OG1	6.24	1.53	1.43
2	2	259	ILE	C-O	6.20	1.31	1.24
3	3	182	THR	CA-CB	6.20	1.62	1.53
3	3	75	ARG	C-N	-6.18	1.24	1.33
3	3	164	THR	N-CA	6.18	1.53	1.46
3	3	178	PRO	CA-CB	-6.17	1.45	1.53
2	2	121	CYS	C-O	6.16	1.31	1.23
1	1	177	PHE	C-N	-6.16	1.25	1.33
4	4	45	LEU	N-CA	6.14	1.55	1.46
2	2	168	ASP	CA-CB	6.14	1.60	1.53
1	1	251	GLU	N-CA	6.12	1.53	1.46
1	1	28	THR	N-CA	-6.10	1.37	1.45
2	2	162	VAL	N-CA	6.10	1.53	1.46
1	1	274	ASN	N-CA	6.10	1.54	1.46
1	1	115	LYS	C-N	-6.09	1.25	1.33
3	3	215	PRO	CA-CB	-6.09	1.44	1.53
4	4	33	LYS	CE-NZ	6.08	1.67	1.49
1	1	24	GLY	N-CA	6.07	1.53	1.44
3	3	110	SER	N-CA	6.05	1.52	1.45
2	2	19	GLY	C-N	-6.05	1.25	1.33
2	2	190	ASN	N-CA	6.04	1.54	1.46
2	2	257	LYS	N-CA	6.04	1.53	1.46
3	3	57	ASN	C-O	6.03	1.31	1.24
1	1	131	LEU	C-O	6.02	1.31	1.23
3	3	155	ILE	N-CA	5.99	1.53	1.46
3	3	36	ILE	N-CA	5.99	1.53	1.46
3	3	135	GLY	C-O	5.99	1.31	1.24
2	2	208	PRO	C-N	-5.98	1.28	1.33
3	3	222	MET	CG-SD	5.96	1.95	1.80
1	1	88	THR	CB-OG1	5.93	1.53	1.43
2	2	180	ASN	C-N	-5.92	1.25	1.33
2	2	17	THR	C-N	-5.90	1.25	1.33
1	1	38	GLU	CB-CG	-5.83	1.34	1.52
3	3	213	ALA	C-O	5.83	1.30	1.23
3	3	219	LEU	C-N	-5.81	1.26	1.33
1	1	276	GLU	N-CA	5.80	1.54	1.45
2	2	55	LYS	N-CA	5.79	1.53	1.46
3	3	116	MET	N-CA	5.79	1.53	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	2	103	ARG	C-O	5.77	1.30	1.23
2	2	135	HIS	CG-CD2	-5.77	1.29	1.35
1	1	287	LYS	C-O	5.75	1.31	1.24
2	2	88	ASP	C-O	5.74	1.32	1.24
2	2	176	THR	N-CA	5.73	1.53	1.45
3	3	38	GLY	CA-C	-5.73	1.43	1.51
2	2	152	ARG	NE-CZ	5.72	1.39	1.33
1	1	274	ASN	CA-C	5.71	1.60	1.52
2	2	54	SER	CA-CB	-5.71	1.44	1.53
4	4	45	LEU	C-O	5.69	1.31	1.23
3	3	41	HIS	CE1-NE2	5.67	1.38	1.32
1	1	285	ASP	C-N	5.67	1.40	1.33
1	1	239	VAL	C-O	5.67	1.30	1.24
3	3	201	THR	C-O	5.66	1.30	1.23
2	2	103	ARG	N-CA	5.66	1.52	1.46
2	2	195	ASN	CA-CB	-5.66	1.44	1.54
3	3	35	HIS	C-N	-5.65	1.26	1.33
1	1	268	ARG	N-CA	5.65	1.52	1.45
3	3	158	GLN	C-O	5.65	1.30	1.24
1	1	25	PRO	CA-CB	-5.64	1.45	1.53
2	2	223	ILE	CA-C	-5.64	1.48	1.52
2	2	63	PHE	C-O	5.64	1.30	1.24
2	2	208	PRO	C-O	5.63	1.30	1.24
2	2	87	LYS	CB-CG	-5.63	1.35	1.52
1	1	63	SER	CB-OG	-5.62	1.30	1.42
1	1	267	GLY	C-O	5.62	1.32	1.24
3	3	82	GLY	N-CA	5.62	1.50	1.45
2	2	259	ILE	N-CA	5.62	1.53	1.46
1	1	180	VAL	C-O	5.62	1.29	1.24
2	2	75	SER	C-O	5.61	1.30	1.23
3	3	172	GLN	CG-CD	-5.58	1.38	1.52
2	2	168	ASP	C-N	-5.58	1.26	1.33
1	1	137	PRO	C-O	5.58	1.31	1.24
2	2	194	ASN	C-O	5.58	1.30	1.23
1	1	254	ILE	CA-CB	5.57	1.61	1.54
3	3	82	GLY	C-N	-5.57	1.26	1.33
3	3	231	THR	CB-OG1	5.56	1.52	1.43
4	4	51	LYS	CE-NZ	5.55	1.66	1.49
3	3	75	ARG	N-CA	5.54	1.52	1.45
3	3	108	SER	CA-CB	-5.54	1.44	1.53
1	1	102	TRP	NE1-CE2	-5.53	1.31	1.37
3	3	140	GLN	C-N	-5.52	1.26	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	2	109	HIS	C-O	5.51	1.30	1.24
3	3	66	SER	N-CA	5.51	1.53	1.46
3	3	61	LYS	CE-NZ	5.50	1.65	1.49
3	3	174	ARG	NE-CZ	5.50	1.39	1.33
2	2	153	GLY	C-N	-5.50	1.25	1.33
2	2	237	SER	C-O	5.49	1.30	1.23
2	2	237	SER	N-CA	5.49	1.52	1.46
2	2	151	GLU	CA-CB	-5.46	1.43	1.53
3	3	77	ASN	CG-OD1	5.45	1.33	1.23
1	1	25	PRO	C-N	-5.45	1.25	1.33
3	3	209	SER	N-CA	5.45	1.52	1.46
2	2	141	SER	N-CA	5.45	1.52	1.45
1	1	277	PRO	N-CA	5.44	1.53	1.47
3	3	40	VAL	C-O	5.44	1.30	1.24
3	3	37	PRO	CA-CB	-5.42	1.45	1.53
2	2	171	TYR	C-O	5.41	1.31	1.24
1	1	161	LYS	CE-NZ	5.41	1.65	1.49
3	3	91	VAL	C-O	5.38	1.30	1.24
1	1	279	ILE	C-O	5.38	1.29	1.24
2	2	61	CYS	CA-C	-5.37	1.47	1.53
1	1	149	GLN	C-O	5.37	1.30	1.24
1	1	270	ASN	CA-C	5.36	1.59	1.52
2	2	103	ARG	CA-CB	-5.35	1.44	1.53
2	2	72	THR	CB-OG1	5.34	1.52	1.43
3	3	74	ASN	CA-CB	5.34	1.61	1.53
3	3	209	SER	C-O	5.34	1.30	1.23
2	2	68	SER	CA-C	-5.34	1.45	1.52
2	2	211	SER	C-O	5.34	1.30	1.23
2	2	148	HIS	ND1-CE1	5.32	1.37	1.32
2	2	256	SER	C-N	-5.32	1.26	1.33
4	4	61	LEU	C-O	5.32	1.30	1.24
2	2	219	SER	N-CA	5.30	1.52	1.46
1	1	30	LYS	CE-NZ	5.30	1.65	1.49
2	2	14	GLN	CD-NE2	5.29	1.44	1.33
2	2	123	LEU	C-N	-5.28	1.26	1.33
3	3	228	ILE	C-O	5.28	1.30	1.24
1	1	33	ILE	C-O	5.27	1.30	1.24
3	3	64	VAL	C-N	-5.26	1.25	1.33
3	3	2	LEU	CA-CB	5.25	1.63	1.53
1	1	89	GLY	C-O	5.25	1.31	1.23
1	1	161	LYS	C-N	-5.25	1.26	1.33
2	2	246	PRO	C-O	5.23	1.29	1.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	2	99	HIS	C-N	-5.21	1.26	1.34
3	3	164	THR	CA-CB	5.21	1.61	1.53
1	1	283	LYS	CE-NZ	5.21	1.65	1.49
2	2	202	PRO	C-O	5.20	1.29	1.23
1	1	54	ARG	C-O	5.20	1.30	1.23
3	3	146	MET	C-O	5.19	1.30	1.24
3	3	77	ASN	C-N	-5.19	1.26	1.33
2	2	38	TRP	CA-C	-5.18	1.45	1.52
3	3	153	TRP	C-O	5.17	1.30	1.24
1	1	252	ALA	C-O	5.15	1.30	1.23
3	3	58	THR	CA-CB	5.15	1.62	1.53
3	3	133	PRO	CA-CB	-5.13	1.47	1.54
2	2	204	ILE	C-N	-5.13	1.26	1.33
1	1	159	ASN	CA-C	-5.12	1.47	1.53
3	3	112	ARG	CA-CB	-5.12	1.45	1.53
2	2	202	PRO	C-N	-5.10	1.26	1.33
3	3	136	ALA	C-O	5.10	1.30	1.23
3	3	205	VAL	C-O	5.10	1.29	1.23
1	1	166	TYR	N-CA	5.10	1.52	1.46
1	1	85	LYS	N-CA	5.08	1.51	1.46
2	2	128	PRO	CA-CB	-5.08	1.46	1.53
1	1	209	ALA	C-N	-5.08	1.26	1.33
2	2	186	HIS	C-O	5.06	1.29	1.23
3	3	65	ASN	CA-CB	5.06	1.62	1.53
2	2	248	CYS	C-N	-5.06	1.26	1.33
3	3	232	VAL	C-O	5.05	1.29	1.23
2	2	233	GLY	C-O	5.05	1.30	1.24
1	1	42	THR	C-O	5.05	1.29	1.23
3	3	34	ILE	C-O	5.04	1.30	1.24
3	3	216	ASP	N-CA	-5.04	1.40	1.46
3	3	109	GLY	C-N	5.02	1.40	1.33
2	2	109	HIS	N-CA	5.02	1.53	1.46
2	2	12	ARG	N-CA	-5.01	1.40	1.46
3	3	164	THR	CA-C	-5.01	1.46	1.52
2	2	220	LEU	C-N	-5.01	1.26	1.33
1	1	246	ARG	CD-NE	-5.00	1.39	1.46
2	2	223	ILE	N-CA	5.00	1.49	1.45
3	3	163	MET	C-N	-5.00	1.26	1.33
3	3	84	ASN	N-CA	5.00	1.51	1.45

All (595) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	3	50	ASP	CA-CB-CG	27.73	140.33	112.60
1	1	285	ASP	CA-CB-CG	-22.21	90.39	112.60
3	3	215	PRO	CA-C-N	20.36	149.20	120.29
3	3	215	PRO	C-N-CA	20.36	149.20	120.29
2	2	87	LYS	CA-CB-CG	19.05	152.21	114.10
2	2	11	ASP	CA-CB-CG	-18.96	93.64	112.60
1	1	145	ASN	OD1-CG-ND2	17.24	139.84	122.60
2	2	193	THR	CA-C-N	16.42	150.15	122.07
2	2	193	THR	C-N-CA	16.42	150.15	122.07
2	2	190	ASN	CA-CB-CG	16.38	128.98	112.60
2	2	194	ASN	CA-CB-CG	-14.89	97.71	112.60
2	2	11	ASP	CA-C-N	14.78	140.54	120.44
2	2	11	ASP	C-N-CA	14.78	140.54	120.44
3	3	57	ASN	CA-CB-CG	-13.74	98.86	112.60
1	1	38	GLU	CB-CG-CD	13.64	135.78	112.60
3	3	74	ASN	CA-CB-CG	-13.47	99.13	112.60
3	3	65	ASN	CA-CB-CG	-13.09	99.51	112.60
1	1	202	ASP	CA-CB-CG	12.96	125.56	112.60
1	1	145	ASN	CA-CB-CG	-12.89	99.71	112.60
2	2	194	ASN	N-CA-CB	-12.65	89.79	110.41
2	2	44	ASP	CA-CB-CG	12.64	125.24	112.60
1	1	94	ARG	CD-NE-CZ	-12.61	106.75	124.40
1	1	256	ARG	NE-CZ-NH2	12.57	130.51	119.20
2	2	67	ASP	CA-CB-CG	-12.45	100.15	112.60
1	1	175	SER	CA-C-N	12.23	138.54	121.66
1	1	175	SER	C-N-CA	12.23	138.54	121.66
2	2	256	SER	CA-C-O	-12.21	105.38	119.79
4	4	30	ASN	CA-CB-CG	-12.10	100.50	112.60
3	3	172	GLN	CB-CG-CD	12.03	133.05	112.60
4	4	45	LEU	N-CA-CB	-11.89	94.13	111.84
4	4	41	ALA	CA-C-O	-11.31	105.46	119.38
3	3	74	ASN	OD1-CG-ND2	11.30	133.90	122.60
2	2	14	GLN	OE1-CD-NE2	11.18	133.78	122.60
1	1	285	ASP	N-CA-CB	-11.05	95.26	110.29
2	2	151	GLU	CA-CB-CG	11.04	136.19	114.10
1	1	25	PRO	CA-C-O	-10.88	108.94	121.56
2	2	88	ASP	CA-CB-CG	-10.83	101.77	112.60
2	2	219	SER	CA-CB-OG	10.64	132.39	111.10
1	1	282	ARG	CD-NE-CZ	-10.62	109.53	124.40
2	2	97	PHE	CA-CB-CG	-10.60	103.20	113.80
4	4	48	ASP	CA-CB-CG	-10.60	102.00	112.60
1	1	141	ASN	CA-CB-CG	-10.45	102.15	112.60
3	3	57	ASN	N-CA-CB	-10.40	92.92	110.49

