



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 08:23 PM UTC

PDB ID : 3GXD / pdb_00003gxd
Title : Crystal structure of Apo acid-beta-glucosidase pH 4.5
Authors : Lieberman, R.L.
Deposited on : 2009-04-02
Resolution : 2.50 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

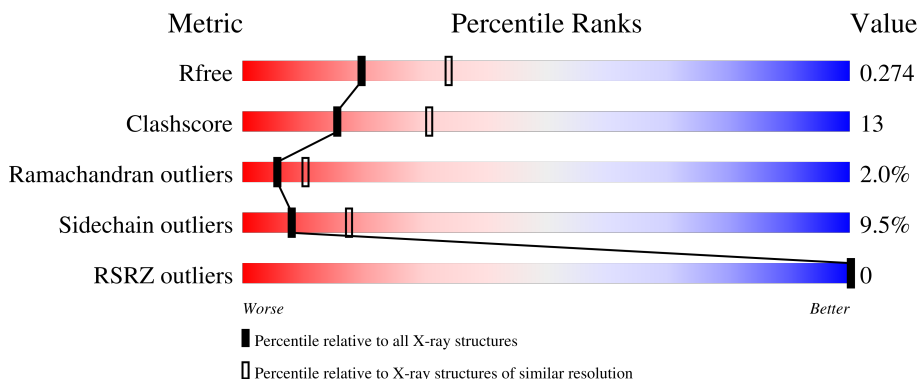
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

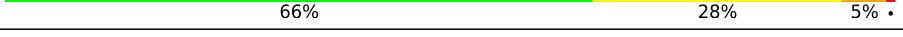
The reported resolution of this entry is 2.50 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	5829 (2.50-2.50)
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)
RSRZ outliers	180081	5833 (2.50-2.50)

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

Mol	Chain	Length	Quality of chain
1	A	497	 69% 26% 5%
1	B	497	 68% 26% 5%
1	C	497	 71% 24% 5%
1	D	497	 66% 28% 5%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard

residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	PO4	A	500	-	-	X	-
2	PO4	A	502	-	-	X	-
2	PO4	B	501	-	-	X	-
2	PO4	C	501	-	-	X	-
2	PO4	D	503	-	-	X	-
3	NAG	D	510	X	-	-	-

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 16277 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.

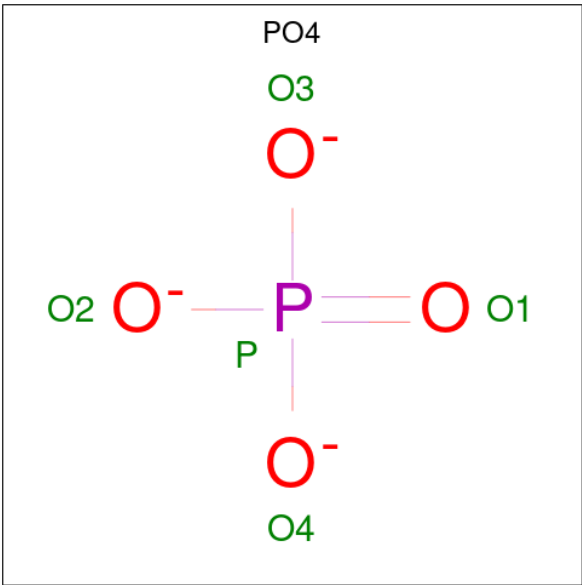
- Molecule 1 is a protein called Glucosylceramidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	497	Total	C	N	O	S	0	0	0
			3930	2532	671	711	16			
1	B	497	Total	C	N	O	S	0	0	0
			3930	2532	671	711	16			
1	C	497	Total	C	N	O	S	0	0	0
			3930	2532	671	711	16			
1	D	497	Total	C	N	O	S	0	0	0
			3930	2532	671	711	16			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	495	HIS	ARG	variant	UNP P04062
B	495	HIS	ARG	variant	UNP P04062
C	495	HIS	ARG	variant	UNP P04062
D	495	HIS	ARG	variant	UNP P04062

