



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 05:21 AM UTC

PDB ID : 3U7U / pdb_00003u7u
Title : Crystal structure of extracellular region of human epidermal growth factor receptor 4 in complex with neuregulin-1 beta
Authors : Liu, P.; Cleveland IV, T.E.; Bouyain, S.; Longo, P.A.; Leahy, D.J.
Deposited on : 2011-10-14
Resolution : 3.03 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

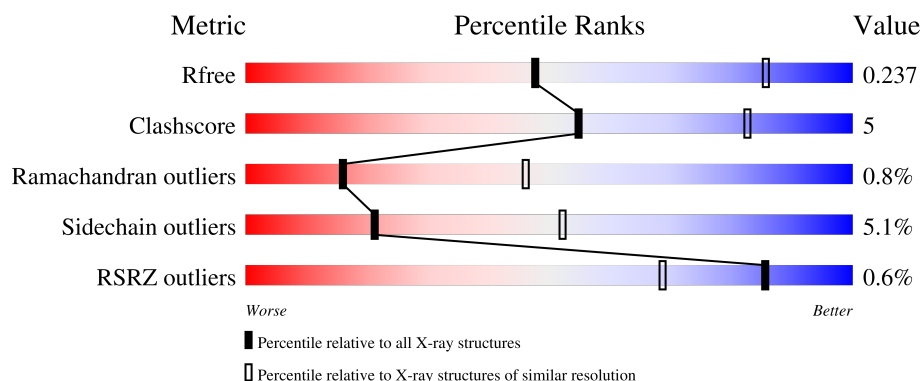
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.03 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	3685 (3.08-3.00)
Clashscore	190562	4007 (3.08-3.00)
Ramachandran outliers	187476	3834 (3.08-3.00)
Sidechain outliers	187428	3836 (3.08-3.00)
RSRZ outliers	180081	3684 (3.08-3.00)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	615	74% 13% • 11%
1	B	615	78% 17% • •
1	C	615	% 80% 15% • •
1	D	615	79% 16% • •
1	E	615	77% 17% • •

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Mol	Chain	Length	Quality of chain
1	F	615	79%15%
2	G	55	2% 82%9%9%
2	H	55	2% 73%20%7%
2	I	55	4% 69%22%9%
2	J	55	2% 71%22%7%
2	K	55	2% 75%15%11%
2	L	55	82%11%7%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 30527 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 Receptor tyrosine-protein kinase erbB-4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	550	Total	C	N	O	S	0	0	0
			4284	2658	746	829	51			
1	B	601	Total	C	N	O	S	0	0	0
			4685	2908	815	904	58			
1	C	598	Total	C	N	O	S	0	0	0
			4649	2879	812	900	58			
1	D	600	Total	C	N	O	S	0	0	0
			4683	2906	815	904	58			
1	E	593	Total	C	N	O	S	0	0	0
			4615	2856	807	894	58			
1	F	591	Total	C	N	O	S	0	0	0
			4595	2843	804	890	58			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	524	ASP	GLY	conflict	UNP Q15303
B	524	ASP	GLY	conflict	UNP Q15303
C	524	ASP	GLY	conflict	UNP Q15303
D	524	ASP	GLY	conflict	UNP Q15303
E	524	ASP	GLY	conflict	UNP Q15303
F	524	ASP	GLY	conflict	UNP Q15303

- Molecule 2 is a protein called Neuregulin 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	G	50	Total	C	N	O	S	0	0	0
			391	243	67	73	8			
2	H	51	Total	C	N	O	S	0	0	0
			398	247	68	75	8			
2	I	50	Total	C	N	O	S	0	0	0
			391	243	67	73	8			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	J	51	Total	C	N	O	S	0	0	0
			398	247	68	75	8			
2	K	49	Total	C	N	O	S	0	0	0
			385	240	66	71	8			
2	L	51	Total	C	N	O	S	0	0	0
			398	247	68	75	8			

- Molecule 3 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			14	8	1	5		
3	A	1	Total	C	N	O	0	0
			14	8	1	5		
3	A	1	Total	C	N	O	0	0
			14	8	1	5		
3	A	1	Total	C	N	O	0	0
			14	8	1	5		
3	B	1	Total	C	N	O	0	0
			14	8	1	5		
3	B	1	Total	C	N	O	0	0
			14	8	1	5		
3	B	1	Total	C	N	O	0	0
			14	8	1	5		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	B	1	Total	C	N	O	0	0
			14	8	1	5		
3	B	1	Total	C	N	O	0	0
			14	8	1	5		
3	C	1	Total	C	N	O	0	0
			14	8	1	5		
3	C	1	Total	C	N	O	0	0
			14	8	1	5		
3	D	1	Total	C	N	O	0	0
			14	8	1	5		
3	D	1	Total	C	N	O	0	0
			14	8	1	5		
3	D	1	Total	C	N	O	0	0
			14	8	1	5		
3	D	1	Total	C	N	O	0	0
			14	8	1	5		
3	D	1	Total	C	N	O	0	0
			14	8	1	5		
3	E	1	Total	C	N	O	0	0
			14	8	1	5		
3	E	1	Total	C	N	O	0	0
			14	8	1	5		
3	E	1	Total	C	N	O	0	0
			14	8	1	5		
3	F	1	Total	C	N	O	0	0
			14	8	1	5		
3	F	1	Total	C	N	O	0	0
			14	8	1	5		
3	F	1	Total	C	N	O	0	0
			14	8	1	5		
3	F	1	Total	C	N	O	0	0
			14	8	1	5		
3	F	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	30	Total	O	0	0
			30	30		

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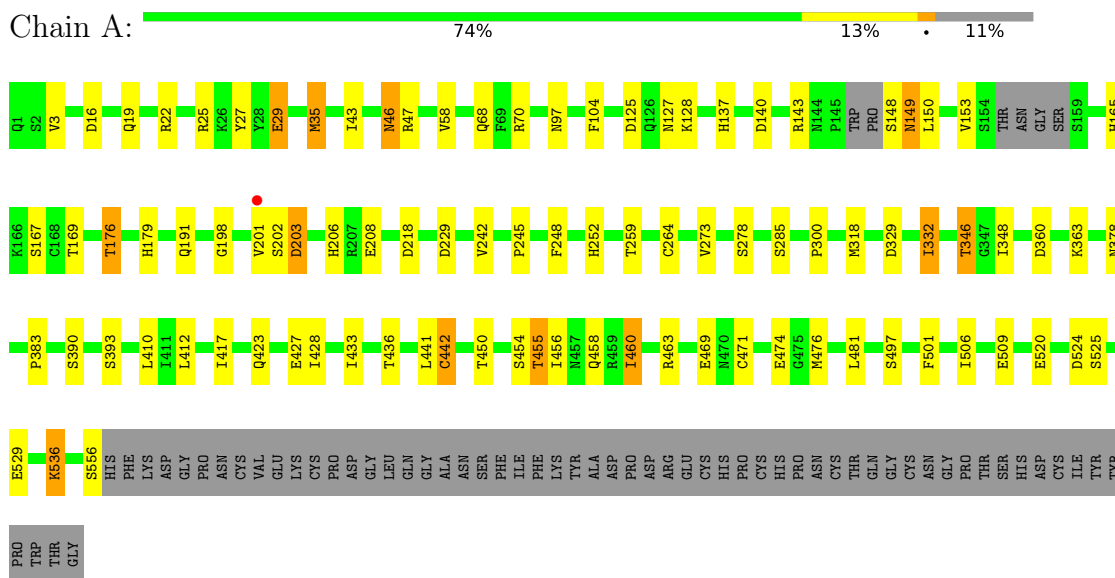
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	63	Total 63	O 63	0	0
4	C	37	Total 37	O 37	0	0
4	D	55	Total 55	O 55	0	0
4	E	33	Total 33	O 33	0	0
4	F	52	Total 52	O 52	0	0
4	G	1	Total 1	O 1	0	0
4	H	9	Total 9	O 9	0	0
4	I	2	Total 2	O 2	0	0
4	J	3	Total 3	O 3	0	0
4	K	2	Total 2	O 2	0	0
4	L	4	Total 4	O 4	0	0

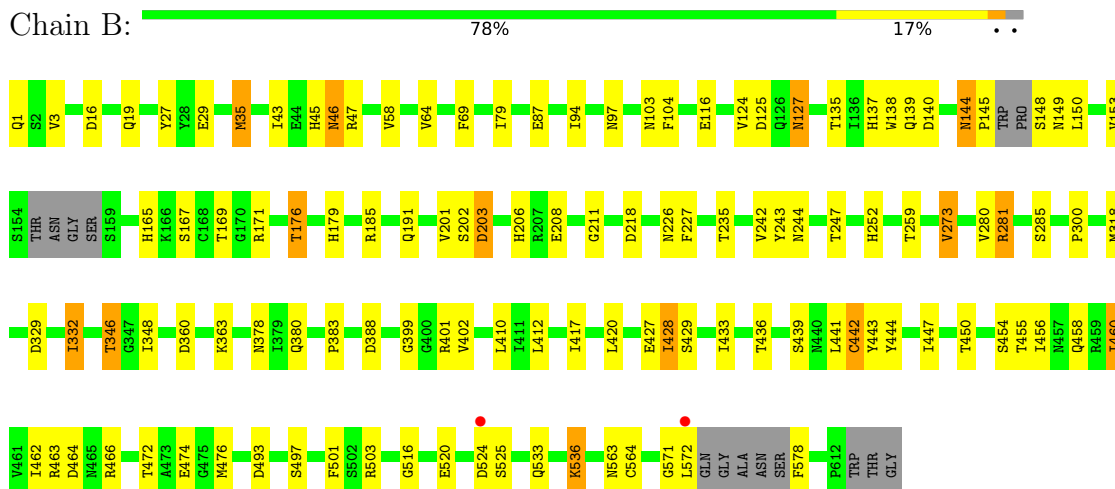
3 Residue-property plots

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.

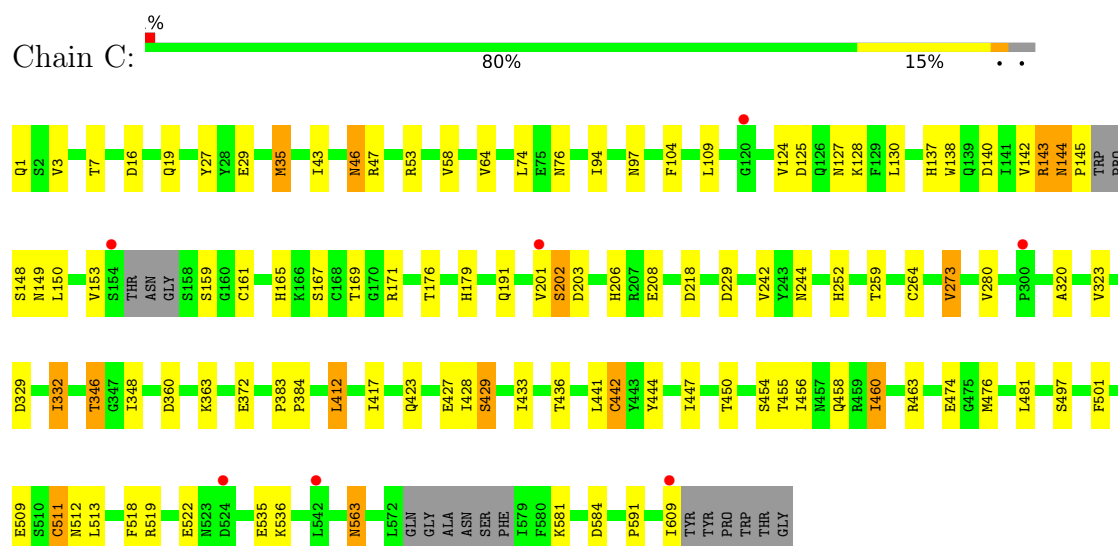
- Molecule 1: Receptor tyrosine-protein kinase erbB-4



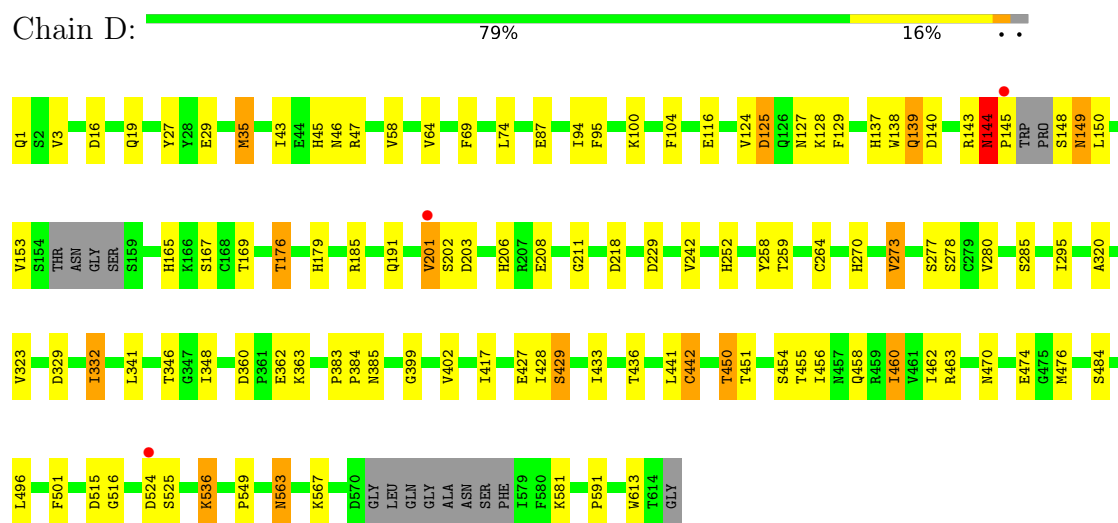
- Molecule 1: Receptor tyrosine-protein kinase erbB-4