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	3	72	ASN	CA-CB-CG	-10.16	102.44	112.60
4	4	48	ASP	O-C-N	10.14	128.33	121.23
1	1	246	ARG	NE-CZ-NH1	10.01	131.51	121.50
1	1	63	SER	CB-CA-C	-10.00	94.20	110.79
1	1	54	ARG	CD-NE-CZ	-9.96	110.45	124.40
4	4	44	SER	CA-C-N	-9.87	107.96	122.07
4	4	44	SER	C-N-CA	-9.87	107.96	122.07
1	1	91	ASP	CA-CB-CG	-9.79	102.81	112.60
1	1	275	THR	CA-C-O	-9.78	109.17	121.88
1	1	285	ASP	N-CA-C	9.75	122.91	110.33
1	1	28	THR	CB-CA-C	-9.73	92.89	111.48
1	1	176	VAL	N-CA-C	9.72	121.72	108.89
1	1	22	SER	CA-C-O	-9.71	109.62	120.69
3	3	33	ARG	CA-C-O	-9.70	110.00	121.05
1	1	208	ASP	CA-CB-CG	-9.69	102.92	112.60
1	1	256	ARG	NE-CZ-NH1	-9.66	111.83	121.50
3	3	137	ARG	NE-CZ-NH1	-9.63	111.87	121.50
1	1	53	THR	CA-CB-OG1	-9.54	95.30	109.60
1	1	246	ARG	CD-NE-CZ	9.44	137.62	124.40
1	1	79	VAL	CA-C-O	-9.42	110.59	120.39
1	1	38	GLU	CA-CB-CG	9.41	132.93	114.10
3	3	86	PHE	CA-CB-CG	9.40	123.20	113.80
3	3	89	ASP	CA-CB-CG	-9.37	103.23	112.60
3	3	57	ASN	CB-CA-C	-9.07	92.36	110.42
2	2	255	ARG	NE-CZ-NH2	-9.06	111.04	119.20
1	1	95	GLU	CB-CG-CD	-9.03	97.25	112.60
1	1	268	ARG	CD-NE-CZ	-9.03	111.76	124.40
4	4	50	SER	CA-C-O	-9.02	109.90	120.10
3	3	196	ILE	CA-C-O	-8.98	111.20	120.27
2	2	195	ASN	CA-CB-CG	8.94	121.54	112.60
2	2	136	GLU	CB-CG-CD	-8.83	97.59	112.60
2	2	250	GLU	CA-CB-CG	8.81	131.72	114.10
4	4	68	ASN	CA-CB-CG	-8.76	103.84	112.60
1	1	270	ASN	CA-CB-CG	8.67	121.27	112.60
1	1	251	GLU	CA-CB-CG	8.64	131.38	114.10
2	2	139	ASN	CA-CB-CG	-8.48	104.12	112.60
2	2	255	ARG	CA-CB-CG	8.48	131.07	114.10
2	2	73	THR	CA-CB-OG1	-8.47	96.89	109.60
1	1	259	ARG	CA-CB-CG	-8.44	97.22	114.10
3	3	174	ARG	CD-NE-CZ	-8.41	112.62	124.40
2	2	168	ASP	CA-C-O	-8.41	110.61	120.62
1	1	165	ASP	CB-CA-C	-8.40	93.70	110.42

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	2	68	SER	N-CA-C	8.38	122.88	110.48
2	2	169	VAL	CA-C-O	-8.38	112.29	121.17
2	2	169	VAL	CB-CA-C	-8.37	101.25	111.97
3	3	74	ASN	CA-C-O	-8.36	109.86	120.55
4	4	41	ALA	N-CA-C	8.35	122.73	112.54
4	4	36	ALA	CA-C-N	-8.33	108.80	122.54
4	4	36	ALA	C-N-CA	-8.33	108.80	122.54
3	3	5	THR	CA-C-O	-8.29	111.11	120.32
3	3	172	GLN	CG-CD-NE2	8.25	128.77	116.40
3	3	219	LEU	CA-C-O	-8.22	111.21	120.66
1	1	82	ILE	CA-C-O	-8.20	113.06	121.67
3	3	182	THR	CA-CB-CG2	8.16	124.37	110.50
3	3	57	ASN	OD1-CG-ND2	8.15	130.75	122.60
4	4	57	LYS	CA-C-O	-8.12	112.33	120.70
1	1	29	GLN	N-CA-C	-8.11	102.43	113.30
2	2	49	ASP	CA-CB-CG	8.09	120.69	112.60
1	1	288	SER	CA-C-O	-8.00	113.07	121.55
3	3	78	GLU	N-CA-C	8.00	120.85	110.53
3	3	233	ALA	CA-C-O	-8.00	112.39	121.19
1	1	164	ASP	CA-C-N	8.00	136.82	121.54
1	1	164	ASP	C-N-CA	8.00	136.82	121.54
3	3	60	THR	CA-CB-OG1	-8.00	97.61	109.60
2	2	187	GLN	CA-CB-CG	7.99	130.09	114.10
2	2	248	CYS	CA-C-O	-7.97	112.29	121.54
1	1	94	ARG	NE-CZ-NH2	-7.95	112.05	119.20
3	3	111	LEU	CA-C-N	-7.94	111.80	123.00
3	3	111	LEU	C-N-CA	-7.94	111.80	123.00
1	1	149	GLN	OE1-CD-NE2	-7.93	114.67	122.60
3	3	231	THR	CA-CB-OG1	-7.91	97.74	109.60
2	2	223	ILE	N-CA-CB	-7.91	101.52	112.27
1	1	118	LEU	O-C-N	7.90	133.63	122.41
1	1	37	ASN	CB-CG-ND2	7.87	128.20	116.40
2	2	216	ASN	CA-C-O	-7.85	112.09	120.80
1	1	274	ASN	O-C-N	7.83	133.01	122.59
2	2	95	ASN	CA-CB-CG	-7.83	104.77	112.60
3	3	216	ASP	N-CA-CB	-7.79	98.63	110.16
4	4	45	LEU	CA-C-O	7.76	130.54	121.54
1	1	282	ARG	CA-C-N	-7.74	111.50	122.41
1	1	282	ARG	C-N-CA	-7.74	111.50	122.41
2	2	109	HIS	CA-C-O	-7.73	110.83	120.57
4	4	37	SER	CB-CA-C	7.71	122.96	110.09
3	3	62	ASP	CA-CB-CG	7.68	120.28	112.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1	64	GLU	CB-CG-CD	7.67	125.64	112.60
2	2	190	ASN	OD1-CG-ND2	-7.66	114.94	122.60
1	1	17	THR	CA-C-N	-7.65	110.26	122.50
1	1	17	THR	C-N-CA	-7.65	110.26	122.50
2	2	240	ILE	CA-C-O	-7.63	112.37	120.39
3	3	137	ARG	CD-NE-CZ	-7.62	113.74	124.40
1	1	61	ASN	CA-CB-CG	-7.61	104.99	112.60
3	3	59	HIS	CA-C-O	7.60	130.47	121.88
3	3	184	ALA	N-CA-C	7.58	122.72	113.17
3	3	142	ARG	CA-CB-CG	7.58	129.25	114.10
2	2	87	LYS	CB-CG-CD	7.56	128.70	111.30
1	1	277	PRO	N-CD-CG	-7.54	91.88	103.20
3	3	79	GLN	OE1-CD-NE2	-7.50	115.10	122.60
1	1	197	TYR	CA-C-O	-7.44	112.37	120.92
4	4	30	ASN	CA-C-O	-7.43	112.22	120.69
1	1	149	GLN	CB-CG-CD	7.41	125.19	112.60
1	1	288	SER	N-CA-C	7.41	120.42	110.35
2	2	98	PHE	CA-C-O	-7.37	110.97	119.60
2	2	140	VAL	CA-C-O	-7.36	113.36	121.23
4	4	45	LEU	CB-CA-C	7.35	122.53	111.80
2	2	107	THR	CA-C-O	-7.34	112.24	120.32
3	3	129	LEU	CA-C-O	-7.32	112.95	120.71
2	2	39	PRO	CA-C-O	-7.31	113.01	121.34
3	3	118	THR	CA-CB-OG1	-7.30	98.65	109.60
2	2	187	GLN	CB-CA-C	7.26	125.39	109.94
2	2	77	GLY	CA-C-O	-7.23	114.82	122.05
3	3	46	ILE	CA-C-O	-7.23	112.45	120.25
3	3	61	LYS	CA-C-O	-7.23	112.68	121.06
2	2	169	VAL	N-CA-C	7.22	117.36	110.42
3	3	124	SER	CA-C-O	-7.22	113.53	121.33
4	4	30	ASN	OD1-CG-ND2	7.22	129.82	122.60
1	1	26	LYS	CA-CB-CG	7.21	128.53	114.10
2	2	180	ASN	CA-CB-CG	-7.21	105.39	112.60
2	2	103	ARG	CD-NE-CZ	-7.20	114.31	124.40
1	1	275	THR	CA-CB-OG1	-7.18	98.83	109.60
2	2	68	SER	O-C-N	-7.18	114.84	122.96
2	2	52	LYS	CA-C-O	-7.17	113.30	121.19
2	2	146	PHE	CA-CB-CG	-7.14	106.66	113.80
2	2	168	ASP	N-CA-CB	-7.14	97.90	109.60
1	1	59	HIS	CA-C-O	-7.12	111.98	120.81
1	1	284	GLY	CA-C-N	7.11	133.60	120.95
1	1	284	GLY	C-N-CA	7.11	133.60	120.95