- Molecule 2 is PHOSPHATE ION (CCD ID: PO4) (formula: O₄P).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	P	0	0
			5	4	1		
2	A	1	Total	O	P	0	0
			5	4	1		
2	A	1	Total	O	P	0	0
			5	4	1		
2	A	1	Total	O	P	0	0
			5	4	1		
2	A	1	Total	O	P	0	0
			5	4	1		
2	A	1	Total	O	P	0	0
			5	4	1		
2	A	1	Total	O	P	0	0
			5	4	1		
2	A	1	Total	O	P	0	0
			5	4	1		
2	A	1	Total	O	P	0	0
			5	4	1		

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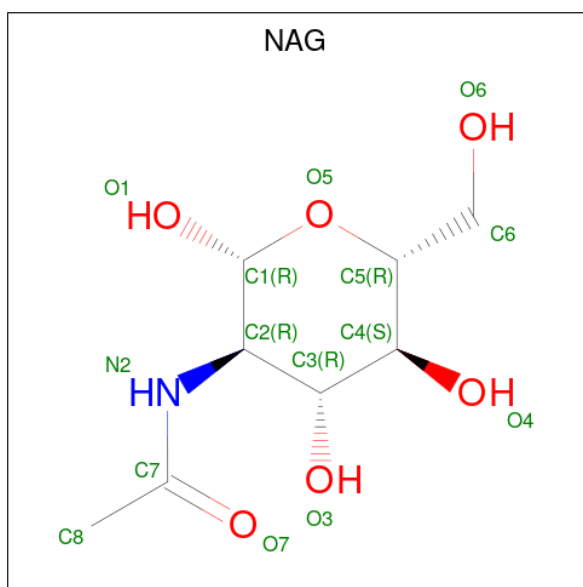
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	P	0	0
			5	4	1		
2	A	1	Total	O	P	0	0
			5	4	1		
2	B	1	Total	O	P	0	0
			5	4	1		
2	B	1	Total	O	P	0	0
			5	4	1		
2	B	1	Total	O	P	0	0
			5	4	1		
2	B	1	Total	O	P	0	0
			5	4	1		
2	B	1	Total	O	P	0	0
			5	4	1		
2	B	1	Total	O	P	0	0
			5	4	1		
2	B	1	Total	O	P	0	0
			5	4	1		
2	B	1	Total	O	P	0	0
			5	4	1		
2	C	1	Total	O	P	0	0
			5	4	1		
2	C	1	Total	O	P	0	0
			5	4	1		
2	C	1	Total	O	P	0	0
			5	4	1		
2	C	1	Total	O	P	0	0
			5	4	1		
2	C	1	Total	O	P	0	0
			5	4	1		
2	C	1	Total	O	P	0	0
			5	4	1		
2	C	1	Total	O	P	0	0
			5	4	1		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	C	1	Total	O	P	0	0
			5	4	1		
2	C	1	Total	O	P	0	0
			5	4	1		
2	C	1	Total	O	P	0	0
			5	4	1		
2	C	1	Total	O	P	0	0
			5	4	1		
2	D	1	Total	O	P	0	0
			5	4	1		
2	D	1	Total	O	P	0	0
			5	4	1		
2	D	1	Total	O	P	0	0
			5	4	1		
2	D	1	Total	O	P	0	0
			5	4	1		
2	D	1	Total	O	P	0	0
			5	4	1		
2	D	1	Total	O	P	0	0
			5	4	1		
2	D	1	Total	O	P	0	0
			5	4	1		
2	D	1	Total	O	P	0	0
			5	4	1		
2	D	1	Total	O	P	0	0
			5	4	1		

- 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	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	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		