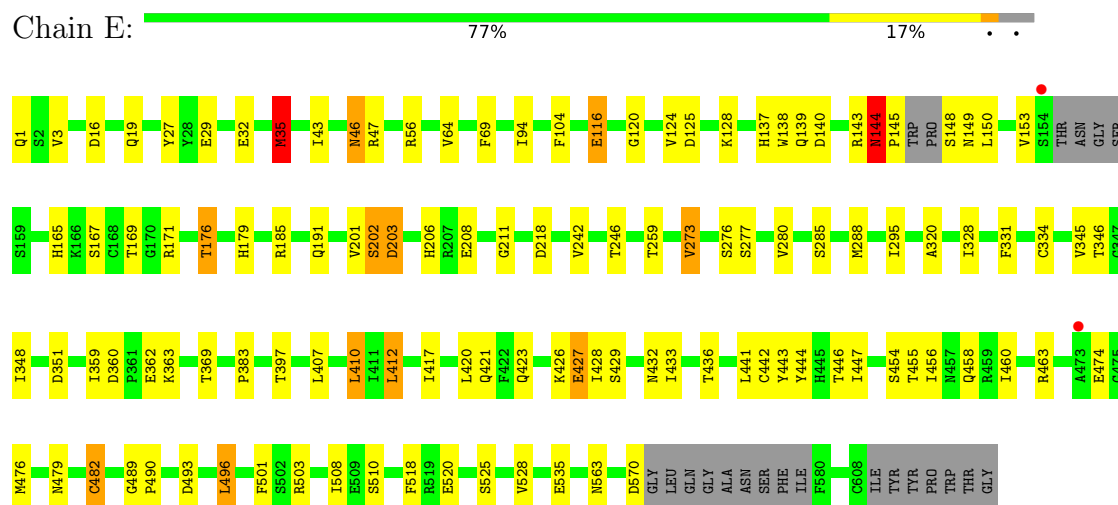
- Molecule 1: Receptor tyrosine-protein kinase erbB-4



• Molecule 1: Receptor tyrosine-protein kinase erbB-4

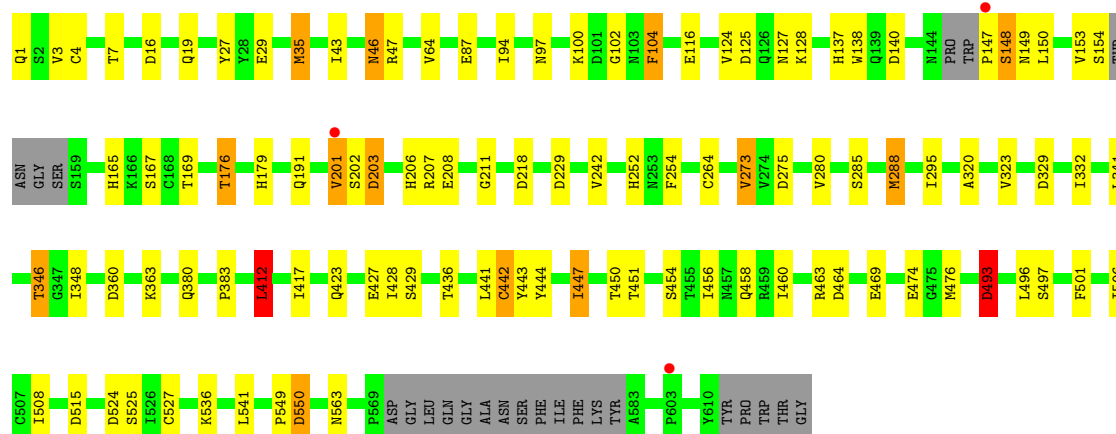


• Molecule 1: Receptor tyrosine-protein kinase erbB-4



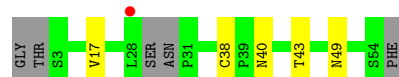
- Molecule 1: Receptor tyrosine-protein kinase erbB-4

Chain F:  79% 15% . .



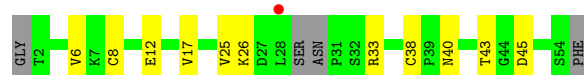
- Molecule 2: Neuregulin 1

Chain G:  2% 82% 9% 9%



- Molecule 2: Neuregulin 1

Chain H:  2% 73% 20% 7%



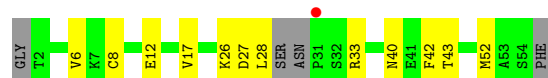
- Molecule 2: Neuregulin 1

Chain I:  4% 69% 22% 9%



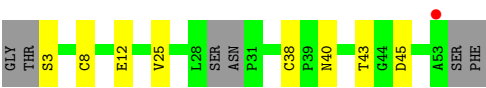
- Molecule 2: Neuregulin 1

Chain J:  2% 71% 22% 7%

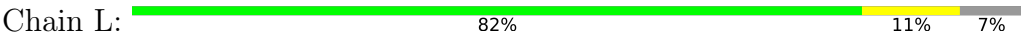


- Molecule 2: Neuregulin 1

Chain K:  2% 75% 15% 11%



● Molecule 2: Neuregulin 1



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	85.73Å 223.51Å 146.92Å 90.00° 99.72° 90.00°	Depositor
Resolution (Å)	49.63 – 3.03 49.63 – 3.03	Depositor EDS
% Data completeness (in resolution range)	(Not available) (49.63-3.03) 98.7 (49.63-3.03)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.91 (at 3.01Å)	Xtriage
Refinement program	BUSTER-TNT BUSTER 2.8.0, BUSTER 2.8.0	Depositor
R, R_{free}	0.190 , 0.227 (Not available) , 0.237	Depositor DCC
R_{free} test set	5198 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	73.3	Xtriage
Anisotropy	0.361	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 85.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	30527	wwPDB-VP
Average B, all atoms (Å ²)	90.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.60% 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 ⓘ

5.1 Standard geometry ⓘ

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

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	0.84	0/4366	1.32	26/5908 (0.4%)
1	B	0.88	2/4783 (0.0%)	1.35	43/6476 (0.7%)
1	C	0.84	1/4743 (0.0%)	1.32	33/6420 (0.5%)
1	D	0.85	1/4782 (0.0%)	1.33	36/6477 (0.6%)
1	E	0.85	2/4709 (0.0%)	1.34	26/6374 (0.4%)
1	F	0.88	1/4688 (0.0%)	1.35	40/6346 (0.6%)
2	G	0.84	0/397	1.37	2/528 (0.4%)
2	H	0.79	0/404	1.34	4/538 (0.7%)
2	I	0.75	0/397	1.32	4/528 (0.8%)
2	J	0.84	0/404	1.31	2/538 (0.4%)
2	K	0.75	0/391	1.38	6/520 (1.2%)
2	L	0.82	0/404	1.39	2/538 (0.4%)
All	All	0.85	7/30468 (0.0%)	1.34	224/41191 (0.5%)

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	F	35	MET	SD-CE	8.17	2.00	1.79
1	E	35	MET	CA-C	-5.56	1.47	1.53
1	B	226	ASN	CA-C	-5.50	1.49	1.52
1	C	244	ASN	CA-C	5.33	1.58	1.52
1	B	318	MET	SD-CE	5.24	1.92	1.79
1	D	144	ASN	CA-C	5.10	1.59	1.52
1	E	410	LEU	CA-C	-5.06	1.46	1.52

All (224) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	47	ARG	N-CA-C	7.76	121.22	110.35
1	E	446	THR	CA-C-N	7.70	131.11	120.49