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	4	47	MET	CA-CB-CG	-7.08	99.95	114.10
2	2	134	SER	CA-C-O	-7.06	113.01	121.05
1	1	285	ASP	CB-CA-C	-7.05	93.81	110.02
3	3	94	THR	O-C-N	7.04	131.65	122.42
2	2	259	ILE	CB-CG1-CD1	-7.04	99.03	113.80
3	3	13	PHE	CA-CB-CG	7.03	120.83	113.80
1	1	85	LYS	CA-C-O	-7.00	113.97	121.38
3	3	164	THR	N-CA-CB	-6.98	99.61	110.57
1	1	28	THR	OG1-CB-CG2	6.98	123.25	109.30
3	3	35	HIS	CA-C-O	-6.97	112.90	120.92
1	1	43	MET	CA-C-O	6.94	126.28	119.75
1	1	285	ASP	CB-CG-OD1	-6.93	102.46	118.40
3	3	109	GLY	CA-C-N	-6.93	110.86	122.64
3	3	109	GLY	C-N-CA	-6.93	110.86	122.64
3	3	121	ALA	CA-C-O	-6.93	112.27	120.10
3	3	66	SER	CB-CA-C	6.91	121.63	110.09
3	3	77	ASN	OD1-CG-ND2	-6.91	115.69	122.60
1	1	270	ASN	O-C-N	6.90	131.39	122.97
2	2	57	ASP	CB-CA-C	-6.88	108.65	116.63
1	1	138	ASP	CA-CB-CG	6.88	119.48	112.60
2	2	9	TYR	CB-CA-C	6.88	121.41	109.65
1	1	35	THR	CA-CB-OG1	-6.87	99.29	109.60
3	3	231	THR	CA-C-O	-6.85	110.49	119.06
4	4	44	SER	O-C-N	6.85	131.70	122.59
2	2	186	HIS	CA-CB-CG	-6.84	106.96	113.80
3	3	65	ASN	OD1-CG-ND2	6.84	129.44	122.60
2	2	219	SER	CB-CA-C	6.84	121.69	109.38
3	3	146	MET	CG-SD-CE	6.82	115.90	100.90
2	2	193	THR	O-C-N	-6.81	115.12	121.79
2	2	14	GLN	CB-CG-CD	-6.81	101.03	112.60
1	1	89	GLY	CA-C-N	-6.81	114.35	122.93
1	1	89	GLY	C-N-CA	-6.81	114.35	122.93
1	1	42	THR	CA-CB-CG2	6.80	122.06	110.50
3	3	202	THR	CA-C-O	6.78	128.49	121.23
1	1	49	ASP	N-CA-C	-6.76	105.32	113.97
3	3	151	VAL	CA-C-O	-6.74	113.57	120.25
3	3	187	LEU	CA-C-O	-6.74	113.10	120.24
1	1	35	THR	N-CA-CB	-6.73	99.11	110.49
2	2	124	VAL	CA-C-O	-6.73	112.78	120.66
3	3	143	ARG	N-CA-C	-6.73	104.02	111.36
1	1	62	GLY	CA-C-N	6.73	129.29	120.28
1	1	62	GLY	C-N-CA	6.73	129.29	120.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	2	170	LEU	CD1-CG-CD2	-6.73	96.00	110.80
3	3	42	ASN	CA-C-O	-6.72	112.93	120.66
4	4	58	ASP	O-C-N	6.72	130.88	123.22
2	2	249	THR	CA-CB-OG1	-6.71	99.53	109.60
1	1	206	HIS	CA-C-O	-6.71	114.10	121.28
2	2	224	PRO	CA-C-O	-6.71	114.05	121.23
3	3	178	PRO	O-C-N	6.70	130.72	123.01
2	2	255	ARG	CB-CG-CD	6.66	126.61	111.30
1	1	288	SER	CB-CA-C	-6.65	97.71	109.62
1	1	282	ARG	NE-CZ-NH2	-6.65	113.22	119.20
3	3	227	THR	CA-CB-OG1	-6.65	99.63	109.60
1	1	95	GLU	CA-CB-CG	-6.64	100.82	114.10
1	1	90	ILE	CA-C-N	-6.62	109.74	122.06
1	1	90	ILE	C-N-CA	-6.62	109.74	122.06
1	1	259	ARG	CA-C-O	-6.62	113.20	120.81
2	2	198	THR	CA-C-O	-6.62	112.97	120.32
1	1	60	PHE	CA-C-O	-6.60	113.63	120.89
3	3	187	LEU	N-CA-CB	-6.59	100.42	110.77
1	1	147	VAL	CA-C-O	-6.59	113.48	120.53
3	3	134	PRO	CA-C-N	-6.59	116.32	123.30
3	3	134	PRO	C-N-CA	-6.59	116.32	123.30
1	1	25	PRO	CA-C-N	6.58	133.40	122.73
1	1	25	PRO	C-N-CA	6.58	133.40	122.73
3	3	202	THR	CA-CB-OG1	-6.58	99.73	109.60
2	2	145	THR	CA-CB-OG1	-6.57	99.75	109.60
2	2	161	GLU	CA-C-N	-6.54	114.52	122.90
2	2	161	GLU	C-N-CA	-6.54	114.52	122.90
2	2	38	TRP	N-CA-CB	-6.53	99.34	110.11
2	2	11	ASP	OD1-CG-OD2	6.52	138.55	122.90
2	2	226	ALA	N-CA-C	-6.52	99.14	109.04
4	4	48	ASP	OD1-CG-OD2	6.52	138.54	122.90
2	2	18	LEU	CB-CA-C	6.51	119.84	110.79
2	2	12	ARG	N-CA-C	6.51	118.17	111.14
2	2	148	HIS	CA-CB-CG	6.50	120.30	113.80
2	2	163	GLY	O-C-N	6.50	130.17	122.50
1	1	277	PRO	CB-CA-C	6.48	119.87	111.64
1	1	176	VAL	N-CA-CB	6.47	117.58	110.53
4	4	36	ALA	N-CA-C	-6.47	105.25	113.01
3	3	205	VAL	CB-CA-C	6.46	120.20	110.90
1	1	256	ARG	CD-NE-CZ	-6.45	115.37	124.40
4	4	39	SER	O-C-N	6.45	130.80	122.23
2	2	142	VAL	CA-C-O	-6.44	113.12	120.66

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	3	182	THR	CA-CB-OG1	-6.44	99.94	109.60
3	3	74	ASN	N-CA-C	6.44	120.46	112.47
3	3	65	ASN	N-CA-CB	-6.44	100.94	110.53
3	3	57	ASN	N-CA-C	6.43	124.50	110.80
2	2	193	THR	CA-C-O	6.43	126.47	119.40
2	2	194	ASN	N-CA-C	6.43	120.54	110.32
3	3	164	THR	CA-CB-OG1	-6.43	99.96	109.60
2	2	247	MET	CB-CA-C	6.42	122.39	109.68
2	2	111	GLN	OE1-CD-NE2	-6.42	116.18	122.60
2	2	69	LYS	CA-CB-CG	6.41	126.91	114.10
3	3	216	ASP	CA-C-N	6.40	129.80	120.71
3	3	216	ASP	C-N-CA	6.40	129.80	120.71
1	1	205	SER	O-C-N	6.39	131.22	122.46
3	3	204	GLN	O-C-N	6.39	130.22	123.06
3	3	172	GLN	OE1-CD-NE2	-6.38	116.22	122.60
1	1	50	SER	CA-C-O	-6.38	110.45	118.43
2	2	203	TYR	CA-C-O	-6.38	113.18	120.58
3	3	99	GLU	CB-CG-CD	6.38	123.44	112.60
3	3	226	GLN	CB-CG-CD	-6.38	101.76	112.60
4	4	44	SER	CA-CB-OG	-6.37	98.36	111.10
1	1	239	VAL	CB-CA-C	6.36	120.04	110.63
3	3	181	TYR	O-C-N	6.35	128.85	122.12
2	2	223	ILE	CA-C-O	-6.35	116.64	119.94
3	3	41	HIS	CA-C-O	-6.34	112.38	119.67
1	1	144	SER	N-CA-CB	-6.33	100.79	110.42
2	2	235	THR	CB-CA-C	-6.33	99.52	109.52
1	1	250	VAL	N-CA-C	6.33	117.82	109.21
2	2	241	THR	CA-C-O	-6.32	114.01	120.71
1	1	137	PRO	CA-C-N	-6.31	113.05	122.39
1	1	137	PRO	C-N-CA	-6.31	113.05	122.39
3	3	80	VAL	CA-C-O	-6.31	113.96	120.71
1	1	265	SER	O-C-N	-6.31	115.95	123.27
3	3	202	THR	N-CA-C	6.29	118.42	108.79
2	2	145	THR	CA-C-O	-6.29	113.84	120.63
1	1	288	SER	N-CA-CB	-6.28	100.80	110.04
3	3	216	ASP	CB-CG-OD2	6.28	132.84	118.40
3	3	63	GLU	CB-CG-CD	-6.28	101.93	112.60
3	3	193	THR	CA-C-O	-6.27	111.54	120.51
3	3	83	THR	CA-CB-OG1	-6.27	100.19	109.60
2	2	103	ARG	CA-CB-CG	6.26	126.62	114.10
2	2	143	LYS	O-C-N	6.26	130.51	122.81
1	1	70	PHE	CA-CB-CG	6.23	120.03	113.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	3	183	SER	N-CA-CB	-6.23	100.82	110.29
4	4	65	PRO	CB-CA-C	-6.23	103.42	111.46
1	1	206	HIS	O-C-N	6.23	129.52	123.29
1	1	282	ARG	NH1-CZ-NH2	6.22	127.38	119.30
1	1	198	ASN	CA-CB-CG	6.21	118.81	112.60
3	3	161	ILE	CA-C-O	-6.20	113.88	120.39
1	1	31	VAL	N-CA-CB	-6.20	102.53	111.21
3	3	196	ILE	N-CA-CB	-6.19	103.41	111.82
1	1	274	ASN	N-CA-CB	6.17	120.92	110.49
1	1	48	SER	CA-C-O	-6.17	108.19	119.36
2	2	28	ALA	CA-C-O	-6.17	114.85	121.94
3	3	6	THR	CB-CA-C	6.17	120.05	109.51
3	3	132	THR	CA-C-O	-6.16	113.92	119.59
1	1	260	ALA	CA-C-O	-6.16	111.51	120.13
2	2	11	ASP	O-C-N	6.16	130.39	122.39
2	2	194	ASN	OD1-CG-ND2	6.15	128.75	122.60
2	2	111	GLN	CB-CG-CD	6.13	123.01	112.60
2	2	238	LEU	N-CA-CB	-6.13	98.78	110.42
1	1	236	LYS	CA-C-O	-6.12	114.25	121.16
2	2	179	GLY	CA-C-O	-6.12	114.21	120.45
3	3	163	MET	CA-CB-CG	-6.11	101.87	114.10
1	1	202	ASP	CB-CA-C	6.11	121.11	112.07
1	1	52	GLU	CA-C-O	-6.10	113.60	120.43
3	3	137	ARG	NE-CZ-NH2	6.09	124.68	119.20
3	3	170	GLY	CA-C-N	6.09	128.66	120.50
3	3	170	GLY	C-N-CA	6.09	128.66	120.50
1	1	252	ALA	CA-C-O	-6.08	113.67	120.66
3	3	193	THR	CA-CB-OG1	-6.08	100.48	109.60
2	2	12	ARG	CD-NE-CZ	-6.08	115.89	124.40
1	1	141	ASN	O-C-N	6.07	129.74	122.27
4	4	43	GLN	OE1-CD-NE2	-6.07	116.53	122.60
1	1	136	GLN	CG-CD-NE2	-6.07	107.30	116.40
2	2	241	THR	CA-CB-OG1	-6.05	100.53	109.60
3	3	8	PRO	CA-C-O	-6.04	114.53	121.36
1	1	68	GLU	CG-CD-OE2	6.04	132.29	118.40
2	2	195	ASN	OD1-CG-ND2	-6.03	116.57	122.60
3	3	36	ILE	CA-C-O	-6.02	111.88	119.95
3	3	30	PRO	O-C-N	6.01	130.18	122.91
1	1	77	VAL	CA-C-O	-6.01	113.25	118.96
3	3	137	ARG	CA-C-O	-6.00	115.03	121.94
1	1	133	THR	CA-CB-OG1	-6.00	100.59	109.60
2	2	86	LEU	CA-C-N	6.00	130.30	120.63

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	2	86	LEU	C-N-CA	6.00	130.30	120.63
3	3	47	ILE	CB-CG1-CD1	-6.00	101.19	113.80
1	1	41	ALA	CA-C-O	-6.00	114.64	121.72
2	2	169	VAL	N-CA-CB	5.99	117.56	110.55
3	3	121	ALA	CB-CA-C	-5.99	99.55	110.63
3	3	41	HIS	N-CA-CB	5.98	119.08	110.40
3	3	174	ARG	NH1-CZ-NH2	5.98	127.07	119.30
2	2	14	GLN	CA-CB-CG	-5.98	102.15	114.10
3	3	194	SER	N-CA-CB	-5.97	100.40	110.49
3	3	158	GLN	CA-C-O	5.95	127.70	120.62
2	2	105	GLY	N-CA-C	-5.94	102.31	112.64
2	2	136	GLU	CG-CD-OE1	-5.94	104.75	118.40
3	3	77	ASN	O-C-N	-5.93	114.71	122.59
3	3	207	LEU	CA-C-O	-5.91	114.23	120.80
3	3	160	THR	CA-CB-OG1	-5.91	100.74	109.60
1	1	22	SER	N-CA-CB	-5.90	100.80	109.95
1	1	265	SER	N-CA-CB	-5.90	100.55	111.53
1	1	55	THR	CA-CB-OG1	-5.90	100.75	109.60
2	2	161	GLU	CA-CB-CG	5.90	125.90	114.10
3	3	1	GLY	O-C-N	-5.90	113.57	123.00
3	3	57	ASN	O-C-N	-5.89	114.75	122.59
1	1	259	ARG	CB-CA-C	-5.89	100.47	109.89
2	2	41	TYR	N-CA-CB	5.89	118.45	110.38
3	3	55	MET	CA-CB-CG	-5.86	102.39	114.10
2	2	226	ALA	O-C-N	5.85	127.86	121.36
3	3	92	PHE	CA-CB-CG	-5.85	107.95	113.80
1	1	270	ASN	CB-CA-C	-5.84	100.29	109.70
1	1	280	LYS	CB-CA-C	-5.84	101.75	110.16
3	3	131	TYR	CA-C-O	-5.84	114.06	120.43
2	2	88	ASP	CA-C-O	-5.83	112.60	119.48
1	1	242	ARG	CD-NE-CZ	-5.82	116.25	124.40
1	1	267	GLY	CA-C-N	-5.82	113.04	122.81
1	1	267	GLY	C-N-CA	-5.82	113.04	122.81
2	2	198	THR	O-C-N	5.82	130.11	123.31
3	3	197	LEU	CB-CA-C	5.81	117.23	108.86
2	2	105	GLY	CA-C-O	-5.80	112.99	122.56
3	3	93	LYS	N-CA-C	5.80	118.38	111.71
2	2	54	SER	CA-C-N	-5.80	115.03	122.98
2	2	54	SER	C-N-CA	-5.80	115.03	122.98
3	3	59	HIS	CA-CB-CG	-5.80	108.00	113.80
2	2	255	ARG	NE-CZ-NH1	5.79	127.29	121.50
4	4	65	PRO	CA-C-O	-5.79	114.74	121.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1	145	ASN	CB-CG-ND2	-5.78	107.73	116.40
2	2	235	THR	OG1-CB-CG2	5.76	120.83	109.30
1	1	68	GLU	CG-CD-OE1	-5.74	105.20	118.40
2	2	189	ILE	CA-C-O	-5.73	113.24	120.69
2	2	210	ASP	N-CA-CB	-5.73	100.56	110.87
1	1	94	ARG	CG-CD-NE	-5.71	99.43	112.00
3	3	137	ARG	O-C-N	5.71	129.67	122.65
2	2	86	LEU	CA-C-O	-5.71	112.88	119.56
3	3	38	GLY	N-CA-C	5.69	123.74	115.32
3	3	66	SER	N-CA-C	-5.69	106.00	113.17
1	1	83	GLN	CB-CG-CD	-5.68	102.94	112.60
3	3	45	GLU	CG-CD-OE2	5.68	131.47	118.40
3	3	112	ARG	CA-CB-CG	5.68	125.45	114.10
3	3	175	TYR	N-CA-CB	-5.68	101.49	110.06
1	1	139	SER	CA-CB-OG	-5.67	99.77	111.10
3	3	42	ASN	CB-CG-ND2	5.66	124.89	116.40
2	2	190	ASN	CB-CA-C	5.66	120.01	110.79
3	3	161	ILE	CA-CB-CG1	-5.66	100.79	110.40
2	2	199	ILE	CA-C-O	-5.65	114.37	120.36
1	1	28	THR	N-CA-C	5.64	118.08	109.95
1	1	232	HIS	CA-CB-CG	-5.64	108.16	113.80
1	1	173	ASN	CB-CA-C	-5.64	103.66	110.15
1	1	94	ARG	NH1-CZ-NH2	5.63	126.62	119.30
3	3	235	THR	CA-CB-OG1	-5.61	101.18	109.60
1	1	208	ASP	CA-C-O	-5.61	114.66	121.28
3	3	180	THR	CA-CB-OG1	-5.61	101.18	109.60
2	2	99	HIS	CA-CB-CG	-5.58	108.22	113.80
1	1	27	HIS	CA-CB-CG	5.58	119.38	113.80
2	2	217	ASN	CB-CA-C	5.58	118.92	109.55
2	2	251	PHE	CA-C-O	-5.58	114.81	121.11
4	4	58	ASP	CA-C-N	5.57	129.02	121.05
4	4	58	ASP	C-N-CA	5.57	129.02	121.05
2	2	262	GLN	OE1-CD-NE2	-5.57	117.03	122.60
2	2	106	TYR	CA-C-O	-5.56	115.33	121.33
2	2	215	HIS	CA-C-O	-5.55	112.50	120.11
1	1	241	ILE	N-CA-CB	-5.55	104.33	110.99
1	1	273	LYS	CG-CD-CE	-5.55	98.54	111.30
3	3	166	PRO	CB-CA-C	5.55	118.62	111.46
2	2	9	TYR	CA-CB-CG	-5.54	103.93	113.90
3	3	190	TRP	CA-C-O	-5.54	115.14	121.40
2	2	94	GLN	CG-CD-NE2	-5.54	108.10	116.40
2	2	68	SER	N-CA-CB	-5.53	101.88	110.29

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	2	168	ASP	CA-C-N	5.53	127.52	120.56
2	2	168	ASP	C-N-CA	5.53	127.52	120.56
3	3	107	TRP	CA-C-O	-5.53	115.16	121.40
1	1	198	ASN	CA-C-O	-5.52	114.09	120.49
2	2	99	HIS	CA-C-N	5.51	128.22	120.28
2	2	99	HIS	C-N-CA	5.51	128.22	120.28
2	2	188	PHE	CA-C-O	-5.51	114.93	121.66
1	1	64	GLU	CA-CB-CG	5.51	125.12	114.10
1	1	235	HIS	CA-CB-CG	-5.51	108.29	113.80
3	3	57	ASN	CA-C-N	5.51	132.08	121.18
3	3	57	ASN	C-N-CA	5.51	132.08	121.18
3	3	76	GLN	CA-C-O	-5.50	115.18	121.68
2	2	192	ARG	CA-C-O	-5.49	111.92	119.05
3	3	140	GLN	CA-CB-CG	-5.49	103.12	114.10
1	1	63	SER	O-C-N	5.48	127.92	122.12
3	3	63	GLU	CG-CD-OE1	-5.47	105.83	118.40
2	2	123	LEU	CA-C-O	-5.46	114.47	120.43
2	2	43	PRO	N-CD-CG	-5.46	95.01	103.20
2	2	167	LYS	CA-C-O	5.46	126.11	119.78
3	3	84	ASN	OD1-CG-ND2	5.46	128.06	122.60
1	1	144	SER	CA-C-N	-5.45	115.37	123.11
1	1	144	SER	C-N-CA	-5.45	115.37	123.11
2	2	26	GLN	OE1-CD-NE2	-5.45	117.15	122.60
2	2	92	PHE	N-CA-C	-5.45	105.03	110.97
2	2	258	SER	O-C-N	5.45	129.51	122.81
2	2	38	TRP	CB-CA-C	5.45	116.25	108.68
3	3	164	THR	CB-CA-C	5.45	119.14	109.72
2	2	187	GLN	CA-C-O	-5.44	114.89	120.99
3	3	34	ILE	CA-C-O	-5.44	113.97	120.78
3	3	168	THR	CA-CB-OG1	-5.44	101.43	109.60
1	1	123	ARG	NE-CZ-NH2	5.43	124.09	119.20
2	2	53	THR	CA-C-O	-5.43	115.54	121.89
1	1	50	SER	CB-CA-C	5.42	117.48	109.29
4	4	50	SER	CA-CB-OG	-5.42	100.26	111.10
1	1	21	ILE	CA-CB-CG1	-5.42	101.19	110.40
2	2	13	VAL	CA-C-O	-5.42	114.56	120.84
2	2	232	THR	CA-CB-OG1	-5.42	101.48	109.60
2	2	63	PHE	CA-CB-CG	5.41	119.21	113.80
3	3	78	GLU	CA-CB-CG	5.40	124.91	114.10
1	1	166	TYR	N-CA-C	-5.40	105.55	111.82
2	2	219	SER	N-CA-C	-5.40	100.89	109.59
3	3	90	GLY	CA-C-O	-5.40	114.87	121.68

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	2	129	GLU	CB-CA-C	-5.40	104.22	111.89
2	2	221	MET	CA-C-O	-5.38	114.34	120.32
2	2	81	LYS	CB-CG-CD	5.37	123.66	111.30
3	3	112	ARG	CB-CA-C	5.37	119.08	110.16
1	1	231	GLU	N-CA-C	-5.37	102.94	110.35
3	3	38	GLY	O-C-N	-5.36	116.00	122.38
3	3	116	MET	CB-CG-SD	-5.36	96.63	112.70
1	1	92	ASN	O-C-N	5.36	129.49	123.28
1	1	288	SER	CA-CB-OG	-5.35	100.41	111.10
2	2	120	GLY	CA-C-O	-5.35	114.41	122.54
3	3	143	ARG	O-C-N	5.34	128.24	122.15
3	3	195	LEU	CA-C-O	-5.34	114.97	121.05
2	2	210	ASP	CA-CB-CG	-5.33	107.27	112.60
1	1	286	ILE	O-C-N	5.33	127.82	121.80
2	2	177	LEU	N-CA-CB	-5.33	101.60	110.23
1	1	282	ARG	O-C-N	5.32	129.35	122.81
3	3	226	GLN	N-CA-C	-5.32	106.74	113.18
3	3	19	ARG	NE-CZ-NH2	5.32	123.98	119.20
4	4	58	ASP	N-CA-CB	5.32	119.08	110.42
2	2	102	GLY	CA-C-O	-5.31	115.46	121.68
3	3	221	LEU	O-C-N	5.31	129.66	122.59
1	1	26	LYS	CG-CD-CE	-5.30	99.10	111.30
2	2	12	ARG	CB-CG-CD	-5.30	99.11	111.30
3	3	161	ILE	N-CA-CB	5.30	118.72	111.41
3	3	222	MET	CB-CG-SD	-5.30	96.80	112.70
2	2	262	GLN	CG-CD-NE2	5.29	124.34	116.40
1	1	185	ARG	NE-CZ-NH2	5.29	123.96	119.20
2	2	72	THR	CA-CB-OG1	-5.28	101.68	109.60
3	3	86	PHE	CB-CA-C	5.28	120.49	111.68
3	3	204	GLN	CA-C-O	-5.28	115.03	121.36
3	3	33	ARG	NE-CZ-NH2	5.27	123.94	119.20
1	1	113	ARG	NE-CZ-NH2	5.27	123.94	119.20
3	3	192	GLN	N-CA-C	-5.27	105.13	112.45
1	1	60	PHE	N-CA-CB	-5.27	102.17	111.39
3	3	56	ASN	CA-C-N	5.27	131.60	121.54
3	3	56	ASN	C-N-CA	5.27	131.60	121.54
2	2	76	LYS	CA-C-O	-5.27	113.46	119.41
2	2	195	ASN	N-CA-C	-5.26	106.64	114.64
1	1	229	VAL	N-CA-C	-5.26	104.94	112.35
2	2	257	LYS	N-CA-CB	5.25	119.36	110.49
4	4	53	THR	CA-CB-OG1	-5.25	101.73	109.60
3	3	77	ASN	CA-CB-CG	-5.25	107.35	112.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	2	168	ASP	OD1-CG-OD2	5.24	135.49	122.90
3	3	94	THR	CA-C-O	-5.24	113.18	119.15
2	2	214	ARG	CD-NE-CZ	-5.24	117.07	124.40
1	1	201	TYR	CA-C-N	-5.23	114.79	122.06
1	1	201	TYR	C-N-CA	-5.23	114.79	122.06
3	3	208	LEU	CA-C-O	-5.23	114.99	120.80
1	1	279	ILE	CA-C-N	5.23	128.76	121.02
1	1	279	ILE	C-N-CA	5.23	128.76	121.02
2	2	20	ASN	CA-CB-CG	5.23	117.83	112.60
1	1	149	GLN	CA-C-O	-5.23	114.72	120.36
3	3	144	GLU	CA-CB-CG	5.22	124.54	114.10
2	2	122	LEU	CA-C-O	-5.22	115.12	121.28
2	2	75	SER	N-CA-CB	-5.22	101.95	109.83
1	1	63	SER	N-CA-C	5.21	116.96	111.28
3	3	158	GLN	CG-CD-OE1	5.21	131.22	120.80
2	2	243	THR	CA-C-O	-5.21	114.70	120.38
2	2	127	ILE	CA-C-O	-5.21	114.21	119.89
1	1	97	LYS	CB-CA-C	-5.20	104.34	111.73
1	1	282	ARG	CB-CA-C	-5.20	100.31	109.62
3	3	67	TYR	N-CA-C	-5.20	106.78	113.23
1	1	259	ARG	N-CA-CB	5.20	117.59	109.85
1	1	268	ARG	CB-CA-C	5.20	119.74	109.66
2	2	8	GLY	CA-C-N	-5.19	113.50	120.87
2	2	8	GLY	C-N-CA	-5.19	113.50	120.87
3	3	138	GLY	N-CA-C	-5.19	101.75	112.34
1	1	136	GLN	OE1-CD-NE2	5.18	127.78	122.60
2	2	18	LEU	N-CA-CB	-5.18	102.78	110.71
2	2	38	TRP	CA-CB-CG	-5.18	103.77	113.60
2	2	213	THR	CA-CB-OG1	-5.17	101.84	109.60
1	1	257	ALA	N-CA-CB	-5.17	101.86	109.98
2	2	259	ILE	CA-C-O	-5.17	115.01	120.39
3	3	233	ALA	O-C-N	5.17	129.23	122.87
3	3	215	PRO	CB-CA-C	5.17	119.24	111.44
2	2	127	ILE	O-C-N	5.16	125.67	120.92
3	3	186	PHE	O-C-N	5.16	129.85	123.15
3	3	45	GLU	CG-CD-OE1	-5.15	106.55	118.40
1	1	23	SER	CA-C-O	-5.15	115.09	121.06
1	1	145	ASN	O-C-N	5.14	129.61	123.13
2	2	181	LEU	N-CA-C	-5.14	106.27	112.54
2	2	165	PRO	CA-C-O	-5.14	115.37	122.15
3	3	186	PHE	CA-CB-CG	-5.14	108.66	113.80
3	3	231	THR	CA-C-N	-5.14	115.39	122.69