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	446	THR	C-N-CA	7.70	131.11	120.49
2	K	3	SER	CA-C-N	7.67	136.19	121.54
2	K	3	SER	C-N-CA	7.67	136.19	121.54
1	E	47	ARG	N-CA-C	7.63	121.04	110.35
1	B	443	TYR	CA-C-N	7.58	131.45	120.38
1	B	443	TYR	C-N-CA	7.58	131.45	120.38
1	D	47	ARG	N-CA-C	7.58	120.96	110.35
1	F	275	ASP	CA-CB-CG	7.56	120.16	112.60
1	A	47	ARG	N-CA-C	7.53	120.89	110.35
1	C	47	ARG	N-CA-C	7.53	120.89	110.35
1	B	47	ARG	N-CA-C	7.49	120.84	110.35
1	E	169	THR	CB-CA-C	7.30	122.09	111.73
1	F	169	THR	CB-CA-C	7.24	122.01	111.73
1	D	524	ASP	CA-CB-CG	7.15	119.75	112.60
1	A	169	THR	CB-CA-C	7.01	121.68	111.73
1	D	442	CYS	CA-C-N	-6.90	111.29	122.26
1	D	442	CYS	C-N-CA	-6.90	111.29	122.26
1	B	401	ARG	N-CA-C	-6.89	104.84	113.18
1	E	496	LEU	N-CA-C	-6.86	105.05	113.41
1	F	493	ASP	CA-CB-CG	6.83	119.43	112.60
1	C	203	ASP	N-CA-C	6.78	121.40	113.20
1	C	169	THR	CB-CA-C	6.71	121.26	111.73
1	D	125	ASP	CA-CB-CG	6.68	119.28	112.60
1	F	443	TYR	CA-C-N	6.59	129.41	120.38
1	F	443	TYR	C-N-CA	6.59	129.41	120.38
1	B	442	CYS	CA-C-N	-6.59	111.79	122.26
1	B	442	CYS	C-N-CA	-6.59	111.79	122.26
1	D	169	THR	CB-CA-C	6.57	121.06	111.73
1	F	125	ASP	CA-CB-CG	6.56	119.16	112.60
1	A	46	ASN	CA-CB-CG	6.54	119.14	112.60
1	F	147	PRO	CA-C-N	6.44	133.83	121.54
1	F	147	PRO	C-N-CA	6.44	133.83	121.54
1	F	550	ASP	CA-CB-CG	6.44	119.04	112.60
1	D	429	SER	N-CA-C	6.43	119.11	111.33
1	B	493	ASP	CA-CB-CG	6.42	119.02	112.60
1	B	169	THR	CB-CA-C	6.41	120.83	111.73
1	E	345	VAL	CA-C-N	6.38	129.69	120.38
1	E	345	VAL	C-N-CA	6.38	129.69	120.38
1	F	429	SER	N-CA-C	6.30	118.15	111.28
1	B	58	VAL	CA-C-N	6.26	128.66	120.28
1	B	58	VAL	C-N-CA	6.26	128.66	120.28
1	D	46	ASN	CA-CB-CG	6.19	118.79	112.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	428	ILE	CA-C-N	6.17	128.56	120.28
1	F	428	ILE	C-N-CA	6.17	128.56	120.28
1	F	46	ASN	CA-CB-CG	6.14	118.74	112.60
1	A	46	ASN	CA-C-N	6.09	130.38	121.31
1	A	46	ASN	C-N-CA	6.09	130.38	121.31
1	B	388	ASP	N-CA-C	6.09	116.46	107.88
1	C	46	ASN	CA-CB-CG	6.08	118.69	112.60
1	A	442	CYS	CA-C-N	-6.08	112.59	122.26
1	A	442	CYS	C-N-CA	-6.08	112.59	122.26
1	B	46	ASN	CA-C-N	6.08	130.37	121.31
1	B	46	ASN	C-N-CA	6.08	130.37	121.31
1	E	46	ASN	CA-C-N	6.07	130.35	121.31
1	E	46	ASN	C-N-CA	6.07	130.35	121.31
1	F	46	ASN	CA-C-N	6.07	130.35	121.31
1	F	46	ASN	C-N-CA	6.07	130.35	121.31
1	F	442	CYS	CA-C-N	-6.06	112.62	122.26
1	F	442	CYS	C-N-CA	-6.06	112.62	122.26
1	C	46	ASN	CA-C-N	6.06	130.34	121.31
1	C	46	ASN	C-N-CA	6.06	130.34	121.31
1	A	285	SER	CA-C-N	6.05	129.50	120.31
1	A	285	SER	C-N-CA	6.05	129.50	120.31
1	B	285	SER	CA-C-N	6.01	129.44	120.31
1	B	285	SER	C-N-CA	6.01	129.44	120.31
1	A	203	ASP	N-CA-C	5.99	120.28	113.15
1	D	46	ASN	CA-C-N	5.97	130.21	121.31
1	D	46	ASN	C-N-CA	5.97	130.21	121.31
1	E	27	TYR	N-CA-C	5.97	117.87	111.36
1	B	378	ASN	CA-CB-CG	5.96	118.56	112.60
1	E	46	ASN	CA-CB-CG	5.95	118.55	112.60
1	B	125	ASP	CA-CB-CG	5.91	118.51	112.60
1	F	46	ASN	N-CA-C	5.87	117.67	111.28
1	B	46	ASN	CA-CB-CG	5.84	118.44	112.60
1	C	27	TYR	N-CA-C	5.83	117.72	111.36
1	C	372	GLU	CB-CG-CD	5.81	122.48	112.60
1	B	428	ILE	CA-C-N	5.79	128.31	120.38
1	B	428	ILE	C-N-CA	5.79	128.31	120.38
1	D	428	ILE	CA-C-N	5.78	128.29	120.38
1	D	428	ILE	C-N-CA	5.78	128.29	120.38
1	E	203	ASP	N-CA-C	5.75	119.92	113.02
1	B	524	ASP	CA-CB-CG	5.74	118.34	112.60
1	C	58	VAL	CA-C-N	5.73	127.95	120.28
1	C	58	VAL	C-N-CA	5.73	127.95	120.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	46	ASN	N-CA-C	5.70	117.49	111.28
1	A	218	ASP	CA-CB-CG	5.69	118.29	112.60
1	D	323	VAL	N-CA-C	-5.68	102.25	109.58
1	E	320	ALA	N-CA-C	5.68	117.62	110.24
2	H	25	VAL	CA-C-N	5.68	129.77	120.63
2	H	25	VAL	C-N-CA	5.68	129.77	120.63
2	K	38	CYS	N-CA-C	5.66	117.20	110.07
1	C	501	PHE	CA-CB-CG	5.65	119.45	113.80
1	F	285	SER	CA-C-N	5.65	128.90	120.31
1	F	285	SER	C-N-CA	5.65	128.90	120.31
1	B	144	ASN	N-CA-C	5.65	119.88	109.10
1	A	27	TYR	N-CA-C	5.60	117.47	111.36
1	A	46	ASN	N-CA-C	5.60	117.39	111.28
1	D	203	ASP	N-CA-C	5.60	119.81	113.15
2	L	38	CYS	N-CA-C	5.59	117.12	110.07
1	D	27	TYR	N-CA-C	5.59	117.45	111.36
1	B	46	ASN	N-CA-C	5.59	117.37	111.28
1	F	218	ASP	CA-CB-CG	5.58	118.18	112.60
1	D	516	GLY	CA-C-N	5.58	128.03	120.38
1	D	516	GLY	C-N-CA	5.58	128.03	120.38
1	A	58	VAL	CA-C-N	5.57	127.74	120.28
1	A	58	VAL	C-N-CA	5.57	127.74	120.28
1	C	74	LEU	CA-C-N	5.56	128.50	120.38
1	C	74	LEU	C-N-CA	5.56	128.50	120.38
1	B	516	GLY	CA-C-N	5.55	127.98	120.38
1	B	516	GLY	C-N-CA	5.55	127.98	120.38
2	J	27	ASP	CA-CB-CG	5.54	118.14	112.60
2	H	45	ASP	CA-CB-CG	5.53	118.13	112.60
1	A	471	CYS	CA-C-N	5.53	128.01	120.54
1	A	471	CYS	C-N-CA	5.53	128.01	120.54
1	A	125	ASP	CA-CB-CG	5.53	118.13	112.60
2	I	38	CYS	N-CA-C	5.52	117.02	110.07
1	D	74	LEU	CA-C-N	5.50	128.41	120.38
1	D	74	LEU	C-N-CA	5.50	128.41	120.38
1	E	144	ASN	CA-CB-CG	5.47	118.07	112.60
1	E	218	ASP	CA-CB-CG	5.47	118.07	112.60
1	B	27	TYR	N-CA-C	5.46	117.31	111.36
1	D	144	ASN	CA-CB-CG	5.45	118.05	112.60
2	L	45	ASP	CA-CB-CG	5.45	118.05	112.60
1	D	285	SER	CA-C-N	5.44	128.59	120.31
1	D	285	SER	C-N-CA	5.44	128.59	120.31
1	D	278	SER	N-CA-C	5.41	118.40	109.85

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	218	ASP	CA-CB-CG	5.41	118.01	112.60
1	C	7	THR	CA-C-N	5.40	129.79	121.53
1	C	7	THR	C-N-CA	5.40	129.79	121.53
1	F	27	TYR	N-CA-C	5.39	117.24	111.36
1	C	46	ASN	N-CA-C	5.36	117.12	111.28
1	E	125	ASP	CA-CB-CG	5.35	117.95	112.60
1	B	439	SER	N-CA-C	5.34	118.59	111.75
1	D	46	ASN	N-CA-C	5.34	117.10	111.28
1	F	412	LEU	N-CA-C	5.34	117.50	109.23
1	B	203	ASP	N-CA-C	5.33	119.49	113.15
1	C	125	ASP	CA-CB-CG	5.32	117.92	112.60
2	G	49	ASN	CA-CB-CG	5.30	117.90	112.60
1	E	116	GLU	N-CA-C	5.29	117.04	108.26
1	C	320	ALA	N-CA-C	5.29	117.69	110.24
1	C	144	ASN	CA-CB-CG	5.28	117.88	112.60
2	H	38	CYS	N-CA-C	5.28	116.72	110.07
1	B	464	ASP	N-CA-C	5.28	118.72	111.54
1	C	423	GLN	N-CA-C	5.27	117.71	111.33
1	B	235	THR	CA-C-N	5.27	130.98	122.29
1	B	235	THR	C-N-CA	5.27	130.98	122.29
1	B	462	ILE	N-CA-CB	5.27	118.31	111.67
1	B	427	GLU	CA-C-N	5.26	127.96	122.96
1	B	427	GLU	C-N-CA	5.26	127.96	122.96
1	E	285	SER	CA-C-N	5.26	129.50	120.72
1	E	285	SER	C-N-CA	5.26	129.50	120.72
1	C	429	SER	N-CA-C	5.25	117.75	111.71
1	C	323	VAL	N-CA-C	-5.25	102.80	109.58
1	C	412	LEU	N-CA-C	5.24	117.36	109.23
1	C	442	CYS	CA-C-N	-5.24	113.93	122.26
1	C	442	CYS	C-N-CA	-5.24	113.93	122.26
1	A	318	MET	CA-C-N	5.23	127.29	120.28
1	A	318	MET	C-N-CA	5.23	127.29	120.28
1	D	427	GLU	N-CA-C	5.23	117.95	108.69
1	F	7	THR	CA-C-N	5.22	129.52	121.53
1	F	7	THR	C-N-CA	5.22	129.52	121.53
1	C	563	ASN	CA-C-N	5.22	128.28	120.87
1	C	563	ASN	C-N-CA	5.22	128.28	120.87
2	G	38	CYS	N-CA-C	5.22	116.64	110.07
1	B	218	ASP	CA-CB-CG	5.21	117.81	112.60
1	A	427	GLU	N-CA-C	5.20	117.89	108.69
1	F	323	VAL	N-CA-C	-5.20	102.88	109.58
1	C	518	PHE	CA-CB-CG	5.18	118.98	113.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	469	GLU	CA-C-N	5.18	127.22	120.28
1	F	469	GLU	C-N-CA	5.18	127.22	120.28
1	B	472	THR	CA-C-N	5.17	127.21	120.28
1	B	472	THR	C-N-CA	5.17	127.21	120.28
1	F	427	GLU	N-CA-C	5.16	117.82	108.69
1	E	518	PHE	CA-C-N	5.15	128.02	120.71
1	E	518	PHE	C-N-CA	5.15	128.02	120.71
1	D	69	PHE	CA-C-N	5.14	127.17	120.28
1	D	69	PHE	C-N-CA	5.14	127.17	120.28
1	E	412	LEU	N-CA-C	5.12	117.17	109.23
1	F	203	ASP	N-CA-C	5.12	119.40	113.20
1	C	427	GLU	N-CA-C	5.12	117.76	108.69
2	I	25	VAL	CA-C-N	5.12	128.87	120.63
2	I	25	VAL	C-N-CA	5.12	128.87	120.63
2	K	25	VAL	CA-C-N	5.11	128.86	120.63
2	K	25	VAL	C-N-CA	5.11	128.86	120.63
1	B	226	ASN	CA-C-O	-5.11	116.86	119.77
1	A	427	GLU	CA-C-N	5.09	127.80	122.96
1	A	427	GLU	C-N-CA	5.09	127.80	122.96
1	F	464	ASP	N-CA-C	5.09	118.46	111.54
2	K	45	ASP	CA-CB-CG	5.08	117.69	112.60
1	D	45	HIS	N-CA-C	5.08	117.21	111.11
1	E	427	GLU	N-CA-C	5.07	117.67	108.69
1	A	469	GLU	CA-C-N	5.06	127.06	120.28
1	A	469	GLU	C-N-CA	5.06	127.06	120.28
1	D	462	ILE	N-CA-CB	5.06	118.05	111.67
1	F	427	GLU	CA-C-N	5.06	127.76	122.96
1	F	427	GLU	C-N-CA	5.06	127.76	122.96
1	B	69	PHE	CA-C-N	5.05	127.05	120.28
1	B	69	PHE	C-N-CA	5.05	127.05	120.28
1	F	320	ALA	N-CA-C	5.05	117.56	110.23
1	D	270	HIS	N-CA-C	5.04	117.43	111.33
1	F	100	LYS	CA-C-N	5.04	127.03	120.28
1	F	100	LYS	C-N-CA	5.04	127.03	120.28
1	C	161	CYS	CA-C-N	5.03	124.88	120.10
1	C	161	CYS	C-N-CA	5.03	124.88	120.10
1	D	320	ALA	N-CA-C	5.03	116.78	110.24
1	F	447	ILE	N-CA-C	5.03	115.59	109.30
1	B	45	HIS	N-CA-C	5.03	117.14	111.11
1	C	584	ASP	CA-CB-CG	5.03	117.63	112.60
1	D	58	VAL	CA-C-N	5.02	127.01	120.28
1	D	58	VAL	C-N-CA	5.02	127.01	120.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	127	ASN	CA-C-N	5.02	127.26	120.38
1	B	127	ASN	C-N-CA	5.02	127.26	120.38
2	I	45	ASP	CA-CB-CG	5.02	117.62	112.60
2	J	42	PHE	N-CA-C	5.02	117.78	109.85
1	F	506	ILE	N-CA-C	5.01	115.53	108.36
1	F	104	PHE	CA-CB-CG	5.01	118.81	113.80
1	A	442	CYS	N-CA-C	5.01	121.65	114.39
1	E	69	PHE	CA-C-N	5.01	126.99	120.28
1	E	69	PHE	C-N-CA	5.01	126.99	120.28
1	D	100	LYS	CA-C-N	5.00	126.98	120.28
1	D	100	LYS	C-N-CA	5.00	126.98	120.28
1	D	218	ASP	CA-CB-CG	5.00	117.60	112.60

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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	4284	0	4089	40	0
1	B	4685	0	4432	51	0
1	C	4649	0	4407	47	0
1	D	4683	0	4427	54	0
1	E	4615	0	4365	49	0
1	F	4595	0	4348	49	0
2	G	391	0	373	1	0
2	H	398	0	380	4	0
2	I	391	0	373	4	0
2	J	398	0	380	5	0
2	K	385	0	368	1	0
2	L	398	0	380	2	0
3	A	56	0	51	0	0
3	B	84	0	78	2	0
3	C	28	0	26	0	0
3	D	70	0	65	7	0
3	E	42	0	39	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	F	84	0	78	2	0
4	A	30	0	0	0	0
4	B	63	0	0	2	0
4	C	37	0	0	1	0
4	D	55	0	0	2	0
4	E	33	0	0	2	0
4	F	52	0	0	2	0
4	G	1	0	0	0	0
4	H	9	0	0	0	0
4	I	2	0	0	0	0
4	J	3	0	0	0	0
4	K	2	0	0	0	0
4	L	4	0	0	0	0
All	All	30527	0	28659	285	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 5.