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	3	231	THR	C-N-CA	-5.14	115.39	122.69
1	1	217	VAL	CB-CA-C	-5.13	105.36	112.24
2	2	152	ARG	CD-NE-CZ	-5.13	117.22	124.40
2	2	143	LYS	CA-C-N	5.12	131.32	121.54
2	2	143	LYS	C-N-CA	5.12	131.32	121.54
1	1	204	TYR	CA-C-O	-5.12	115.64	121.58
3	3	125	ALA	CA-C-O	-5.11	115.48	121.10
2	2	259	ILE	CA-C-N	-5.11	112.68	122.13
2	2	259	ILE	C-N-CA	-5.11	112.68	122.13
3	3	109	GLY	N-CA-C	5.11	117.50	111.63
1	1	98	LEU	O-C-N	5.10	129.88	122.43
2	2	119	SER	O-C-N	5.10	129.34	123.17
1	1	27	HIS	CA-C-O	-5.10	113.09	122.62
1	1	285	ASP	CA-C-N	-5.09	111.95	120.30
1	1	285	ASP	C-N-CA	-5.09	111.95	120.30
3	3	82	GLY	N-CA-C	-5.09	103.03	110.87
2	2	126	VAL	CA-C-O	-5.08	115.09	120.53
2	2	65	THR	CA-CB-OG1	-5.08	101.98	109.60
3	3	1	GLY	N-CA-C	5.07	128.01	113.30
3	3	174	ARG	NE-CZ-NH2	-5.07	114.64	119.20
1	1	40	GLY	N-CA-C	-5.07	108.12	115.27
2	2	119	SER	CA-C-O	-5.07	115.67	121.40
2	2	215	HIS	CA-CB-CG	5.07	118.87	113.80
2	2	235	THR	CA-C-O	5.07	125.44	120.17
2	2	25	THR	CA-C-O	5.07	126.49	120.66
3	3	75	ARG	CD-NE-CZ	-5.07	117.31	124.40
1	1	165	ASP	CB-CG-OD2	5.06	130.04	118.40
3	3	217	PHE	N-CA-C	5.06	117.57	110.23
2	2	168	ASP	CB-CG-OD1	-5.06	106.76	118.40
1	1	133	THR	CA-C-O	-5.06	115.39	121.11
1	1	83	GLN	OE1-CD-NE2	5.06	127.66	122.60
3	3	95	THR	CA-CB-OG1	-5.05	102.02	109.60
3	3	177	ASP	N-CA-CB	-5.05	103.02	110.14
2	2	170	LEU	N-CA-C	-5.05	106.81	112.87
3	3	158	GLN	CB-CA-C	5.05	118.34	110.67
1	1	270	ASN	N-CA-CB	5.04	117.71	109.69
1	1	66	ASP	CA-C-O	-5.04	115.64	121.19
3	3	146	MET	CB-CA-C	5.03	120.43	110.17
2	2	261	PRO	CA-C-N	5.03	130.75	121.70
2	2	261	PRO	C-N-CA	5.03	130.75	121.70
1	1	65	THR	N-CA-C	-5.03	106.07	113.61
1	1	76	CYS	CA-C-O	-5.03	115.03	120.81

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1	282	ARG	CG-CD-NE	-5.02	100.95	112.00
1	1	160	PRO	N-CD-CG	-5.02	95.67	103.20
2	2	121	CYS	N-CA-CB	-5.02	102.31	110.59
3	3	217	PHE	CA-C-O	-5.02	115.67	121.19
2	2	32	VAL	O-C-N	5.01	128.25	123.14
1	1	68	GLU	N-CA-C	-5.01	106.01	111.82

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	1	259	ARG	Sidechain
1	1	268	ARG	Sidechain
2	2	12	ARG	Sidechain
2	2	255	ARG	Sidechain

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	1	2170	0	2107	233	0
2	2	1952	0	1926	120	0
3	3	1849	0	1832	149	0
4	4	297	0	294	29	0
5	1	21	0	21	6	0
All	All	6289	0	6180	464	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 37.

All (464) 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)
3:3:57:ASN:CB	3:3:57:ASN:CA	1.75	1.58
4:4:33:LYS:CE	4:4:33:LYS:NZ	1.67	1.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:52:LYS:NZ	2:2:52:LYS:CE	1.68	1.54
1:1:285:ASP:CB	1:1:285:ASP:CA	1.79	1.54
1:1:152:TYR:CE2	1:1:154:PRO:HG3	1.58	1.39
1:1:152:TYR:CD2	1:1:154:PRO:HG3	1.69	1.28
5:1:290:S57:C6B	5:1:290:S57:CL	2.27	1.18
3:3:179:ASP:OD2	3:3:182:THR:HB	1.41	1.16
5:1:290:S57:CL	5:1:290:S57:H6B1	1.82	1.14
2:2:158:SER:OG	2:2:167:LYS:HE2	1.46	1.14
1:1:105:ASN:HD21	1:1:266:ILE:HG12	1.19	1.07
1:1:285:ASP:CA	1:1:285:ASP:OD1	2.00	1.07
1:1:258:PRO:HG2	3:3:99:GLU:HG2	1.36	1.06
1:1:47:PRO:HA	3:3:164:THR:HG21	1.34	1.05
2:2:12:ARG:NH1	2:2:12:ARG:HG3	1.69	1.05
1:1:154:PRO:HB2	1:1:155:PRO:HD2	1.35	1.05
1:1:191:VAL:HG23	1:1:191:VAL:O	1.57	1.03
2:2:255:ARG:HG2	2:2:256:SER:H	1.24	1.03
1:1:152:TYR:C	1:1:154:PRO:HD3	1.83	1.02
1:1:282:ARG:HG3	3:3:57:ASN:HB3	1.41	1.02
3:3:16:THR:HG23	3:3:16:THR:O	1.55	1.02
1:1:154:PRO:CB	1:1:155:PRO:HD2	1.92	1.00
1:1:70:PHE:O	1:1:115:LYS:NZ	1.95	0.98
3:3:57:ASN:CB	3:3:57:ASN:N	2.28	0.97
2:2:136:GLU:HB3	2:2:140:VAL:HG21	1.44	0.97
3:3:57:ASN:CB	3:3:57:ASN:C	2.37	0.96
5:1:290:S57:CL	5:1:290:S57:H6B2	2.02	0.96
1:1:136:GLN:HE21	1:1:235:HIS:CD2	1.84	0.95
1:1:285:ASP:CA	1:1:285:ASP:CG	2.37	0.95
1:1:224:MET:HE2	1:1:226:PHE:CZ	2.01	0.95
3:3:16:THR:O	3:3:16:THR:CG2	2.13	0.95
1:1:191:VAL:O	1:1:191:VAL:CG2	2.12	0.94
1:1:83:GLN:HG3	1:1:85:LYS:HE2	1.47	0.94
1:1:154:PRO:CB	1:1:155:PRO:CD	2.45	0.94
1:1:285:ASP:CB	1:1:285:ASP:C	2.40	0.93
1:1:152:TYR:CE2	1:1:154:PRO:CG	2.51	0.93
1:1:220:HIS:O	1:1:221:MET:HG2	1.69	0.93
1:1:197:TYR:CE1	1:1:221:MET:HE1	2.04	0.93
1:1:152:TYR:CD2	1:1:154:PRO:CG	2.52	0.92
3:3:25:LEU:HD23	3:3:25:LEU:H	1.33	0.92
2:2:41:TYR:CE2	2:2:55:LYS:HD3	2.05	0.92
1:1:105:ASN:ND2	1:1:266:ILE:HG12	1.85	0.92
1:1:285:ASP:CB	1:1:285:ASP:N	2.34	0.91

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:153:VAL:HG21	1:1:159:ASN:HA	1.50	0.91
2:2:235:THR:HG23	2:2:236:PRO:HD2	1.53	0.91
2:2:12:ARG:HG3	2:2:12:ARG:HH11	1.27	0.91
1:1:28:THR:HB	1:1:30:LYS:H	1.35	0.90
1:1:58:MET:HE1	3:3:216:ASP:O	1.71	0.90
2:2:11:ASP:HB2	4:4:68:ASN:OD1	1.71	0.90
3:3:175:TYR:HB2	3:3:182:THR:HG21	1.53	0.90
3:3:27:ASN:O	3:3:28:TYR:O	1.90	0.89
3:3:57:ASN:CA	3:3:57:ASN:CG	2.45	0.89
1:1:92:ASN:ND2	1:1:95:GLU:HB2	1.87	0.89
1:1:285:ASP:OD1	1:1:285:ASP:HA	1.73	0.88
1:1:129:THR:OG1	1:1:185:ARG:HD2	1.74	0.88
1:1:105:ASN:HD21	1:1:266:ILE:CG1	1.87	0.88
3:3:198:PRO:HD2	3:3:201:THR:HG21	1.55	0.88
2:2:20:ASN:ND2	2:2:62:ARG:HE	1.72	0.87
1:1:47:PRO:HA	3:3:164:THR:CG2	2.03	0.87
1:1:94:ARG:CZ	1:1:101:ASP:OD2	2.21	0.87
1:1:218:LEU:O	1:1:220:HIS:N	2.06	0.86
1:1:154:PRO:HB2	1:1:155:PRO:CD	2.05	0.85
1:1:224:MET:HE2	1:1:226:PHE:HZ	1.40	0.85
1:1:153:VAL:O	1:1:153:VAL:HG22	1.74	0.85
2:2:12:ARG:HH11	2:2:12:ARG:CG	1.89	0.85
2:2:116:LYS:HB3	3:3:121:ALA:HB3	1.57	0.85
3:3:26:PRO:O	3:3:28:TYR:N	2.10	0.85
1:1:125:ASP:OD1	1:1:189:PRO:HA	1.76	0.84
1:1:90:ILE:HD13	1:1:90:ILE:N	1.92	0.84
1:1:121:TYR:O	1:1:122:VAL:HG23	1.77	0.84
3:3:25:LEU:HD23	3:3:25:LEU:N	1.90	0.84
1:1:282:ARG:HD2	1:1:285:ASP:O	1.78	0.84
2:2:158:SER:OG	2:2:167:LYS:CE	2.27	0.82
2:2:10:SER:OG	2:2:12:ARG:HB2	1.78	0.82
2:2:52:LYS:NZ	2:2:52:LYS:CD	2.43	0.82
1:1:248:LYS:HE3	4:4:38:THR:O	1.80	0.82
1:1:94:ARG:NH2	1:1:101:ASP:OD2	2.13	0.82
1:1:152:TYR:O	1:1:154:PRO:HD3	1.80	0.81
2:2:136:GLU:CB	2:2:140:VAL:HG21	2.09	0.81
4:4:59:LEU:HD21	4:4:61:LEU:HD13	1.61	0.81
1:1:38:GLU:CD	3:3:116:MET:HE2	2.05	0.81
1:1:58:MET:CE	3:3:216:ASP:HA	2.11	0.80
2:2:9:TYR:HD1	2:2:9:TYR:N	1.77	0.80
4:4:68:ASN:OD1	4:4:68:ASN:N	2.11	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:9:TYR:N	2:2:9:TYR:CD1	2.43	0.79
1:1:58:MET:HE1	3:3:216:ASP:C	2.08	0.78
1:1:136:GLN:NE2	1:1:235:HIS:NE2	2.32	0.78
1:1:105:ASN:O	1:1:106:LEU:HB2	1.83	0.78
2:2:262:GLN:HE21	2:2:262:GLN:C	1.91	0.78
3:3:26:PRO:C	3:3:28:TYR:H	1.92	0.78
1:1:282:ARG:HG3	3:3:57:ASN:CB	2.15	0.77
3:3:21:SER:O	4:4:37:SER:HB2	1.83	0.77
2:2:255:ARG:HG2	2:2:256:SER:N	2.00	0.77
3:3:79:GLN:HB2	3:3:190:TRP:CZ3	2.19	0.76
1:1:94:ARG:NH1	1:1:94:ARG:HG2	2.00	0.76
3:3:18:ASP:OD1	4:4:40:SER:HB2	1.86	0.75
1:1:188:VAL:HG12	1:1:189:PRO:O	1.87	0.75
1:1:152:TYR:O	1:1:154:PRO:CD	2.35	0.75
1:1:270:ASN:HA	2:2:133:ALA:HB1	1.68	0.75
3:3:179:ASP:OD2	3:3:182:THR:CB	2.31	0.74
2:2:174:ASN:C	2:2:174:ASN:HD22	1.93	0.74
3:3:197:LEU:HB3	3:3:201:THR:CG2	2.18	0.74
1:1:89:GLY:C	1:1:90:ILE:HD13	2.13	0.74
4:4:43:GLN:HG2	4:4:45:LEU:HB2	1.70	0.73
2:2:188:PHE:O	2:2:194:ASN:ND2	2.22	0.73
1:1:282:ARG:CG	3:3:57:ASN:HB3	2.18	0.73
1:1:47:PRO:CA	3:3:164:THR:HG21	2.15	0.72
1:1:58:MET:HE1	3:3:216:ASP:HA	1.71	0.71
1:1:258:PRO:CG	3:3:99:GLU:HG2	2.16	0.71
2:2:53:THR:HG22	2:2:252:SER:HB2	1.71	0.71
2:2:20:ASN:HD21	2:2:62:ARG:HE	1.39	0.71
4:4:33:LYS:NZ	4:4:33:LYS:CD	2.52	0.71
1:1:19:ALA:HB2	1:1:58:MET:HG2	1.72	0.71
2:2:230:VAL:CG2	2:2:234:ALA:HB3	2.20	0.71
1:1:215:ILE:HG12	1:1:215:ILE:O	1.91	0.70
3:3:57:ASN:CA	3:3:57:ASN:OD1	2.38	0.70
1:1:197:TYR:HE1	1:1:221:MET:HE1	1.55	0.70
2:2:39:PRO:HG2	2:2:247:MET:HE2	1.74	0.70
2:2:235:THR:CG2	2:2:236:PRO:HD2	2.21	0.70
1:1:123:ARG:HD2	1:1:195:SER:O	1.92	0.69
2:2:195:ASN:OD1	2:2:196:THR:HG23	1.92	0.69
3:3:98:GLY:O	3:3:102:GLN:HG3	1.92	0.69
2:2:230:VAL:HG23	2:2:234:ALA:HB3	1.74	0.69
2:2:136:GLU:HB3	2:2:140:VAL:CG2	2.21	0.69
1:1:151:MET:SD	1:1:170:SER:HB2	2.33	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:4:29:ILE:HG22	4:4:29:ILE:O	1.94	0.68
1:1:125:ASP:HB2	1:1:248:LYS:O	1.94	0.67
1:1:208:ASP:HB3	1:1:211:THR:HG22	1.74	0.67
1:1:83:GLN:CG	1:1:85:LYS:HE2	2.24	0.67
3:3:61:LYS:HD3	3:3:63:GLU:OE2	1.95	0.67
1:1:278:VAL:HG12	3:3:62:ASP:OD2	1.95	0.67
2:2:84:ASP:OD1	2:2:87:LYS:HE2	1.94	0.67
1:1:146:LEU:HD13	1:1:228:ILE:HD13	1.77	0.66
2:2:155:ASP:C	2:2:155:ASP:OD1	2.37	0.66
3:3:89:ASP:HA	3:3:93:LYS:HD2	1.78	0.66
1:1:152:TYR:C	1:1:154:PRO:CD	2.65	0.66
1:1:121:TYR:C	1:1:122:VAL:HG23	2.21	0.66
1:1:151:MET:HG3	1:1:175:SER:HB3	1.76	0.66
3:3:197:LEU:HB3	3:3:201:THR:HG22	1.77	0.66
1:1:208:ASP:HB3	1:1:211:THR:CG2	2.25	0.66
1:1:285:ASP:CB	1:1:285:ASP:H	2.09	0.65
2:2:256:SER:O	2:2:257:LYS:HB3	1.96	0.65
2:2:149:PRO:HG3	2:2:154:ILE:HG13	1.78	0.64
1:1:58:MET:HE1	3:3:216:ASP:CA	2.27	0.64
1:1:186:PHE:CZ	5:1:290:S57:H13	2.31	0.64
3:3:27:ASN:C	3:3:28:TYR:O	2.41	0.64
3:3:79:GLN:HB2	3:3:190:TRP:CE3	2.32	0.64
2:2:12:ARG:HH21	3:3:157:LEU:HD21	1.63	0.64
2:2:23:ILE:HD11	2:2:243:THR:HG21	1.79	0.64
1:1:158:PRO:HB2	1:1:167:THR:HG22	1.80	0.64
2:2:12:ARG:NH1	4:4:68:ASN:O	2.31	0.64
1:1:60:PHE:CE2	3:3:218:LYS:HB3	2.33	0.64
2:2:11:ASP:H	4:4:68:ASN:CG	2.06	0.63
2:2:39:PRO:CG	2:2:247:MET:HE2	2.29	0.63
3:3:18:ASP:CG	4:4:40:SER:HB2	2.22	0.63
3:3:25:LEU:N	3:3:25:LEU:CD2	2.62	0.63
1:1:220:HIS:C	1:1:221:MET:CG	2.72	0.63
1:1:87:ALA:HA	1:1:90:ILE:HG12	1.80	0.63
3:3:75:ARG:O	3:3:194:SER:HB2	1.99	0.62
2:2:40:GLU:HG3	2:2:41:TYR:O	2.00	0.62
1:1:102:TRP:CZ3	1:1:243:VAL:HG11	2.33	0.62
2:2:13:VAL:O	2:2:14:GLN:HG2	1.99	0.61
2:2:38:TRP:CZ3	4:4:57:LYS:HD2	2.36	0.61
1:1:121:TYR:O	1:1:122:VAL:CG2	2.46	0.61
2:2:133:ALA:O	2:2:166:VAL:HG12	2.01	0.61
3:3:57:ASN:ND2	3:3:91:VAL:HG13	2.15	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:123:ARG:O	1:1:251:GLU:N	2.34	0.61
1:1:281:LYS:HD2	3:3:59:HIS:O	2.01	0.61
3:3:55:MET:HG3	3:3:55:MET:O	1.99	0.61
1:1:90:ILE:N	1:1:90:ILE:CD1	2.62	0.61
3:3:175:TYR:H	3:3:182:THR:HG21	1.66	0.60
3:3:56:ASN:HB3	3:3:66:SER:HA	1.83	0.60
3:3:76:GLN:O	3:3:78:GLU:N	2.34	0.60
1:1:265:SER:HB3	1:1:268:ARG:HG2	1.83	0.60
1:1:159:ASN:HD22	1:1:160:PRO:CD	2.15	0.60
1:1:51:ILE:HD13	3:3:166:PRO:HG3	1.82	0.59
1:1:221:MET:O	1:1:222:GLY:O	2.20	0.59
3:3:131:TYR:HB3	3:3:149:THR:HB	1.82	0.59
2:2:256:SER:O	2:2:257:LYS:CB	2.50	0.59
1:1:94:ARG:NH1	1:1:94:ARG:CG	2.60	0.59
1:1:259:ARG:HD2	1:1:263:TYR:CE1	2.38	0.59
1:1:205:SER:HB3	1:1:217:VAL:HG13	1.85	0.59
3:3:26:PRO:C	3:3:28:TYR:N	2.55	0.58
1:1:154:PRO:O	1:1:157:ALA:HB3	2.02	0.58
3:3:180:THR:O	3:3:183:SER:HB3	2.02	0.58
1:1:43:MET:HE3	1:1:43:MET:HA	1.85	0.57
2:2:177:LEU:HD11	3:3:94:THR:HG21	1.86	0.57
2:2:204:ILE:HG12	3:3:37:PRO:HG2	1.87	0.57
2:2:64:TYR:CD1	2:2:89:MET:HB3	2.39	0.57
1:1:285:ASP:HB3	1:1:287:LYS:N	2.18	0.57
2:2:221:MET:HE2	2:2:223:ILE:HD11	1.87	0.57
1:1:176:VAL:HG23	5:1:290:S57:H11	1.87	0.57
1:1:214:GLY:HA2	2:2:131:GLN:NE2	2.20	0.57
2:2:52:LYS:NZ	2:2:52:LYS:HD3	2.20	0.57
3:3:57:ASN:HB3	3:3:57:ASN:C	2.28	0.57
3:3:179:ASP:OD2	3:3:182:THR:CG2	2.53	0.57
1:1:43:MET:HG3	1:1:44:PRO:HD2	1.87	0.56
1:1:58:MET:HE3	3:3:216:ASP:HA	1.85	0.56
1:1:171:ALA:O	1:1:172:SER:CB	2.53	0.56
3:3:175:TYR:H	3:3:182:THR:CG2	2.19	0.56
1:1:85:LYS:HB3	1:1:236:LYS:HG3	1.87	0.56
2:2:174:ASN:C	2:2:174:ASN:ND2	2.63	0.56
1:1:201:TYR:HD2	1:1:214:GLY:O	1.89	0.56
1:1:136:GLN:NE2	1:1:235:HIS:CD2	2.64	0.56
1:1:114:LYS:NZ	3:3:99:GLU:OE2	2.37	0.56
1:1:125:ASP:N	1:1:248:LYS:O	2.37	0.56
2:2:10:SER:OG	2:2:12:ARG:CB	2.53	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:3:53:ILE:HD11	3:3:211:ILE:HB	1.87	0.56
4:4:44:SER:O	4:4:45:LEU:C	2.48	0.56
1:1:236:LYS:HE3	1:1:238:LEU:HD13	1.88	0.56
1:1:154:PRO:HB3	1:1:155:PRO:HD2	1.85	0.55
2:2:189:ILE:HA	2:2:194:ASN:ND2	2.21	0.55
4:4:43:GLN:O	4:4:45:LEU:HB3	2.05	0.55
2:2:77:GLY:O	2:2:156:LEU:HB2	2.07	0.55
2:2:230:VAL:HG23	2:2:231:PRO:O	2.05	0.55
1:1:228:ILE:HD11	1:1:239:VAL:HG21	1.88	0.55
3:3:199:PRO:O	3:3:200:GLU:HB2	2.05	0.55
2:2:38:TRP:CD1	2:2:39:PRO:HD2	2.42	0.55
1:1:105:ASN:O	1:1:106:LEU:CD1	2.55	0.55
1:1:154:PRO:HB3	1:1:155:PRO:CD	2.35	0.55
1:1:79:VAL:HG22	1:1:242:ARG:HG2	1.89	0.54
1:1:266:ILE:HD12	3:3:235:THR:HA	1.88	0.54
2:2:8:GLY:C	2:2:9:TYR:HD1	2.14	0.54
3:3:198:PRO:O	3:3:201:THR:HB	2.07	0.54
4:4:59:LEU:HD21	4:4:61:LEU:CD1	2.34	0.54
2:2:230:VAL:HB	2:2:231:PRO:HD2	1.89	0.54
3:3:63:GLU:C	3:3:65:ASN:H	2.14	0.54
1:1:126:SER:O	1:1:187:SER:HB2	2.08	0.54
2:2:38:TRP:HZ3	4:4:57:LYS:HD2	1.70	0.54
1:1:35:THR:HG23	3:3:160:THR:HB	1.90	0.54
2:2:170:LEU:CD2	3:3:64:VAL:HA	2.38	0.54
1:1:105:ASN:HD21	1:1:266:ILE:CD1	2.19	0.54
3:3:193:THR:O	3:3:194:SER:CB	2.55	0.54
3:3:197:LEU:HB3	3:3:201:THR:HG21	1.87	0.54
3:3:55:MET:HA	3:3:91:VAL:HG11	1.90	0.54
1:1:130:ILE:CG2	1:1:178:PHE:CZ	2.92	0.53
3:3:117:TYR:CD1	3:3:155:ILE:HD13	2.44	0.53
1:1:273:LYS:O	1:1:274:ASN:C	2.52	0.53
1:1:105:ASN:O	1:1:106:LEU:CB	2.53	0.53
1:1:190:TYR:OH	1:1:196:ALA:C	2.52	0.53
1:1:271:TYR:HB2	1:1:272:PRO:HD2	1.89	0.53
2:2:235:THR:CG2	2:2:236:PRO:CD	2.86	0.53
1:1:152:TYR:O	1:1:154:PRO:HD2	2.09	0.53
1:1:153:VAL:O	1:1:153:VAL:CG2	2.45	0.53
3:3:86:PHE:CD1	3:3:178:PRO:HB3	2.44	0.53
2:2:12:ARG:NH2	3:3:157:LEU:HD21	2.24	0.52
1:1:122:VAL:HG12	1:1:124:PHE:CE2	2.44	0.52
1:1:170:SER:O	1:1:170:SER:OG	2.22	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:205:SER:HB3	1:1:217:VAL:CG1	2.39	0.52
1:1:88:THR:O	1:1:90:ILE:HD13	2.10	0.52
1:1:83:GLN:HG3	1:1:85:LYS:CE	2.31	0.52
1:1:88:THR:O	1:1:90:ILE:CD1	2.58	0.52
1:1:112:LEU:O	1:1:112:LEU:HG	2.09	0.52
1:1:153:VAL:N	1:1:154:PRO:HD3	2.25	0.52
1:1:276:GLU:HB3	1:1:277:PRO:CD	2.39	0.52
1:1:74:ALA:HB3	3:3:15:THR:HB	1.91	0.52
1:1:236:LYS:NZ	1:1:238:LEU:HD11	2.25	0.52