All (285) 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:D:143:ARG:O	1:D:145:PRO:HD3	1.69	0.90
1:C:145:PRO:HB2	1:F:254:PHE:HB3	1.52	0.88
1:E:3:VAL:HG13	1:E:35:MET:HG3	1.57	0.87
1:D:3:VAL:HG13	1:D:35:MET:HG3	1.56	0.87
1:D:206:HIS:HD2	1:D:208:GLU:H	1.20	0.86
1:F:46:ASN:HA	4:F:624:HOH:O	1.76	0.85
1:A:206:HIS:HD2	1:A:208:GLU:H	1.22	0.85
1:C:3:VAL:HG13	1:C:35:MET:HG3	1.58	0.85
1:A:3:VAL:HG13	1:A:35:MET:HG3	1.60	0.83
1:B:206:HIS:HD2	1:B:208:GLU:H	1.21	0.82
1:B:3:VAL:HG13	1:B:35:MET:HG3	1.61	0.82
1:F:206:HIS:HD2	1:F:208:GLU:H	1.26	0.82
1:E:206:HIS:HD2	1:E:208:GLU:H	1.27	0.79
1:E:397:THR:HG22	1:E:427:GLU:HB3	1.67	0.77
1:B:466:ARG:NH1	3:B:1005:NAG:H2	2.01	0.76
1:C:206:HIS:HD2	1:C:208:GLU:H	1.34	0.74
1:E:143:ARG:O	1:E:145:PRO:HD3	1.88	0.73
1:B:206:HIS:CD2	1:B:208:GLU:H	2.06	0.73
1:C:143:ARG:O	1:C:145:PRO:HD3	1.89	0.73
1:D:143:ARG:C	1:D:145:PRO:HD3	2.14	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:466:ARG:HH12	3:B:1005:NAG:H2	1.54	0.71
1:C:145:PRO:HB2	1:F:254:PHE:CB	2.22	0.69
1:A:206:HIS:CD2	1:A:208:GLU:H	2.10	0.68
1:D:385:ASN:HD22	3:D:1004:NAG:H83	1.58	0.68
1:F:3:VAL:HG13	1:F:35:MET:HG3	1.73	0.68
1:C:455:THR:H	1:C:458:GLN:HE21	1.40	0.68
1:D:206:HIS:CD2	1:D:208:GLU:H	2.07	0.67
1:F:3:VAL:HG13	1:F:35:MET:CG	2.25	0.67
1:B:46:ASN:HA	4:B:657:HOH:O	1.96	0.65
1:C:97:ASN:H	1:C:127:ASN:ND2	1.95	0.65
1:E:206:HIS:CD2	1:E:208:GLU:H	2.12	0.65
1:B:454:SER:H	1:B:458:GLN:HE22	1.45	0.65
1:A:137:HIS:HD2	1:A:140:ASP:HB2	1.62	0.64
1:C:137:HIS:HD2	1:C:140:ASP:HB2	1.62	0.64
1:A:455:THR:H	1:A:458:GLN:HE21	1.47	0.63
1:C:53:ARG:O	1:C:76:ASN:ND2	2.32	0.62
1:D:148:SER:C	1:D:150:LEU:H	2.07	0.62
1:C:206:HIS:CD2	1:C:208:GLU:H	2.19	0.61
1:D:454:SER:H	1:D:458:GLN:NE2	1.98	0.61
1:F:423:GLN:HE21	1:F:493:ASP:HB2	1.65	0.61
1:D:167:SER:HA	4:D:632:HOH:O	1.99	0.61
1:F:417:ILE:HD12	1:F:441:LEU:HD13	1.83	0.60
1:D:148:SER:O	1:D:150:LEU:N	2.28	0.59
1:B:165:HIS:HD2	1:B:167:SER:H	1.50	0.59
1:F:206:HIS:CD2	1:F:208:GLU:H	2.14	0.59
1:E:444:TYR:HA	1:E:447:ILE:HD12	1.83	0.59
1:B:137:HIS:HD2	1:B:140:ASP:HB2	1.67	0.58
1:F:97:ASN:H	1:F:127:ASN:HD22	1.50	0.58
1:F:165:HIS:HD2	1:F:167:SER:H	1.51	0.58
1:F:3:VAL:CG1	1:F:35:MET:HG3	2.32	0.58
1:D:501:PHE:CD2	1:D:525:SER:HA	2.39	0.58
1:F:451:THR:HG22	3:F:1004:NAG:HN2	1.68	0.58
1:A:97:ASN:HD22	1:A:127:ASN:HD21	1.52	0.57
1:F:102:GLY:HA3	4:F:626:HOH:O	2.04	0.57
1:F:137:HIS:HD2	1:F:140:ASP:HB2	1.69	0.57
1:A:25:ARG:CD	3:D:1005:NAG:H62	2.34	0.57
1:B:501:PHE:CD2	1:B:525:SER:HA	2.39	0.57
1:D:139:GLN:O	1:D:185:ARG:NH2	2.37	0.57
1:A:390:SER:O	1:A:393:SER:HB2	2.04	0.57
1:A:25:ARG:HD3	3:D:1005:NAG:H62	1.86	0.56
1:A:454:SER:H	1:A:458:GLN:NE2	2.02	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:417:ILE:HD12	1:E:441:LEU:HD13	1.87	0.56
1:B:417:ILE:HD12	1:B:441:LEU:HD13	1.88	0.56
1:C:165:HIS:HD2	1:C:167:SER:H	1.53	0.56
1:C:202:SER:HB3	1:D:201:VAL:HB	1.86	0.56
1:E:165:HIS:HD2	1:E:167:SER:H	1.53	0.56
1:E:501:PHE:CD2	1:E:525:SER:HA	2.41	0.56
1:D:258:TYR:HA	1:D:277:SER:O	2.05	0.56
1:D:360:ASP:HB3	1:D:363:LYS:HG3	1.88	0.55
1:B:571:GLY:HA2	1:B:578:PHE:HA	1.88	0.55
1:E:328:ILE:HD13	1:E:359:ILE:HD11	1.88	0.55
1:E:137:HIS:HD2	1:E:140:ASP:HB2	1.72	0.55
1:F:501:PHE:CD2	1:F:525:SER:HA	2.41	0.55
1:A:248:PHE:HB2	1:B:281:ARG:HG3	1.87	0.55
1:D:454:SER:H	1:D:458:GLN:HE22	1.54	0.55
1:F:454:SER:H	1:F:458:GLN:NE2	2.04	0.55
1:A:165:HIS:HD2	1:A:167:SER:H	1.53	0.55
1:E:407:LEU:HD23	1:E:432:ASN:HB2	1.89	0.55
2:I:5:LEU:HD21	2:I:35:LEU:HD21	1.87	0.55
1:A:501:PHE:CD2	1:A:525:SER:HA	2.41	0.54
1:D:124:VAL:HB	1:D:153:VAL:HG22	1.89	0.54
1:F:87:GLU:OE2	2:L:33:ARG:HD3	2.07	0.54
1:C:417:ILE:HD12	1:C:441:LEU:HD13	1.89	0.54
1:A:417:ILE:HD12	1:A:441:LEU:HD13	1.88	0.54
1:B:454:SER:H	1:B:458:GLN:NE2	2.05	0.54
1:C:124:VAL:HB	1:C:153:VAL:HG22	1.88	0.54
1:B:399:GLY:O	1:B:429:SER:HB2	2.06	0.54
1:C:97:ASN:H	1:C:127:ASN:HD22	1.55	0.54
1:D:165:HIS:HD2	1:D:167:SER:H	1.53	0.54
1:F:360:ASP:HB3	1:F:363:LYS:HG3	1.89	0.54
1:D:137:HIS:HD2	1:D:140:ASP:HB2	1.73	0.54
1:D:417:ILE:HD12	1:D:441:LEU:HD13	1.89	0.54
1:B:360:ASP:HB3	1:B:363:LYS:HG3	1.90	0.54
1:E:124:VAL:HB	1:E:153:VAL:HG22	1.89	0.54
1:A:346:THR:HG21	2:G:17:VAL:HG11	1.89	0.54
1:C:481:LEU:HD21	1:C:509:GLU:HG3	1.90	0.53
1:C:360:ASP:HB3	1:C:363:LYS:HG3	1.90	0.53
1:E:346:THR:HG23	1:E:351:ASP:HB2	1.91	0.53
1:E:454:SER:H	1:E:458:GLN:HE22	1.57	0.53
1:F:116:GLU:HB2	1:F:211:GLY:HA2	1.90	0.53
1:B:124:VAL:HB	1:B:153:VAL:HG22	1.90	0.53
1:B:97:ASN:HD22	1:B:127:ASN:HD21	1.56	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:116:GLU:HB2	1:E:211:GLY:HA2	1.91	0.53
1:E:479:ASN:O	1:E:482:CYS:HB2	2.09	0.53
1:A:360:ASP:HB3	1:A:363:LYS:HG3	1.90	0.52
1:E:426:LYS:NZ	4:E:638:HOH:O	2.41	0.52
1:C:444:TYR:HA	1:C:447:ILE:HD12	1.92	0.52
1:A:378:ASN:HA	1:A:410:LEU:HB2	1.91	0.52
1:A:97:ASN:H	1:A:127:ASN:HD22	1.58	0.51
1:E:273:VAL:HG13	1:E:280:VAL:HG23	1.92	0.51
1:E:360:ASP:HB3	1:E:363:LYS:HG3	1.92	0.51
1:A:148:SER:C	1:A:150:LEU:H	2.18	0.51
1:F:124:VAL:HB	1:F:153:VAL:HG22	1.92	0.51
1:E:176:THR:H	1:E:179:HIS:HD2	1.58	0.51
1:D:273:VAL:HG13	1:D:280:VAL:HG23	1.93	0.51
1:C:329:ASP:O	1:C:332:ILE:HG12	2.11	0.50
1:C:346:THR:HG21	2:I:17:VAL:HG11	1.94	0.50
1:F:423:GLN:NE2	1:F:493:ASP:HB2	2.26	0.50
1:F:454:SER:H	1:F:458:GLN:HE22	1.59	0.50
1:B:346:THR:HG21	2:H:17:VAL:HG11	1.93	0.50
1:B:116:GLU:HB2	1:B:211:GLY:HA2	1.95	0.49
1:A:329:ASP:O	1:A:332:ILE:HG12	2.12	0.49
1:C:176:THR:H	1:C:179:HIS:HD2	1.57	0.49
1:D:329:ASP:O	1:D:332:ILE:HG12	2.12	0.49
1:C:176:THR:H	1:C:179:HIS:CD2	2.30	0.49
1:F:273:VAL:HG13	1:F:280:VAL:HG23	1.94	0.49
1:E:139:GLN:O	1:E:185:ARG:NH2	2.44	0.49
1:F:329:ASP:O	1:F:332:ILE:HG12	2.12	0.49
1:B:444:TYR:HA	1:B:447:ILE:HD12	1.95	0.49
1:E:176:THR:H	1:E:179:HIS:CD2	2.31	0.49
1:B:148:SER:C	1:B:150:LEU:H	2.21	0.48
1:F:346:THR:HG21	2:L:17:VAL:HG11	1.95	0.48
1:B:455:THR:H	1:B:458:GLN:HE21	1.61	0.48
1:F:176:THR:H	1:F:179:HIS:HD2	1.61	0.48
2:I:6:VAL:HG13	2:I:26:LYS:HE2	1.96	0.48
1:D:176:THR:H	1:D:179:HIS:HD2	1.59	0.48
1:A:22:ARG:HD2	1:D:484:SER:HB2	1.94	0.48
1:C:148:SER:C	1:C:150:LEU:H	2.21	0.48
1:C:138:TRP:HE1	1:C:153:VAL:HG21	1.79	0.48
1:F:4:CYS:O	1:F:35:MET:HB2	2.13	0.48
1:B:176:THR:H	1:B:179:HIS:HD2	1.62	0.48
1:F:444:TYR:HA	1:F:447:ILE:HD12	1.94	0.48
1:E:443:TYR:CG	1:E:489:GLY:HA2	2.49	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:171:ARG:HH21	1:F:295:ILE:CD1	2.27	0.48
1:C:97:ASN:HD22	1:C:127:ASN:HD21	1.60	0.47
1:C:273:VAL:HG13	1:C:280:VAL:HG23	1.96	0.47
4:D:646:HOH:O	2:J:52:MET:HE3	2.14	0.47
1:F:138:TRP:HE1	1:F:153:VAL:HG21	1.78	0.47
1:F:148:SER:C	1:F:150:LEU:H	2.23	0.47
1:F:474:GLU:HB3	1:F:476:MET:HE2	1.96	0.47
1:A:97:ASN:HD22	1:A:127:ASN:ND2	2.11	0.47
1:B:329:ASP:O	1:B:332:ILE:HG12	2.15	0.47
1:C:511:CYS:HB3	1:C:513:LEU:HG	1.97	0.47
1:B:171:ARG:HH21	1:E:295:ILE:HD11	1.80	0.47
1:A:176:THR:H	1:A:179:HIS:HD2	1.62	0.47
1:C:454:SER:H	1:C:458:GLN:NE2	2.11	0.47
1:E:148:SER:C	1:E:150:LEU:H	2.22	0.47
1:B:474:GLU:HB3	1:B:476:MET:HE2	1.97	0.47
1:D:16:ASP:HB3	1:D:19:GLN:HB2	1.97	0.47
1:E:276:SER:OG	1:E:277:SER:N	2.48	0.47
1:C:512:ASN:HB3	1:C:519:ARG:HA	1.97	0.47
1:D:116:GLU:HB2	1:D:211:GLY:HA2	1.96	0.47
1:C:16:ASP:HB3	1:C:19:GLN:HB2	1.97	0.46
1:A:16:ASP:HB3	1:A:19:GLN:HB2	1.97	0.46
1:E:474:GLU:HB3	1:E:476:MET:HE2	1.97	0.46
1:D:176:THR:H	1:D:179:HIS:CD2	2.32	0.46
1:D:348:ILE:HD12	1:D:383:PRO:HD3	1.97	0.46
1:E:16:ASP:HB3	1:E:19:GLN:HB2	1.98	0.46
1:E:138:TRP:HE1	1:E:153:VAL:HG21	1.81	0.46
1:C:137:HIS:CD2	1:C:140:ASP:HB2	2.48	0.46
1:B:176:THR:H	1:B:179:HIS:CD2	2.34	0.45
1:A:348:ILE:HD12	1:A:383:PRO:HD3	1.98	0.45
1:D:450:THR:HG22	3:D:1005:NAG:H2	1.97	0.45
1:E:421:GLN:NE2	1:E:490:PRO:HD2	2.31	0.45
1:B:420:LEU:HG	1:B:441:LEU:HD11	1.98	0.45
1:B:139:GLN:O	1:B:185:ARG:NH2	2.50	0.45
1:D:362:GLU:OE1	3:D:1004:NAG:O4	2.24	0.45
1:F:16:ASP:HB3	1:F:19:GLN:HB2	1.99	0.45
1:B:428:ILE:HD13	1:B:433:ILE:HD11	1.97	0.45
1:D:138:TRP:HE1	1:D:153:VAL:HG21	1.82	0.45
1:A:176:THR:H	1:A:179:HIS:CD2	2.35	0.45
1:B:16:ASP:HB3	1:B:19:GLN:HB2	1.99	0.45
1:A:245:PRO:HG3	1:B:227:PHE:CE2	2.52	0.45
1:B:87:GLU:OE2	2:H:33:ARG:HD3	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:455:THR:H	1:D:458:GLN:HE21	1.65	0.45
1:B:35:MET:HE2	1:B:35:MET:HB3	1.90	0.44
1:B:533:GLN:HB3	1:B:564:CYS:HB2	1.99	0.44
1:F:176:THR:H	1:F:179:HIS:CD2	2.34	0.44
1:B:144:ASN:HA	1:B:145:PRO:HD3	1.77	0.44
1:C:171:ARG:NH2	1:F:295:ILE:HD12	2.32	0.44
1:B:348:ILE:HD12	1:B:383:PRO:HD3	1.99	0.44
1:B:380:GLN:HG2	1:B:412:LEU:HD21	2.00	0.44
1:D:436:THR:HA	1:D:463:ARG:O	2.18	0.44
1:C:348:ILE:HD12	1:C:383:PRO:HD3	1.98	0.44
1:C:474:GLU:HB3	1:C:476:MET:HE2	1.99	0.44
1:D:229:ASP:HB2	1:D:264:CYS:SG	2.57	0.44
1:E:202:SER:HB3	1:F:201:VAL:HB	1.98	0.44
1:E:46:ASN:HA	4:E:626:HOH:O	2.16	0.44
1:E:508:ILE:HD12	1:E:510:SER:O	2.18	0.44
1:F:64:VAL:O	1:F:94:ILE:HA	2.18	0.44
1:D:144:ASN:HD22	1:D:148:SER:HB3	1.83	0.44
1:F:451:THR:HG22	3:F:1004:NAG:N2	2.32	0.44
1:A:300:PRO:HG2	1:B:300:PRO:HG2	2.00	0.44
2:J:6:VAL:HG13	2:J:26:LYS:HE2	1.99	0.44
1:E:331:PHE:HA	1:E:334:CYS:SG	2.58	0.43
1:E:348:ILE:HD12	1:E:383:PRO:HD3	1.99	0.43
1:F:436:THR:HA	1:F:463:ARG:O	2.18	0.43
1:A:137:HIS:CD2	1:A:140:ASP:HB2	2.48	0.43
1:D:549:PRO:HG2	1:D:563:ASN:HB3	1.99	0.43
1:E:421:GLN:HE21	1:E:490:PRO:HD2	1.83	0.43
1:F:341:LEU:HD23	1:F:341:LEU:HA	1.94	0.43
1:B:138:TRP:HE1	1:B:153:VAL:HG21	1.82	0.43
1:A:436:THR:HA	1:A:463:ARG:O	2.18	0.43
1:D:95:PHE:HA	1:D:125:ASP:O	2.18	0.43
1:E:420:LEU:HG	1:E:441:LEU:HD11	2.01	0.43
1:C:428:ILE:HD13	1:C:433:ILE:HD11	2.01	0.43
1:D:383:PRO:HA	1:D:384:PRO:HD3	1.89	0.43
2:H:6:VAL:HG13	2:H:26:LYS:HE2	1.99	0.43
2:I:8:CYS:HB3	2:I:12:GLU:HB2	2.01	0.43
1:E:454:SER:H	1:E:458:GLN:NE2	2.16	0.43
1:A:474:GLU:HB3	1:A:476:MET:HE2	1.99	0.43
1:A:29:GLU:OE1	3:D:1005:NAG:O4	2.37	0.43
1:E:428:ILE:HD13	1:E:433:ILE:HD11	2.00	0.43
1:D:346:THR:HG21	2:J:17:VAL:HG11	2.01	0.42
1:C:436:THR:HA	1:C:463:ARG:O	2.18	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:229:ASP:HB2	1:A:264:CYS:SG	2.59	0.42
1:D:474:GLU:HB3	1:D:476:MET:HE2	2.00	0.42
1:E:120:GLY:H	1:E:144:ASN:ND2	2.17	0.42
1:F:3:VAL:HG13	1:F:35:MET:HG2	1.98	0.42
1:F:508:ILE:HD11	1:F:527:CYS:SG	2.59	0.42
1:F:549:PRO:HB2	1:F:563:ASN:HB2	2.01	0.42
1:A:198:GLY:HA3	1:A:203:ASP:OD2	2.20	0.42
1:B:103:ASN:HA	4:B:626:HOH:O	2.19	0.42
1:B:436:THR:HA	1:B:463:ARG:O	2.19	0.42
1:C:109:LEU:HG	1:C:130:LEU:HD11	2.01	0.42
1:D:206:HIS:CD2	1:D:208:GLU:HB2	2.54	0.42
1:D:433:ILE:HB	1:D:460:ILE:HD12	2.01	0.42
1:B:273:VAL:HG13	1:B:280:VAL:HG23	2.00	0.42
1:D:127:ASN:O	1:D:129:PHE:N	2.49	0.42
1:E:436:THR:HA	1:E:463:ARG:O	2.20	0.42
1:B:64:VAL:O	1:B:94:ILE:HA	2.20	0.42
1:C:433:ILE:HB	1:C:460:ILE:HD12	2.00	0.42
1:C:581:LYS:HG2	1:C:591:PRO:HA	2.00	0.42
1:A:481:LEU:HD21	1:A:509:GLU:HG2	2.02	0.42
1:D:451:THR:HG22	3:D:1005:NAG:C7	2.49	0.42
1:E:288:MET:HE3	1:E:288:MET:HB2	1.94	0.42
1:C:138:TRP:O	1:C:142:VAL:HG23	2.19	0.42
1:C:229:ASP:HB2	1:C:264:CYS:SG	2.60	0.42
1:B:244:ASN:OD1	1:B:247:THR:HG23	2.20	0.41
1:C:171:ARG:HH21	1:F:295:ILE:HD12	1.85	0.41
1:C:383:PRO:HA	1:C:384:PRO:HD3	1.91	0.41
1:D:143:ARG:O	1:D:145:PRO:CD	2.55	0.41
1:D:295:ILE:HD11	1:E:171:ARG:HH21	1.85	0.41
1:E:64:VAL:O	1:E:94:ILE:HA	2.20	0.41
1:E:503:ARG:HD3	1:E:520:GLU:OE1	2.21	0.41
1:D:399:GLY:O	1:D:429:SER:HB2	2.21	0.41
1:E:32:GLU:HG2	1:E:56:ARG:HE	1.85	0.41
2:J:8:CYS:HB3	2:J:12:GLU:HB2	2.01	0.41
1:C:64:VAL:O	1:C:94:ILE:HA	2.21	0.41
1:D:148:SER:C	1:D:150:LEU:N	2.78	0.41
1:A:433:ILE:HB	1:A:460:ILE:HD12	2.03	0.41
1:C:46:ASN:HA	4:C:619:HOH:O	2.20	0.41
1:D:35:MET:HE2	1:D:35:MET:HB3	1.91	0.41
2:K:8:CYS:HB3	2:K:12:GLU:HB2	2.03	0.41
1:D:501:PHE:HD2	1:D:525:SER:HA	1.84	0.41
2:H:8:CYS:HB3	2:H:12:GLU:HB2	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:428:ILE:HD13	1:A:433:ILE:HD11	2.03	0.41
1:A:410:LEU:HD12	1:A:412:LEU:HD22	2.02	0.40
1:D:87:GLU:OE2	2:J:33:ARG:HD3	2.21	0.40
1:D:581:LYS:HG2	1:D:591:PRO:HA	2.03	0.40
1:E:423:GLN:HE21	1:E:493:ASP:HB2	1.86	0.40
1:D:64:VAL:O	1:D:94:ILE:HA	2.21	0.40
1:D:341:LEU:HD23	1:D:341:LEU:HA	1.91	0.40
1:E:35:MET:HE2	1:E:35:MET:HB3	1.84	0.40
1:B:165:HIS:CD2	1:B:167:SER:H	2.35	0.40
1:B:433:ILE:HB	1:B:460:ILE:HD12	2.02	0.40
1:F:380:GLN:HG2	1:F:412:LEU:HD21	2.03	0.40
1:A:278:SER:HB3	1:B:243:TYR:CD1	2.56	0.40
1:B:79:ILE:HA	1:B:116:GLU:O	2.21	0.40
1:F:229:ASP:HB2	1:F:264:CYS:SG	2.61	0.40
1:F:288:MET:HE3	1:F:288:MET:HB2	1.83	0.40
1:A:520:GLU:HG2	1:A:529:GLU:HA	2.03	0.40
1:B:503:ARG:NH1	1:B:520:GLU:OE2	2.55	0.40
1:C:35:MET:HE2	1:C:35:MET:HB3	1.87	0.40
1:F:348:ILE:HD12	1:F:383:PRO:HD3	2.02	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	544/615 (88%)	508 (93%)	31 (6%)	5 (1%)	14	44
1	B	593/615 (96%)	558 (94%)	33 (6%)	2 (0%)	36	67
1	C	590/615 (96%)	548 (93%)	37 (6%)	5 (1%)	16	46
1	D	592/615 (96%)	553 (93%)	35 (6%)	4 (1%)	18	49
1	E	585/615 (95%)	544 (93%)	38 (6%)	3 (0%)	24	57