3:3:216:ASP:O	3:3:218:LYS:HE3	2.09	0.52
1:1:103:LYS:O	1:1:104:ILE:C	2.53	0.52
2:2:66:LEU:HD12	2:2:89:MET:HE3	1.91	0.52
1:1:159:ASN:HD22	1:1:160:PRO:HD3	1.74	0.52
2:2:262:GLN:C	2:2:262:GLN:NE2	2.66	0.51
4:4:44:SER:C	4:4:46:SER:N	2.68	0.51
1:1:129:THR:HG1	1:1:185:ARG:HD2	1.73	0.51
1:1:236:LYS:HE3	1:1:238:LEU:CD1	2.40	0.51
2:2:177:LEU:CD1	3:3:94:THR:HG21	2.40	0.51
3:3:75:ARG:NH1	3:3:78:GLU:OE2	2.41	0.51
1:1:273:LYS:O	1:1:274:ASN:O	2.28	0.51
3:3:193:THR:O	3:3:194:SER:HB3	2.08	0.51
3:3:214:CYS:HB3	3:3:215:PRO:HD2	1.92	0.51
1:1:149:GLN:HA	1:1:176:VAL:O	2.10	0.51
2:2:34:CYS:HB2	2:2:202:PRO:CD	2.41	0.51
1:1:38:GLU:OE1	3:3:116:MET:HE2	2.10	0.51
1:1:265:SER:HB2	2:2:138:GLY:O	2.11	0.51
3:3:210:PHE:N	3:3:210:PHE:CD1	2.77	0.51
1:1:94:ARG:CG	1:1:94:ARG:HH11	2.24	0.51
1:1:92:ASN:CG	1:1:95:GLU:HB2	2.36	0.50
2:2:171:TYR:HA	2:2:176:THR:O	2.11	0.50
1:1:65:THR:HG22	3:3:104:TYR:CZ	2.46	0.50
2:2:139:ASN:N	2:2:139:ASN:OD1	2.44	0.50
1:1:114:LYS:NZ	3:3:227:THR:OG1	2.43	0.50
2:2:255:ARG:CG	2:2:256:SER:H	2.00	0.50
1:1:60:PHE:CD2	3:3:218:LYS:HB3	2.46	0.50
1:1:220:HIS:O	1:1:221:MET:CG	2.47	0.50
3:3:24:ALA:HB3	3:3:25:LEU:HD23	1.94	0.50
2:2:158:SER:HG	2:2:167:LYS:HE2	1.71	0.50
1:1:125:ASP:CG	1:1:249:HIS:HD1	2.20	0.49
2:2:13:VAL:C	2:2:14:GLN:CG	2.85	0.49
2:2:143:LYS:HG2	2:2:163:GLY:O	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:37:GLU:CD	3:3:35:HIS:HE2	2.19	0.49
2:2:235:THR:HG22	2:2:236:PRO:N	2.22	0.49
3:3:28:TYR:CG	3:3:29:GLU:N	2.70	0.49
1:1:58:MET:O	1:1:59:HIS:HB2	2.13	0.49
1:1:130:ILE:HG21	1:1:178:PHE:CZ	2.48	0.49
2:2:19:GLY:HA2	2:2:58:THR:HG22	1.94	0.49
3:3:95:THR:O	3:3:99:GLU:HB2	2.13	0.49
2:2:34:CYS:HB2	2:2:202:PRO:HD2	1.94	0.49
3:3:181:TYR:CD1	3:3:181:TYR:C	2.91	0.49
1:1:224:MET:CE	1:1:226:PHE:CZ	2.88	0.48
1:1:151:MET:SD	1:1:170:SER:CB	3.01	0.48
3:3:54:PRO:O	3:3:91:VAL:HG12	2.12	0.48
3:3:125:ALA:HB3	3:3:155:ILE:HD12	1.95	0.48
3:3:129:LEU:O	3:3:150:HIS:HA	2.13	0.48
2:2:10:SER:CB	4:4:68:ASN:OXT	2.61	0.48
2:2:170:LEU:HD21	3:3:64:VAL:HA	1.94	0.48
1:1:280:LYS:HE3	3:3:89:ASP:OD1	2.13	0.48
2:2:135:HIS:CD2	2:2:160:ASN:HB3	2.49	0.48
3:3:61:LYS:O	3:3:61:LYS:HG2	2.07	0.48
3:3:115:LEU:HD22	3:3:129:LEU:HD21	1.96	0.48
1:1:224:MET:HE2	1:1:226:PHE:CE1	2.48	0.48
3:3:190:TRP:CD1	3:3:190:TRP:N	2.81	0.48
3:3:112:ARG:NH1	3:3:112:ARG:HG2	2.28	0.48
1:1:134:ALA:HB2	1:1:180:VAL:HG11	1.96	0.48
1:1:87:ALA:CA	1:1:90:ILE:HG12	2.44	0.47
3:3:112:ARG:HD3	3:3:162:VAL:CG1	2.43	0.47
3:3:195:LEU:C	3:3:196:ILE:HG12	2.40	0.47
1:1:121:TYR:C	1:1:122:VAL:CG2	2.88	0.47
1:1:221:MET:O	1:1:222:GLY:C	2.58	0.47
1:1:153:VAL:C	1:1:157:ALA:HB3	2.39	0.47
1:1:165:ASP:HB3	1:1:167:THR:H	1.79	0.47
2:2:13:VAL:C	2:2:14:GLN:HG2	2.39	0.47
1:1:83:GLN:OE1	1:1:236:LYS:HD2	2.15	0.47
1:1:105:ASN:O	1:1:106:LEU:HD12	2.15	0.47
1:1:268:ARG:CZ	2:2:139:ASN:HB2	2.44	0.47
2:2:13:VAL:HA	2:2:25:THR:O	2.14	0.47
2:2:177:LEU:CD1	3:3:94:THR:CG2	2.93	0.47
1:1:98:LEU:HD23	1:1:98:LEU:HA	1.76	0.47
1:1:119:PHE:HB2	1:1:122:VAL:HG21	1.96	0.47
1:1:206:HIS:ND1	1:1:206:HIS:N	2.62	0.47
2:2:63:PHE:CD1	2:2:245:ALA:HB2	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:4:43:GLN:O	4:4:44:SER:C	2.58	0.47
1:1:213:TYR:OH	2:2:131:GLN:HA	2.15	0.47
1:1:127:GLU:HA	1:1:187:SER:HA	1.96	0.47
1:1:268:ARG:HH11	1:1:268:ARG:HD3	1.50	0.47
1:1:152:TYR:CD2	1:1:154:PRO:CD	2.97	0.46
1:1:224:MET:CE	1:1:226:PHE:CE1	2.98	0.46
2:2:130:HIS:ND1	2:2:219:SER:OG	2.47	0.46
1:1:120:THR:CB	1:1:254:ILE:HB	2.46	0.46
2:2:170:LEU:HD23	3:3:64:VAL:CG2	2.45	0.46
4:4:59:LEU:HG	4:4:60:MET:N	2.27	0.46
4:4:61:LEU:HD12	4:4:61:LEU:HA	1.62	0.46
1:1:215:ILE:C	1:1:217:VAL:H	2.24	0.46
1:1:125:ASP:OD2	1:1:249:HIS:ND1	2.35	0.46
2:2:156:LEU:HD11	2:2:173:MET:SD	2.56	0.46
1:1:130:ILE:HG22	1:1:178:PHE:CZ	2.51	0.46
1:1:236:LYS:HE2	1:1:236:LYS:HB3	1.83	0.46
2:2:158:SER:HG	2:2:167:LYS:CE	2.26	0.46
3:3:101:VAL:HG22	3:3:219:LEU:HD11	1.98	0.46
1:1:120:THR:HB	1:1:254:ILE:HB	1.97	0.46
3:3:55:MET:CE	3:3:91:VAL:HG21	2.46	0.46
1:1:87:ALA:HB2	1:1:98:LEU:CD1	2.46	0.45
2:2:148:HIS:N	2:2:149:PRO:CD	2.79	0.45
2:2:195:ASN:OD1	2:2:195:ASN:C	2.59	0.45
1:1:96:ALA:C	1:1:97:LYS:HG2	2.40	0.45
3:3:57:ASN:CB	3:3:57:ASN:H	2.26	0.45
1:1:150:ALA:O	1:1:175:SER:HA	2.16	0.45
2:2:190:ASN:H	2:2:194:ASN:CB	2.30	0.45
2:2:228:LEU:CD1	2:2:238:LEU:HD22	2.47	0.45
1:1:31:VAL:HG11	1:1:34:LEU:HD12	1.98	0.45
3:3:50:ASP:HA	3:3:212:SER:HB3	1.97	0.45
2:2:170:LEU:HD23	3:3:64:VAL:HG22	1.99	0.45
3:3:55:MET:HE2	3:3:91:VAL:HG21	1.98	0.45
1:1:64:GLU:O	1:1:64:GLU:HG2	2.17	0.45
2:2:91:VAL:HG12	2:2:95:ASN:HD22	1.82	0.45
1:1:28:THR:HG22	1:1:29:GLN:H	1.81	0.45
1:1:154:PRO:HA	1:1:222:GLY:HA3	1.99	0.45
2:2:190:ASN:H	2:2:194:ASN:HB3	1.82	0.45
3:3:192:GLN:HE21	3:3:192:GLN:HA	1.81	0.45
1:1:221:MET:C	1:1:222:GLY:O	2.59	0.44
1:1:285:ASP:HB3	1:1:288:SER:H	1.82	0.44
2:2:259:ILE:HG21	2:2:259:ILE:HD13	1.74	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:43:MET:HA	1:1:43:MET:CE	2.46	0.44
1:1:198:ASN:HB3	1:1:200:PHE:O	2.17	0.44
1:1:207:ASP:HA	2:2:144:TYR:CE2	2.52	0.44
1:1:268:ARG:NH1	3:3:236:GLU:O	2.46	0.44
3:3:57:ASN:N	3:3:57:ASN:HB2	2.25	0.44
3:3:61:LYS:O	3:3:63:GLU:HG3	2.17	0.44
1:1:289:TYR:CE2	3:3:138:GLY:HA3	2.53	0.44
3:3:116:MET:HG3	3:3:159:SER:OG	2.17	0.44
4:4:43:GLN:O	4:4:45:LEU:CB	2.65	0.44
4:4:59:LEU:CD2	4:4:61:LEU:HD13	2.41	0.44
1:1:176:VAL:CG2	5:1:290:S57:H11	2.46	0.44
3:3:197:LEU:HD21	3:3:205:VAL:HG11	1.99	0.44
1:1:105:ASN:ND2	1:1:266:ILE:CD1	2.80	0.44
1:1:105:ASN:ND2	1:1:266:ILE:CG1	2.62	0.44
2:2:10:SER:OG	4:4:68:ASN:OXT	2.35	0.44
3:3:84:ASN:OD1	3:3:84:ASN:C	2.60	0.44
3:3:221:LEU:C	3:3:221:LEU:HD23	2.43	0.44
1:1:282:ARG:CG	3:3:57:ASN:CB	2.89	0.44
2:2:146:PHE:CG	2:2:164:GLY:HA2	2.52	0.44
1:1:289:TYR:CD2	3:3:138:GLY:HA3	2.53	0.44
4:4:43:GLN:HG3	4:4:45:LEU:H	1.82	0.44
1:1:47:PRO:HB3	3:3:166:PRO:HB3	1.99	0.43
1:1:286:ILE:HG23	3:3:81:PHE:HA	2.00	0.43
3:3:208:LEU:HA	3:3:208:LEU:HD12	1.73	0.43
1:1:109:LEU:HD13	1:1:109:LEU:HA	1.93	0.43
2:2:190:ASN:O	2:2:191:LEU:C	2.61	0.43
1:1:38:GLU:N	3:3:116:MET:HE1	2.34	0.43
1:1:132:ALA:O	1:1:181:GLY:N	2.41	0.43
1:1:129:THR:OG1	1:1:185:ARG:CD	2.57	0.43
3:3:57:ASN:HD21	3:3:91:VAL:HG13	1.84	0.43
2:2:91:VAL:HG12	2:2:95:ASN:ND2	2.34	0.43
3:3:61:LYS:HG2	3:3:63:GLU:HG3	2.00	0.43
1:1:102:TRP:CH2	1:1:243:VAL:HG11	2.53	0.43
1:1:130:ILE:HG22	1:1:130:ILE:O	2.18	0.43
2:2:10:SER:CB	2:2:12:ARG:HB2	2.48	0.43
3:3:112:ARG:HG2	3:3:112:ARG:HH11	1.83	0.43
1:1:285:ASP:C	1:1:285:ASP:HB3	2.38	0.43
2:2:70:THR:HG22	2:2:72:THR:HG22	2.01	0.43
3:3:151:VAL:HG11	3:3:161:ILE:HD11	2.01	0.43
2:2:95:ASN:HB3	2:2:251:PHE:CE2	2.53	0.43
1:1:188:VAL:HG22	3:3:25:LEU:HD21	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:4:43:GLN:C	4:4:45:LEU:N	2.74	0.42
1:1:215:ILE:C	1:1:217:VAL:N	2.78	0.42
1:1:89:GLY:C	1:1:90:ILE:CD1	2.89	0.42
1:1:206:HIS:NE2	1:1:208:ASP:HB2	2.34	0.42
3:3:174:ARG:HD2	3:3:182:THR:O	2.19	0.42
1:1:87:ALA:HB2	1:1:98:LEU:HD11	2.02	0.42
3:3:153:TRP:CD1	3:3:153:TRP:C	2.97	0.42
2:2:122:LEU:HD23	2:2:224:PRO:HA	2.02	0.42
2:2:225:ILE:O	3:3:68:LEU:HD21	2.19	0.42
3:3:226:GLN:HE21	3:3:226:GLN:HB2	1.21	0.42
2:2:40:GLU:O	2:2:40:GLU:CG	2.61	0.42
2:2:228:LEU:HD11	2:2:238:LEU:HD22	2.02	0.42
2:2:235:THR:CG2	2:2:236:PRO:N	2.79	0.42
1:1:93:HIS:CE1	1:1:163:TRP:HD1	2.38	0.42
1:1:105:ASN:HB3	1:1:106:LEU:H	1.18	0.42
1:1:285:ASP:HB3	1:1:288:SER:N	2.34	0.42
3:3:27:ASN:O	3:3:28:TYR:C	2.58	0.42
3:3:44:LEU:HA	3:3:44:LEU:HD23	1.79	0.42
1:1:130:ILE:HD11	1:1:224:MET:HE1	2.02	0.42
1:1:190:TYR:OH	1:1:196:ALA:N	2.53	0.42
1:1:289:TYR:CZ	3:3:139:PRO:HD2	2.55	0.42
4:4:43:GLN:HG2	4:4:43:GLN:O	2.18	0.42
1:1:261:LEU:HD11	2:2:171:TYR:CD2	2.55	0.41
1:1:286:ILE:HD13	1:1:286:ILE:HG21	1.77	0.41
2:2:69:LYS:O	2:2:239:PRO:HA	2.20	0.41
1:1:188:VAL:HG13	3:3:25:LEU:HD21	2.03	0.41
3:3:47:ILE:HG21	3:3:47:ILE:HD13	1.51	0.41
3:3:113:PHE:CE2	3:3:115:LEU:HD13	2.55	0.41
1:1:86:ASP:OD1	1:1:88:THR:HB	2.21	0.41
1:1:87:ALA:C	1:1:90:ILE:HG12	2.45	0.41
1:1:124:PHE:CD1	1:1:124:PHE:O	2.73	0.41
2:2:187:GLN:HE21	2:2:187:GLN:HB2	1.57	0.41
2:2:235:THR:HG22	2:2:237:SER:N	2.35	0.41
3:3:167:TRP:HZ2	3:3:172:GLN:HA	1.86	0.41
2:2:43:PRO:HG2	2:2:46:ASP:HB2	2.02	0.41
3:3:137:ARG:HH11	3:3:137:ARG:HD3	1.22	0.41
1:1:146:LEU:HA	1:1:230:ASN:OD1	2.20	0.41
1:1:165:ASP:CB	1:1:167:THR:OG1	2.69	0.41
1:1:54:ARG:HH11	1:1:54:ARG:HD2	1.55	0.41
3:3:64:VAL:O	3:3:64:VAL:HG12	2.21	0.41
1:1:78:HIS:NE2	1:1:80:THR:HB	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:3:157:LEU:HD23	3:3:157:LEU:O	2.21	0.41
1:1:152:TYR:CD2	1:1:154:PRO:HD3	2.56	0.40
1:1:153:VAL:N	1:1:154:PRO:CD	2.84	0.40
1:1:159:ASN:HD22	1:1:160:PRO:HD2	1.84	0.40
2:2:13:VAL:HG22	2:2:26:GLN:HA	2.03	0.40
3:3:214:CYS:HB3	3:3:215:PRO:CD	2.51	0.40
3:3:231:THR:C	3:3:232:VAL:HG13	2.45	0.40
1:1:220:HIS:C	1:1:221:MET:HG2	2.32	0.40
1:1:265:SER:OG	2:2:139:ASN:HB3	2.21	0.40
3:3:101:VAL:HG13	3:3:176:THR:HB	2.04	0.40
2:2:172:ASN:CG	2:2:181:LEU:HD13	2.47	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	1	271/289 (94%)	236 (87%)	26 (10%)	9 (3%)	3	17
2	2	253/262 (97%)	233 (92%)	18 (7%)	2 (1%)	16	50
3	3	234/236 (99%)	212 (91%)	17 (7%)	5 (2%)	5	27
4	4	38/68 (56%)	34 (90%)	3 (8%)	1 (3%)	4	23
All	All	796/855 (93%)	715 (90%)	64 (8%)	17 (2%)	5	27

All (17) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	1	106	LEU
1	1	139	SER
1	1	172	SER
1	1	219	ASN

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Mol	Chain	Res	Type
3	3	27	ASN
3	3	28	TYR
3	3	57	ASN
3	3	77	ASN
1	1	165	ASP
1	1	222	GLY
2	2	255	ARG
2	2	257	LYS
1	1	104	ILE
1	1	153	VAL
4	4	47	MET
1	1	154	PRO
3	3	26	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	1	239/253 (94%)	185 (77%)	54 (23%)	1	5
2	2	223/229 (97%)	178 (80%)	45 (20%)	1	7
3	3	209/209 (100%)	169 (81%)	40 (19%)	1	8
4	4	33/57 (58%)	20 (61%)	13 (39%)	0	1
All	All	704/748 (94%)	552 (78%)	152 (22%)	1	6

All (152) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	1	18	VAL
1	1	21	ILE
1	1	22	SER
1	1	23	SER
1	1	28	THR
1	1	29	GLN
1	1	30	LYS
1	1	38	GLU

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Mol	Chain	Res	Type
1	1	43	MET
1	1	47	PRO
1	1	81	GLU
1	1	90	ILE
1	1	95	GLU
1	1	97	LYS
1	1	103	LYS
1	1	104	ILE
1	1	105	ASN
1	1	106	LEU
1	1	109	LEU
1	1	115	LYS
1	1	118	LEU
1	1	130	ILE
1	1	136	GLN
1	1	137	PRO
1	1	138	ASP
1	1	144	SER
1	1	145	ASN
1	1	153	VAL
1	1	159	ASN
1	1	165	ASP
1	1	170	SER
1	1	172	SER
1	1	173	ASN
1	1	176	VAL
1	1	183	THR
1	1	184	SER
1	1	185	ARG
1	1	191	VAL
1	1	202	ASP
1	1	215	ILE
1	1	216	THR
1	1	220	HIS
1	1	224	MET
1	1	240	LYS
1	1	248	LYS
1	1	254	ILE
1	1	256	ARG
1	1	266	ILE
1	1	268	ARG
1	1	273	LYS

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Mol	Chain	Res	Type
1	1	274	ASN
1	1	275	THR
1	1	278	VAL
1	1	287	LYS
2	2	12	ARG
2	2	20	ASN
2	2	26	GLN
2	2	49	ASP
2	2	52	LYS
2	2	66	LEU
2	2	69	LYS
2	2	73	THR
2	2	76	LYS
2	2	81	LYS
2	2	87	LYS
2	2	103	ARG
2	2	116	LYS
2	2	119	SER
2	2	136	GLU
2	2	141	SER
2	2	143	LYS
2	2	145	THR
2	2	151	GLU
2	2	152	ARG
2	2	156	LEU
2	2	165	PRO
2	2	166	VAL
2	2	167	LYS
2	2	169	VAL
2	2	170	LEU
2	2	174	ASN
2	2	187	GLN
2	2	192	ARG
2	2	195	ASN
2	2	209	ILE
2	2	211	SER
2	2	217	ASN
2	2	225	ILE
2	2	230	VAL
2	2	232	THR
2	2	236	PRO
2	2	238	LEU

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Mol	Chain	Res	Type
2	2	247	MET
2	2	250	GLU
2	2	254	ILE
2	2	255	ARG
2	2	256	SER
2	2	259	ILE
2	2	262	GLN
3	3	12	GLN
3	3	16	THR
3	3	21	SER
3	3	25	LEU
3	3	29	GLU
3	3	33	ARG
3	3	46	ILE
3	3	55	MET
3	3	60	THR
3	3	61	LYS
3	3	65	ASN
3	3	91	VAL
3	3	94	THR
3	3	101	VAL
3	3	112	ARG
3	3	114	SER
3	3	115	LEU
3	3	137	ARG
3	3	146	MET
3	3	157	LEU
3	3	158	GLN
3	3	159	SER
3	3	164	THR
3	3	172	GLN
3	3	174	ARG
3	3	179	ASP
3	3	182	THR
3	3	192	GLN
3	3	194	SER
3	3	196	ILE
3	3	201	THR
3	3	208	LEU
3	3	211	ILE
3	3	218	LYS
3	3	219	LEU

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Mol	Chain	Res	Type
3	3	220	ARG
3	3	223	LYS
3	3	226	GLN
3	3	228	ILE
3	3	230	GLN
4	4	29	ILE
4	4	33	LYS
4	4	40	SER
4	4	43	GLN
4	4	45	LEU
4	4	46	SER
4	4	47	MET
4	4	50	SER
4	4	51	LYS
4	4	59	LEU
4	4	61	LEU
4	4	67	LEU
4	4	68	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	1	61	ASN
1	1	105	ASN
1	1	136	GLN
1	1	159	ASN
2	2	20	ASN
2	2	94	GLN
2	2	111	GLN
2	2	135	HIS
2	2	174	ASN
2	2	187	GLN
2	2	262	GLN
3	3	27	ASN
3	3	65	ASN
3	3	74	ASN
3	3	140	GLN
3	3	192	GLN
3	3	226	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

1 ligand is 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
5	S57	1	290	-	22,22,22	1.25	2 (9%)	27,27,27	1.74	7 (25%)

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
5	S57	1	290	-	-	6/12/12/12	0/2/2/2

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	1	290	S57	C5C-C4C	-2.40	1.29	1.35
5	1	290	S57	O4-C1	-2.28	1.36	1.42

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	1	290	S57	C4C-N3-C2C	3.96	113.07	105.47
5	1	290	S57	C4C-C5C-N1	3.45	112.25	106.57
5	1	290	S57	C5C-N1-C2C	-3.36	102.52	106.71
5	1	290	S57	C5C-C4C-N3	-3.33	103.57	109.92
5	1	290	S57	C6B-O1-C1A	2.39	123.46	117.69
5	1	290	S57	C6A-C1A-C2A	2.27	122.23	118.87
5	1	290	S57	O1-C1A-C2A	-2.15	113.83	116.39

There are no chirality outliers.

All (6) torsion outliers are listed below:

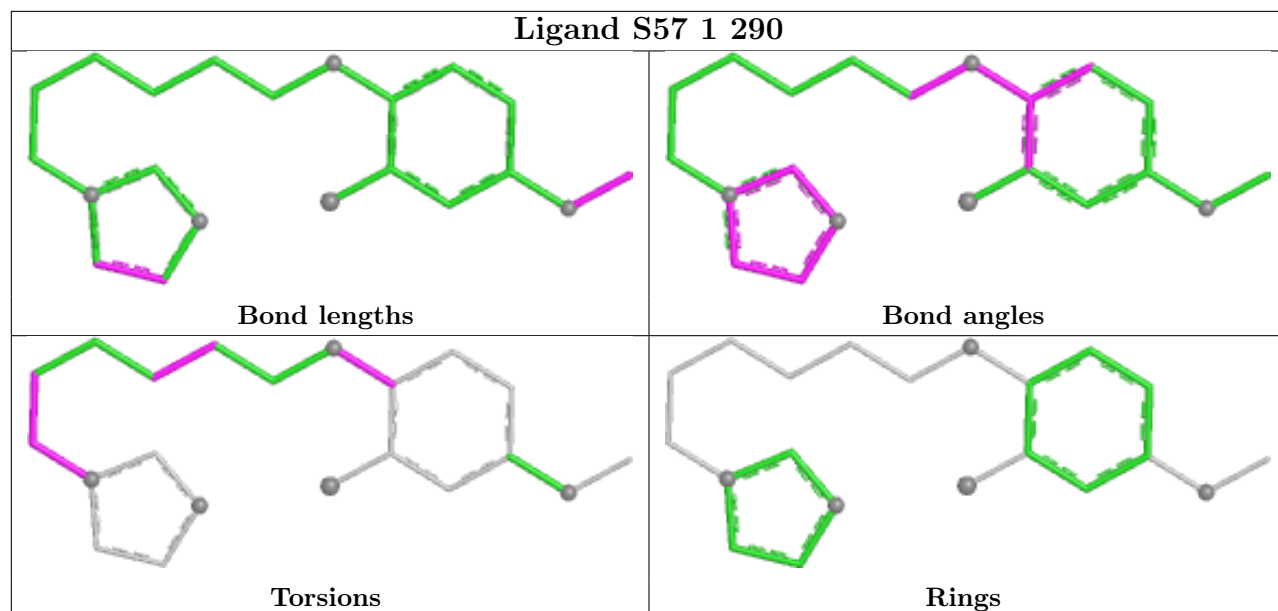
Mol	Chain	Res	Type	Atoms
5	1	290	S57	C2A-C1A-O1-C6B
5	1	290	S57	C6A-C1A-O1-C6B
5	1	290	S57	C2B-C1B-N1-C2C
5	1	290	S57	C2B-C1B-N1-C5C
5	1	290	S57	C3B-C4B-C5B-C6B
5	1	290	S57	N1-C1B-C2B-C3B

There are no ring outliers.

1 monomer is involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	1	290	S57	6	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



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

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.