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	F	583/615 (95%)	546 (94%)	32 (6%)	5 (1%)	14	44
2	G	46/55 (84%)	43 (94%)	2 (4%)	1 (2%)	5	23
2	H	47/55 (86%)	43 (92%)	3 (6%)	1 (2%)	5	24
2	I	46/55 (84%)	43 (94%)	2 (4%)	1 (2%)	5	23
2	J	47/55 (86%)	44 (94%)	2 (4%)	1 (2%)	5	24
2	K	45/55 (82%)	41 (91%)	3 (7%)	1 (2%)	5	23
2	L	47/55 (86%)	44 (94%)	2 (4%)	1 (2%)	5	24
All	All	3765/4020 (94%)	3515 (93%)	220 (6%)	30 (1%)	16	46

All (30) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	149	ASN
1	B	149	ASN
1	C	149	ASN
1	C	159	SER
1	D	128	LYS
1	D	144	ASN
1	D	149	ASN
1	E	128	LYS
1	E	144	ASN
1	E	149	ASN
1	F	148	SER
1	F	149	ASN
1	A	128	LYS
1	F	128	LYS
1	A	423	GLN
1	A	536	LYS
1	B	536	LYS
1	C	128	LYS
1	D	536	LYS
2	G	40	ASN
2	H	40	ASN
2	I	40	ASN
2	J	40	ASN
2	K	40	ASN
2	L	40	ASN
1	C	536	LYS
1	F	536	LYS
1	A	524	ASP

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Mol	Chain	Res	Type
1	F	524	ASP
1	C	144	ASN

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	488/544 (90%)	459 (94%)	29 (6%)	18	47
1	B	534/544 (98%)	506 (95%)	28 (5%)	21	51
1	C	531/544 (98%)	504 (95%)	27 (5%)	21	52
1	D	534/544 (98%)	506 (95%)	28 (5%)	21	51
1	E	527/544 (97%)	498 (94%)	29 (6%)	19	50
1	F	525/544 (96%)	498 (95%)	27 (5%)	21	52
2	G	45/49 (92%)	44 (98%)	1 (2%)	45	71
2	H	46/49 (94%)	45 (98%)	1 (2%)	45	71
2	I	45/49 (92%)	44 (98%)	1 (2%)	45	71
2	J	46/49 (94%)	44 (96%)	2 (4%)	26	57
2	K	44/49 (90%)	43 (98%)	1 (2%)	44	70
2	L	46/49 (94%)	45 (98%)	1 (2%)	45	71
All	All	3411/3558 (96%)	3236 (95%)	175 (5%)	21	52

All (175) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	29	GLU
1	A	35	MET
1	A	43	ILE
1	A	46	ASN
1	A	68	GLN
1	A	70	ARG
1	A	104	PHE
1	A	143	ARG

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Mol	Chain	Res	Type
1	A	149	ASN
1	A	153	VAL
1	A	176	THR
1	A	191	GLN
1	A	201	VAL
1	A	202	SER
1	A	242	VAL
1	A	252	HIS
1	A	259	THR
1	A	273	VAL
1	A	332	ILE
1	A	346	THR
1	A	442	CYS
1	A	450	THR
1	A	455	THR
1	A	456	ILE
1	A	460	ILE
1	A	497	SER
1	A	506	ILE
1	A	536	LYS
1	A	556	SER
1	B	1	GLN
1	B	29	GLU
1	B	35	MET
1	B	43	ILE
1	B	104	PHE
1	B	135	THR
1	B	176	THR
1	B	191	GLN
1	B	201	VAL
1	B	202	SER
1	B	203	ASP
1	B	242	VAL
1	B	252	HIS
1	B	259	THR
1	B	273	VAL
1	B	281	ARG
1	B	332	ILE
1	B	346	THR
1	B	402	VAL
1	B	410	LEU
1	B	442	CYS

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Mol	Chain	Res	Type
1	B	450	THR
1	B	456	ILE
1	B	460	ILE
1	B	497	SER
1	B	536	LYS
1	B	563	ASN
1	B	572	LEU
1	C	1	GLN
1	C	29	GLU
1	C	35	MET
1	C	43	ILE
1	C	104	PHE
1	C	143	ARG
1	C	191	GLN
1	C	201	VAL
1	C	202	SER
1	C	242	VAL
1	C	252	HIS
1	C	259	THR
1	C	273	VAL
1	C	332	ILE
1	C	346	THR
1	C	412	LEU
1	C	429	SER
1	C	442	CYS
1	C	450	THR
1	C	456	ILE
1	C	460	ILE
1	C	497	SER
1	C	511	CYS
1	C	522	GLU
1	C	535	GLU
1	C	563	ASN
1	C	609	ILE
1	D	1	GLN
1	D	29	GLU
1	D	35	MET
1	D	43	ILE
1	D	104	PHE
1	D	139	GLN
1	D	149	ASN
1	D	176	THR

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Mol	Chain	Res	Type
1	D	191	GLN
1	D	201	VAL
1	D	202	SER
1	D	242	VAL
1	D	252	HIS
1	D	259	THR
1	D	273	VAL
1	D	332	ILE
1	D	402	VAL
1	D	442	CYS
1	D	450	THR
1	D	456	ILE
1	D	460	ILE
1	D	470	ASN
1	D	496	LEU
1	D	515	ASP
1	D	536	LYS
1	D	563	ASN
1	D	567	LYS
1	D	613	TRP
1	E	1	GLN
1	E	29	GLU
1	E	35	MET
1	E	43	ILE
1	E	104	PHE
1	E	176	THR
1	E	191	GLN
1	E	201	VAL
1	E	202	SER
1	E	203	ASP
1	E	242	VAL
1	E	246	THR
1	E	259	THR
1	E	273	VAL
1	E	362	GLU
1	E	369	THR
1	E	410	LEU
1	E	412	LEU
1	E	429	SER
1	E	442	CYS
1	E	455	THR
1	E	456	ILE

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Mol	Chain	Res	Type
1	E	460	ILE
1	E	482	CYS
1	E	496	LEU
1	E	528	VAL
1	E	535	GLU
1	E	563	ASN
1	E	570	ASP
1	F	1	GLN
1	F	29	GLU
1	F	43	ILE
1	F	104	PHE
1	F	154	SER
1	F	176	THR
1	F	191	GLN
1	F	201	VAL
1	F	202	SER
1	F	203	ASP
1	F	207	ARG
1	F	242	VAL
1	F	252	HIS
1	F	273	VAL
1	F	288	MET
1	F	346	THR
1	F	412	LEU
1	F	442	CYS
1	F	450	THR
1	F	456	ILE
1	F	460	ILE
1	F	493	ASP
1	F	496	LEU
1	F	497	SER
1	F	515	ASP
1	F	541	LEU
1	F	550	ASP
2	G	43	THR
2	H	43	THR
2	I	43	THR
2	J	28	LEU
2	J	43	THR
2	K	43	THR
2	L	43	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (85)

such sidechains are listed below:

Mol	Chain	Res	Type
1	A	119	ASN
1	A	126	GLN
1	A	127	ASN
1	A	165	HIS
1	A	179	HIS
1	A	206	HIS
1	A	293	ASN
1	A	354	ASN
1	A	445	HIS
1	A	458	GLN
1	B	9	ASN
1	B	68	GLN
1	B	126	GLN
1	B	127	ASN
1	B	165	HIS
1	B	179	HIS
1	B	206	HIS
1	B	270	HIS
1	B	338	ASN
1	B	354	ASN
1	B	415	GLN
1	B	445	HIS
1	B	458	GLN
1	B	557	HIS
1	B	590	HIS
1	C	9	ASN
1	C	126	GLN
1	C	127	ASN
1	C	165	HIS
1	C	179	HIS
1	C	206	HIS
1	C	354	ASN
1	C	378	ASN
1	C	423	GLN
1	C	445	HIS
1	C	458	GLN
1	C	480	HIS
1	C	601	ASN
1	D	119	ASN
1	D	126	GLN
1	D	144	ASN
1	D	165	HIS

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Mol	Chain	Res	Type
1	D	179	HIS
1	D	206	HIS
1	D	252	HIS
1	D	338	ASN
1	D	354	ASN
1	D	445	HIS
1	D	458	GLN
1	D	479	ASN
1	D	590	HIS
1	E	68	GLN
1	E	119	ASN
1	E	126	GLN
1	E	144	ASN
1	E	165	HIS
1	E	179	HIS
1	E	206	HIS
1	E	354	ASN
1	E	421	GLN
1	E	445	HIS
1	E	458	GLN
1	E	523	ASN
1	E	533	GLN
1	E	590	HIS
1	E	606	HIS
1	F	9	ASN
1	F	68	GLN
1	F	119	ASN
1	F	126	GLN
1	F	127	ASN
1	F	144	ASN
1	F	165	HIS
1	F	179	HIS
1	F	206	HIS
1	F	354	ASN
1	F	445	HIS
1	F	458	GLN
1	F	545	HIS
1	F	551	ASN
1	F	590	HIS
2	G	40	ASN
2	G	49	ASN
2	I	18	ASN

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Mol	Chain	Res	Type
2	K	18	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

26 ligands 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$
3	NAG	D	1001	1	14,14,15	1.50	3 (21%)	17,19,21	2.93	7 (41%)
3	NAG	E	1003	1	14,14,15	2.34	4 (28%)	17,19,21	2.10	6 (35%)
3	NAG	D	1003	1	14,14,15	1.26	1 (7%)	17,19,21	2.15	5 (29%)
3	NAG	F	1005	1	14,14,15	1.80	3 (21%)	17,19,21	2.38	7 (41%)
3	NAG	B	1003	1	14,14,15	1.69	2 (14%)	17,19,21	2.23	8 (47%)
3	NAG	A	1001	1	14,14,15	1.27	2 (14%)	17,19,21	3.21	9 (52%)
3	NAG	B	1001	1	14,14,15	1.35	1 (7%)	17,19,21	3.15	8 (47%)
3	NAG	D	1004	1	14,14,15	1.71	3 (21%)	17,19,21	2.18	5 (29%)
3	NAG	E	1002	1	14,14,15	1.29	1 (7%)	17,19,21	2.04	6 (35%)
3	NAG	F	1004	1	14,14,15	2.33	4 (28%)	17,19,21	2.72	8 (47%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	NAG	F	1002	1	14,14,15	1.27	1 (7%)	17,19,21	2.28	6 (35%)
3	NAG	D	1005	1	14,14,15	1.48	2 (14%)	17,19,21	3.00	9 (52%)
3	NAG	B	1002	1	14,14,15	1.58	2 (14%)	17,19,21	2.32	6 (35%)
3	NAG	B	1004	1	14,14,15	3.68	8 (57%)	17,19,21	4.44	10 (58%)
3	NAG	F	1001	1	14,14,15	1.64	3 (21%)	17,19,21	3.69	10 (58%)
3	NAG	A	1004	1	14,14,15	2.28	3 (21%)	17,19,21	4.09	11 (64%)
3	NAG	C	1002	1	14,14,15	1.62	3 (21%)	17,19,21	2.00	6 (35%)
3	NAG	B	1006	1	14,14,15	1.90	5 (35%)	17,19,21	2.58	8 (47%)
3	NAG	B	1005	1	14,14,15	2.72	5 (35%)	17,19,21	2.80	8 (47%)
3	NAG	E	1001	1	14,14,15	1.31	2 (14%)	17,19,21	3.33	9 (52%)
3	NAG	A	1003	1	14,14,15	1.25	1 (7%)	17,19,21	1.78	5 (29%)
3	NAG	F	1003	1	14,14,15	1.09	1 (7%)	17,19,21	2.17	7 (41%)
3	NAG	D	1002	1	14,14,15	1.73	4 (28%)	17,19,21	2.07	5 (29%)
3	NAG	A	1002	1	14,14,15	1.64	3 (21%)	17,19,21	2.53	9 (52%)
3	NAG	C	1001	1	14,14,15	1.18	0	17,19,21	3.54	8 (47%)
3	NAG	F	1006	1	14,14,15	2.25	4 (28%)	17,19,21	1.24	2 (11%)

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
3	NAG	D	1001	1	-	2/6/23/26	0/1/1/1
3	NAG	E	1003	1	-	2/6/23/26	0/1/1/1
3	NAG	D	1003	1	-	1/6/23/26	0/1/1/1
3	NAG	F	1005	1	-	1/6/23/26	0/1/1/1
3	NAG	B	1003	1	-	4/6/23/26	0/1/1/1
3	NAG	A	1001	1	-	2/6/23/26	0/1/1/1
3	NAG	B	1001	1	-	2/6/23/26	0/1/1/1
3	NAG	D	1004	1	-	2/6/23/26	0/1/1/1
3	NAG	E	1002	1	-	0/6/23/26	0/1/1/1
3	NAG	F	1004	1	-	1/6/23/26	0/1/1/1
3	NAG	F	1002	1	-	0/6/23/26	0/1/1/1
3	NAG	D	1005	1	-	0/6/23/26	0/1/1/1
3	NAG	B	1002	1	-	0/6/23/26	0/1/1/1
3	NAG	B	1004	1	-	0/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	NAG	F	1001	1	-	2/6/23/26	0/1/1/1
3	NAG	A	1004	1	-	2/6/23/26	0/1/1/1
3	NAG	C	1002	1	-	0/6/23/26	0/1/1/1
3	NAG	B	1006	1	-	0/6/23/26	0/1/1/1
3	NAG	B	1005	1	-	1/6/23/26	0/1/1/1
3	NAG	E	1001	1	-	2/6/23/26	0/1/1/1
3	NAG	A	1003	1	-	1/6/23/26	0/1/1/1
3	NAG	F	1003	1	-	2/6/23/26	0/1/1/1
3	NAG	D	1002	1	-	0/6/23/26	0/1/1/1
3	NAG	A	1002	1	-	0/6/23/26	0/1/1/1
3	NAG	C	1001	1	-	2/6/23/26	0/1/1/1
3	NAG	F	1006	1	-	1/6/23/26	0/1/1/1

All (71) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	1004	NAG	C1-C2	9.54	1.65	1.52
3	A	1004	NAG	C1-C2	6.61	1.61	1.52
3	B	1005	NAG	C1-C2	6.41	1.61	1.52
3	F	1004	NAG	C1-C2	6.20	1.60	1.52
3	E	1003	NAG	C1-C2	5.54	1.59	1.52
3	B	1004	NAG	C7-N2	5.15	1.51	1.34
3	F	1006	NAG	C1-C2	5.14	1.59	1.52
3	B	1005	NAG	C4-C5	4.99	1.63	1.53
3	E	1003	NAG	C3-C2	4.48	1.61	1.52
3	B	1003	NAG	C1-C2	4.41	1.58	1.52
3	B	1004	NAG	C2-N2	4.39	1.53	1.46
3	D	1002	NAG	C1-C2	4.18	1.58	1.52
3	F	1005	NAG	C1-C2	4.01	1.57	1.52
3	F	1001	NAG	C2-N2	-3.96	1.39	1.46
3	F	1006	NAG	C3-C2	3.67	1.60	1.52
3	C	1002	NAG	C1-C2	3.52	1.57	1.52
3	D	1004	NAG	C1-C2	3.49	1.57	1.52
3	B	1006	NAG	C1-C2	3.44	1.57	1.52
3	B	1004	NAG	C8-C7	3.42	1.57	1.50
3	D	1005	NAG	C1-C2	3.32	1.56	1.52
3	B	1005	NAG	C4-C3	3.14	1.60	1.52
3	A	1002	NAG	C1-C2	3.13	1.56	1.52
3	B	1004	NAG	O5-C1	-3.12	1.38	1.43
3	D	1003	NAG	C1-C2	3.09	1.56	1.52
3	F	1006	NAG	C4-C5	2.96	1.59	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	E	1001	NAG	C2-N2	-2.92	1.41	1.46
3	B	1004	NAG	O7-C7	2.89	1.29	1.23
3	E	1003	NAG	C4-C3	2.86	1.59	1.52
3	F	1005	NAG	C4-C5	2.84	1.59	1.53
3	B	1004	NAG	C4-C5	2.80	1.59	1.53
3	B	1006	NAG	C4-C3	2.80	1.59	1.52
3	F	1004	NAG	O5-C5	-2.80	1.38	1.43
3	B	1004	NAG	O5-C5	-2.77	1.38	1.43
3	A	1004	NAG	C3-C2	2.75	1.58	1.52
3	B	1006	NAG	C3-C2	2.74	1.58	1.52
3	D	1001	NAG	O3-C3	2.72	1.49	1.43
3	D	1001	NAG	C2-N2	-2.70	1.41	1.46
3	B	1002	NAG	C1-C2	2.66	1.56	1.52
3	A	1003	NAG	C1-C2	2.63	1.55	1.52
3	D	1004	NAG	C4-C3	2.63	1.59	1.52
3	B	1001	NAG	O5-C5	2.58	1.48	1.43
3	E	1002	NAG	C1-C2	2.57	1.55	1.52
3	F	1004	NAG	C7-N2	2.48	1.42	1.34
3	F	1001	NAG	C4-C3	2.45	1.58	1.52
3	D	1002	NAG	C3-C2	2.45	1.57	1.52
3	D	1004	NAG	O5-C5	2.44	1.48	1.43
3	F	1006	NAG	O5-C5	2.44	1.48	1.43
3	D	1005	NAG	C6-C5	2.43	1.60	1.51
3	F	1001	NAG	C8-C7	2.41	1.55	1.50
3	F	1004	NAG	O5-C1	-2.40	1.39	1.43
3	D	1001	NAG	O5-C5	2.39	1.48	1.43
3	B	1003	NAG	C3-C2	2.38	1.57	1.52
3	A	1004	NAG	C2-N2	2.38	1.50	1.46
3	D	1002	NAG	C4-C3	2.36	1.58	1.52
3	B	1006	NAG	C4-C5	2.35	1.58	1.53
3	B	1005	NAG	C3-C2	2.29	1.57	1.52
3	B	1002	NAG	C7-N2	2.28	1.41	1.34
3	C	1002	NAG	O5-C1	2.26	1.47	1.43
3	E	1003	NAG	C2-N2	2.24	1.50	1.46
3	A	1002	NAG	O5-C5	2.23	1.47	1.43
3	D	1002	NAG	O5-C1	2.20	1.47	1.43
3	F	1005	NAG	C4-C3	2.20	1.58	1.52
3	E	1001	NAG	O3-C3	2.17	1.48	1.43
3	A	1001	NAG	C3-C2	2.16	1.57	1.52
3	F	1002	NAG	O5-C1	2.14	1.47	1.43
3	A	1002	NAG	C7-N2	2.13	1.41	1.34
3	C	1002	NAG	C3-C2	2.12	1.57	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	1006	NAG	O5-C5	2.07	1.47	1.43
3	A	1001	NAG	O5-C5	2.07	1.47	1.43
3	F	1003	NAG	C4-C3	2.05	1.57	1.52
3	B	1005	NAG	C7-N2	2.03	1.40	1.34

All (188) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	1004	NAG	C2-N2-C7	11.60	138.45	122.90
3	A	1004	NAG	C1-O5-C5	-9.20	99.85	112.19
3	C	1001	NAG	C1-C2-N2	-8.89	96.43	110.43
3	A	1001	NAG	C1-C2-N2	-8.79	96.58	110.43
3	F	1001	NAG	C1-C2-N2	-8.65	96.81	110.43
3	E	1001	NAG	C1-C2-N2	-8.00	97.83	110.43
3	D	1001	NAG	C1-C2-N2	-7.74	98.23	110.43
3	B	1004	NAG	C1-C2-N2	7.35	122.02	110.43
3	B	1001	NAG	C1-C2-N2	-7.12	99.21	110.43
3	A	1004	NAG	O4-C4-C3	-6.55	94.95	110.38
3	F	1001	NAG	C1-O5-C5	6.48	120.87	112.19
3	D	1004	NAG	C1-O5-C5	6.21	120.51	112.19
3	F	1002	NAG	C1-O5-C5	6.19	120.49	112.19
3	D	1005	NAG	C6-C5-C4	6.19	128.21	113.02
3	A	1004	NAG	O5-C5-C6	6.07	119.48	107.66
3	D	1005	NAG	O5-C5-C4	-6.01	96.21	110.83
3	A	1001	NAG	C4-C3-C2	5.87	119.62	111.02
3	C	1001	NAG	C4-C3-C2	5.73	119.41	111.02
3	A	1002	NAG	C1-O5-C5	5.67	119.78	112.19
3	B	1002	NAG	C1-O5-C5	5.62	119.71	112.19
3	B	1006	NAG	C1-O5-C5	5.61	119.70	112.19
3	E	1001	NAG	C1-O5-C5	5.57	119.65	112.19
3	B	1001	NAG	C4-C3-C2	5.55	119.15	111.02
3	F	1001	NAG	C4-C3-C2	5.52	119.11	111.02
3	B	1004	NAG	O5-C1-C2	-5.45	102.86	111.29
3	D	1002	NAG	C1-O5-C5	5.45	119.48	112.19
3	E	1003	NAG	C4-C3-C2	5.36	118.87	111.02
3	C	1001	NAG	C1-O5-C5	5.36	119.36	112.19
3	D	1003	NAG	C4-C3-C2	5.26	118.72	111.02
3	E	1001	NAG	C4-C3-C2	5.25	118.71	111.02
3	E	1002	NAG	C1-O5-C5	5.17	119.12	112.19
3	A	1004	NAG	C4-C3-C2	5.01	118.36	111.02
3	F	1005	NAG	O5-C1-C2	4.93	118.91	111.29
3	B	1004	NAG	O7-C7-N2	4.80	130.47	121.98

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	1005	NAG	C1-C2-N2	4.77	117.94	110.43
3	A	1004	NAG	C1-C2-N2	-4.73	102.97	110.43
3	F	1004	NAG	O5-C5-C4	-4.68	99.43	110.83
3	C	1002	NAG	C1-O5-C5	4.66	118.44	112.19
3	B	1001	NAG	O7-C7-C8	4.62	130.28	122.05
3	D	1001	NAG	C1-O5-C5	4.61	118.37	112.19
3	A	1002	NAG	C4-C3-C2	4.61	117.78	111.02
3	B	1005	NAG	C2-N2-C7	4.60	129.07	122.90
3	E	1001	NAG	O5-C1-C2	4.57	118.36	111.29
3	F	1003	NAG	C8-C7-N2	-4.54	108.59	116.12
3	B	1005	NAG	C6-C5-C4	4.52	124.12	113.02
3	B	1004	NAG	O5-C5-C6	-4.46	98.99	107.66
3	C	1001	NAG	O7-C7-C8	4.45	129.97	122.05
3	F	1003	NAG	C4-C3-C2	4.42	117.50	111.02
3	F	1005	NAG	C4-C3-C2	4.40	117.47	111.02
3	D	1001	NAG	C4-C3-C2	4.38	117.44	111.02
3	F	1004	NAG	O5-C1-C2	-4.37	104.53	111.29
3	A	1004	NAG	O3-C3-C2	4.36	118.46	109.40
3	F	1001	NAG	O7-C7-C8	4.32	129.74	122.05
3	E	1003	NAG	O5-C5-C6	4.31	116.06	107.66
3	D	1003	NAG	C8-C7-N2	-4.29	109.00	116.12
3	F	1001	NAG	O5-C1-C2	4.26	117.88	111.29
3	F	1005	NAG	C1-O5-C5	4.24	117.87	112.19
3	B	1006	NAG	O5-C1-C2	4.23	117.83	111.29
3	F	1002	NAG	C4-C3-C2	4.21	117.19	111.02
3	B	1005	NAG	C1-O5-C5	-4.12	106.66	112.19
3	F	1004	NAG	C4-C3-C2	4.08	117.00	111.02
3	A	1004	NAG	C6-C5-C4	4.07	123.02	113.02
3	B	1003	NAG	C3-C4-C5	-4.07	102.85	110.23
3	B	1004	NAG	C6-C5-C4	4.06	122.98	113.02
3	B	1001	NAG	C1-O5-C5	4.04	117.61	112.19
3	B	1004	NAG	O7-C7-C8	-4.03	114.87	122.05
3	B	1006	NAG	C4-C3-C2	3.97	116.83	111.02
3	F	1004	NAG	O5-C5-C6	-3.95	99.97	107.66
3	C	1001	NAG	O5-C1-C2	3.87	117.28	111.29
3	A	1002	NAG	O3-C3-C2	-3.84	101.43	109.40
3	A	1003	NAG	C8-C7-N2	-3.82	109.79	116.12
3	B	1002	NAG	C8-C7-N2	-3.77	109.87	116.12
3	A	1003	NAG	C4-C3-C2	3.76	116.52	111.02
3	A	1004	NAG	C2-N2-C7	3.75	127.92	122.90
3	E	1002	NAG	C4-C3-C2	3.74	116.50	111.02
3	B	1005	NAG	O5-C5-C6	-3.71	100.44	107.66

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	1002	NAG	O3-C3-C2	-3.71	101.69	109.40
3	B	1004	NAG	C3-C4-C5	3.70	116.94	110.23
3	D	1005	NAG	C4-C3-C2	3.68	116.41	111.02
3	E	1001	NAG	O7-C7-C8	3.59	128.45	122.05
3	B	1003	NAG	C2-N2-C7	3.57	127.69	122.90
3	A	1001	NAG	O5-C1-C2	3.57	116.81	111.29
3	B	1002	NAG	C4-C3-C2	3.56	116.24	111.02
3	D	1005	NAG	C3-C4-C5	-3.56	103.78	110.23
3	B	1003	NAG	O5-C5-C6	3.53	114.54	107.66
3	C	1002	NAG	C4-C3-C2	3.50	116.15	111.02
3	B	1004	NAG	O5-C5-C4	-3.49	102.33	110.83
3	D	1001	NAG	O5-C1-C2	3.46	116.64	111.29
3	B	1005	NAG	C4-C3-C2	3.45	116.08	111.02
3	C	1001	NAG	O3-C3-C4	3.44	118.49	110.38
3	B	1001	NAG	C8-C7-N2	-3.40	110.48	116.12
3	F	1001	NAG	O4-C4-C5	-3.31	101.18	109.32
3	D	1005	NAG	O5-C1-C2	-3.30	106.18	111.29
3	D	1004	NAG	O3-C3-C4	3.29	118.13	110.38
3	F	1006	NAG	O5-C5-C4	3.27	118.79	110.83
3	F	1004	NAG	C6-C5-C4	3.26	121.02	113.02
3	B	1003	NAG	C1-O5-C5	-3.23	107.86	112.19
3	D	1005	NAG	O5-C5-C6	3.21	113.91	107.66
3	F	1004	NAG	O3-C3-C4	3.18	117.87	110.38
3	B	1001	NAG	O3-C3-C4	3.11	117.72	110.38
3	D	1005	NAG	C1-O5-C5	-3.11	108.02	112.19
3	B	1006	NAG	O5-C5-C4	3.09	118.35	110.83
3	F	1005	NAG	O5-C5-C6	-3.07	101.69	107.66
3	A	1001	NAG	O7-C7-C8	3.07	127.51	122.05
3	B	1001	NAG	O5-C1-C2	3.04	115.99	111.29
3	B	1003	NAG	C1-C2-N2	3.01	115.17	110.43
3	B	1006	NAG	C3-C4-C5	3.01	115.69	110.23
3	B	1002	NAG	O7-C7-N2	2.99	127.27	121.98
3	B	1004	NAG	O4-C4-C3	-2.98	103.35	110.38
3	F	1001	NAG	C8-C7-N2	-2.97	111.19	116.12
3	F	1004	NAG	C2-N2-C7	2.96	126.87	122.90
3	B	1002	NAG	C2-N2-C7	-2.93	118.97	122.90
3	A	1001	NAG	C1-O5-C5	2.93	116.11	112.19
3	C	1001	NAG	C8-C7-N2	-2.91	111.29	116.12
3	A	1002	NAG	C1-C2-N2	2.89	114.99	110.43
3	A	1004	NAG	C8-C7-N2	-2.88	111.34	116.12
3	B	1006	NAG	C1-C2-N2	2.88	114.97	110.43
3	F	1003	NAG	O3-C3-C4	2.88	117.16	110.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	1003	NAG	O7-C7-C8	2.86	127.15	122.05
3	F	1004	NAG	O7-C7-N2	2.86	127.03	121.98
3	D	1004	NAG	C1-C2-N2	2.85	114.93	110.43
3	D	1001	NAG	O3-C3-C4	2.85	117.09	110.38
3	D	1001	NAG	C3-C4-C5	2.84	115.38	110.23
3	A	1002	NAG	C8-C7-N2	-2.82	111.44	116.12
3	A	1001	NAG	C8-C7-N2	-2.79	111.49	116.12
3	D	1001	NAG	O7-C7-C8	2.79	127.02	122.05
3	E	1003	NAG	C2-N2-C7	2.77	126.61	122.90
3	C	1002	NAG	C1-C2-N2	2.75	114.77	110.43
3	B	1005	NAG	C8-C7-N2	-2.75	111.56	116.12
3	A	1001	NAG	O4-C4-C5	-2.74	102.57	109.32
3	C	1001	NAG	O4-C4-C5	-2.73	102.59	109.32
3	A	1003	NAG	C1-C2-N2	2.68	114.66	110.43
3	F	1003	NAG	O5-C5-C4	-2.64	104.41	110.83
3	F	1001	NAG	O3-C3-C4	2.64	116.59	110.38
3	E	1001	NAG	C3-C4-C5	2.62	114.98	110.23
3	D	1005	NAG	O7-C7-N2	2.62	126.61	121.98
3	F	1005	NAG	C1-C2-N2	2.62	114.56	110.43
3	C	1002	NAG	O3-C3-C2	-2.61	103.98	109.40
3	E	1002	NAG	O3-C3-C2	-2.59	104.02	109.40
3	E	1001	NAG	O3-C3-C4	2.57	116.43	110.38
3	E	1002	NAG	C1-C2-N2	2.56	114.47	110.43
3	F	1002	NAG	O5-C5-C6	-2.54	102.71	107.66
3	D	1003	NAG	O3-C3-C4	2.54	116.36	110.38
3	B	1003	NAG	O3-C3-C4	2.50	116.27	110.38
3	B	1003	NAG	C6-C5-C4	2.50	119.15	113.02
3	E	1001	NAG	C8-C7-N2	-2.48	112.01	116.12
3	F	1005	NAG	O4-C4-C3	-2.47	104.55	110.38
3	C	1002	NAG	C8-C7-N2	-2.45	112.06	116.12
3	F	1002	NAG	O7-C7-N2	2.44	126.30	121.98
3	E	1001	NAG	C6-C5-C4	-2.44	107.04	113.02
3	F	1002	NAG	C8-C7-N2	-2.43	112.09	116.12
3	E	1002	NAG	O3-C3-C4	-2.38	104.77	110.38
3	B	1001	NAG	C3-C4-C5	2.34	114.48	110.23
3	D	1002	NAG	C2-N2-C7	-2.32	119.79	122.90
3	D	1003	NAG	C2-N2-C7	2.31	126.00	122.90
3	E	1003	NAG	O7-C7-N2	2.30	126.04	121.98
3	B	1006	NAG	C8-C7-N2	-2.28	112.33	116.12
3	F	1001	NAG	C3-C4-C5	2.27	114.35	110.23
3	D	1002	NAG	O5-C1-C2	2.27	114.80	111.29
3	D	1004	NAG	O7-C7-N2	-2.24	118.03	121.98

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1001	NAG	O5-C5-C6	2.23	112.01	107.66
3	F	1003	NAG	O7-C7-N2	2.22	125.90	121.98
3	A	1004	NAG	O5-C5-C4	-2.21	105.45	110.83
3	B	1006	NAG	O4-C4-C5	-2.21	103.89	109.32
3	A	1002	NAG	C2-N2-C7	-2.20	119.94	122.90
3	D	1002	NAG	C4-C3-C2	2.19	114.23	111.02
3	A	1002	NAG	O5-C5-C6	-2.19	103.40	107.66
3	D	1004	NAG	C2-N2-C7	2.16	125.79	122.90
3	A	1001	NAG	O3-C3-C4	2.13	115.39	110.38
3	F	1003	NAG	C1-C2-N2	2.11	113.76	110.43
3	B	1003	NAG	O3-C3-C2	2.11	113.78	109.40
3	A	1003	NAG	C2-N2-C7	2.10	125.71	122.90
3	A	1002	NAG	O7-C7-N2	2.10	125.69	121.98
3	F	1003	NAG	O5-C5-C6	2.10	111.74	107.66
3	D	1005	NAG	O3-C3-C4	2.09	115.31	110.38
3	C	1002	NAG	O3-C3-C4	-2.08	105.47	110.38
3	B	1002	NAG	C1-C2-N2	2.08	113.71	110.43
3	A	1004	NAG	O7-C7-C8	2.08	125.75	122.05
3	E	1003	NAG	C8-C7-N2	-2.07	112.69	116.12
3	B	1005	NAG	C3-C4-C5	2.06	113.97	110.23
3	F	1006	NAG	C4-C3-C2	2.05	114.02	111.02
3	E	1003	NAG	C6-C5-C4	2.05	118.04	113.02
3	A	1003	NAG	O7-C7-N2	2.04	125.59	121.98
3	F	1002	NAG	O3-C3-C2	-2.04	105.17	109.40
3	F	1005	NAG	O3-C3-C4	2.04	115.18	110.38
3	A	1002	NAG	O5-C1-C2	2.03	114.43	111.29
3	F	1001	NAG	C6-C5-C4	-2.03	108.04	113.02
3	E	1002	NAG	C8-C7-N2	-2.02	112.76	116.12

There are no chirality outliers.

All (30) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	F	1004	NAG	C3-C2-N2-C7
3	A	1001	NAG	O5-C5-C6-O6
3	B	1001	NAG	O5-C5-C6-O6
3	C	1001	NAG	O5-C5-C6-O6
3	D	1001	NAG	O5-C5-C6-O6
3	B	1003	NAG	C4-C5-C6-O6
3	E	1001	NAG	O5-C5-C6-O6
3	F	1001	NAG	O5-C5-C6-O6
3	A	1004	NAG	C4-C5-C6-O6

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Mol	Chain	Res	Type	Atoms
3	E	1003	NAG	O5-C5-C6-O6
3	E	1003	NAG	C4-C5-C6-O6
3	B	1001	NAG	C4-C5-C6-O6
3	A	1001	NAG	C4-C5-C6-O6
3	C	1001	NAG	C4-C5-C6-O6
3	D	1001	NAG	C4-C5-C6-O6
3	F	1001	NAG	C4-C5-C6-O6
3	E	1001	NAG	C4-C5-C6-O6
3	F	1003	NAG	O5-C5-C6-O6
3	B	1003	NAG	C8-C7-N2-C2
3	B	1003	NAG	O7-C7-N2-C2
3	D	1004	NAG	C8-C7-N2-C2
3	D	1004	NAG	O7-C7-N2-C2
3	F	1006	NAG	O5-C5-C6-O6
3	A	1004	NAG	O5-C5-C6-O6
3	B	1003	NAG	O5-C5-C6-O6
3	A	1003	NAG	O5-C5-C6-O6
3	F	1003	NAG	C4-C5-C6-O6
3	D	1003	NAG	O5-C5-C6-O6
3	F	1005	NAG	O5-C5-C6-O6
3	B	1005	NAG	C3-C2-N2-C7

There are no ring outliers.

4 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	D	1004	NAG	2	0
3	F	1004	NAG	2	0
3	D	1005	NAG	5	0
3	B	1005	NAG	2	0

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	550/615 (89%)	-0.21	1 (0%) 91 83	47, 85, 249, 280	0
1	B	601/615 (97%)	-0.33	2 (0%) 90 79	45, 69, 115, 151	0
1	C	598/615 (97%)	-0.13	7 (1%) 76 54	50, 93, 173, 229	0
1	D	600/615 (97%)	-0.36	3 (0%) 87 72	45, 77, 117, 172	0
1	E	593/615 (96%)	-0.21	2 (0%) 90 79	45, 93, 164, 228	0
1	F	591/615 (96%)	-0.33	3 (0%) 87 72	43, 72, 155, 278	0
2	G	50/55 (90%)	0.15	1 (2%) 65 41	68, 98, 142, 151	0
2	H	51/55 (92%)	-0.16	1 (1%) 65 41	60, 85, 130, 140	0
2	I	50/55 (90%)	0.01	2 (4%) 42 23	85, 104, 143, 147	0
2	J	51/55 (92%)	-0.03	1 (1%) 65 41	75, 100, 136, 140	0
2	K	49/55 (89%)	0.13	1 (2%) 65 41	87, 110, 143, 158	0
2	L	51/55 (92%)	-0.12	0 100 100	62, 86, 126, 143	0
All	All	3835/4020 (95%)	-0.24	24 (0%) 85 69	43, 83, 156, 280	0

All (24) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	G	28	LEU	3.3
1	F	201	VAL	3.1
1	C	524	ASP	3.0
1	D	201	VAL	3.0
1	C	201	VAL	2.9
1	C	154	SER	2.9
1	E	154	SER	2.8
1	B	572	LEU	2.7
2	K	53	ALA	2.6
2	H	28	LEU	2.6
1	C	300	PRO	2.6

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Mol	Chain	Res	Type	RSRZ
2	I	28	LEU	2.5
1	B	524	ASP	2.5
1	C	542	LEU	2.5
1	F	603	PRO	2.4
1	F	147	PRO	2.4
1	A	201	VAL	2.4
1	D	524	ASP	2.3
1	E	473	ALA	2.1
1	C	120	GLY	2.1
1	D	145	PRO	2.1
1	C	609	ILE	2.1
2	I	54	SER	2.0
2	J	31	PRO	2.0

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

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($\text{\AA}^2$)	Q<0.9
3	NAG	B	1003	14/15	0.43	0.11	140,145,150,152	0
3	NAG	F	1005	14/15	0.66	0.14	126,130,135,136	0
3	NAG	D	1003	14/15	0.67	0.10	126,131,134,137	0
3	NAG	A	1003	14/15	0.67	0.10	145,151,158,160	0
3	NAG	D	1004	14/15	0.74	0.15	125,129,134,135	0
3	NAG	B	1004	14/15	0.76	0.16	89,93,97,97	0
3	NAG	D	1005	14/15	0.79	0.15	108,111,116,118	0
3	NAG	A	1004	14/15	0.80	0.13	117,121,125,127	0
3	NAG	F	1006	14/15	0.81	0.14	127,129,135,136	0
3	NAG	B	1005	14/15	0.82	0.10	100,105,108,111	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	NAG	E	1003	14/15	0.82	0.14	147,149,154,158	0
3	NAG	B	1006	14/15	0.84	0.12	118,121,125,125	0
3	NAG	C	1001	14/15	0.84	0.10	72,75,80,81	0
3	NAG	D	1001	14/15	0.84	0.12	66,70,74,74	0
3	NAG	F	1003	14/15	0.85	0.09	118,123,128,130	0
3	NAG	E	1001	14/15	0.87	0.12	66,70,74,74	0
3	NAG	A	1001	14/15	0.88	0.09	69,72,77,78	0
3	NAG	A	1002	14/15	0.90	0.10	71,76,78,80	0
3	NAG	B	1002	14/15	0.90	0.10	81,86,88,89	0
3	NAG	D	1002	14/15	0.92	0.10	73,77,80,81	0
3	NAG	F	1004	14/15	0.92	0.09	77,81,84,85	0
3	NAG	C	1002	14/15	0.92	0.09	72,77,81,82	0
3	NAG	F	1001	14/15	0.92	0.07	55,59,63,63	0
3	NAG	E	1002	14/15	0.93	0.09	77,82,85,87	0
3	NAG	F	1002	14/15	0.93	0.09	70,74,77,78	0
3	NAG	B	1001	14/15	0.93	0.07	60,64,67,68	0

6.5 Other polymers

There are no such residues in this entry.