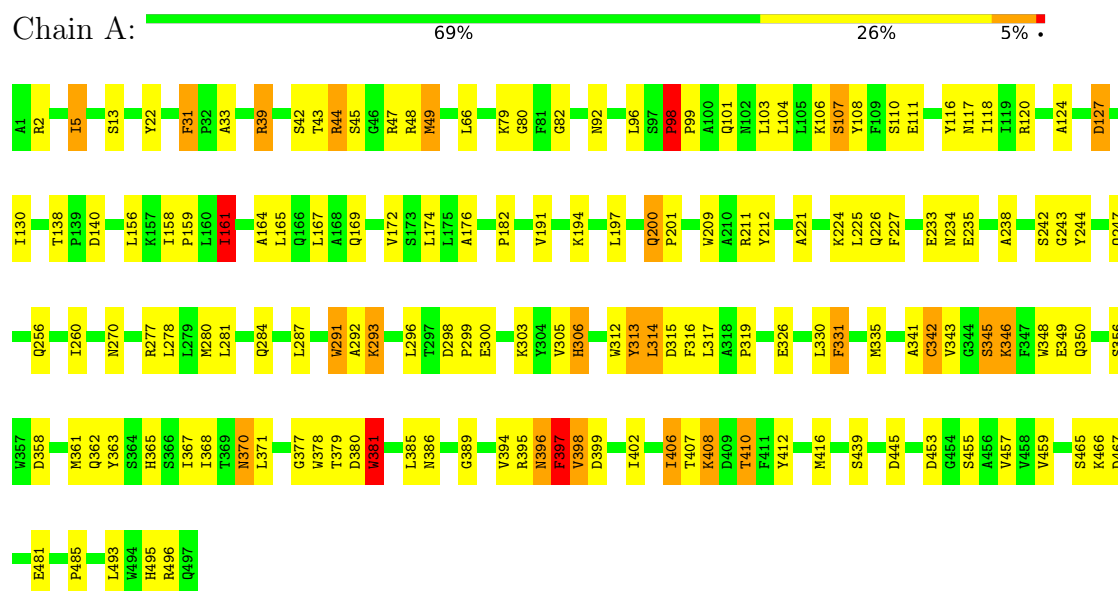
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	61	Total	O	0	0
			61	61		
4	B	43	Total	O	0	0
			43	43		
4	C	59	Total	O	0	0
			59	59		
4	D	60	Total	O	0	0
			60	60		

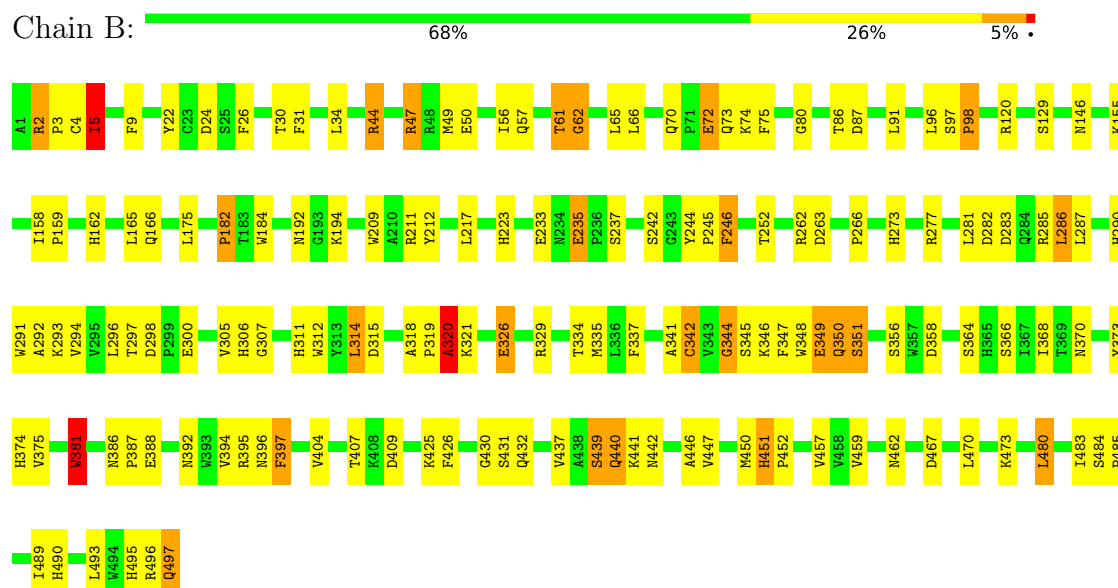
3 Residue-property plots

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: Glucosylceramidase

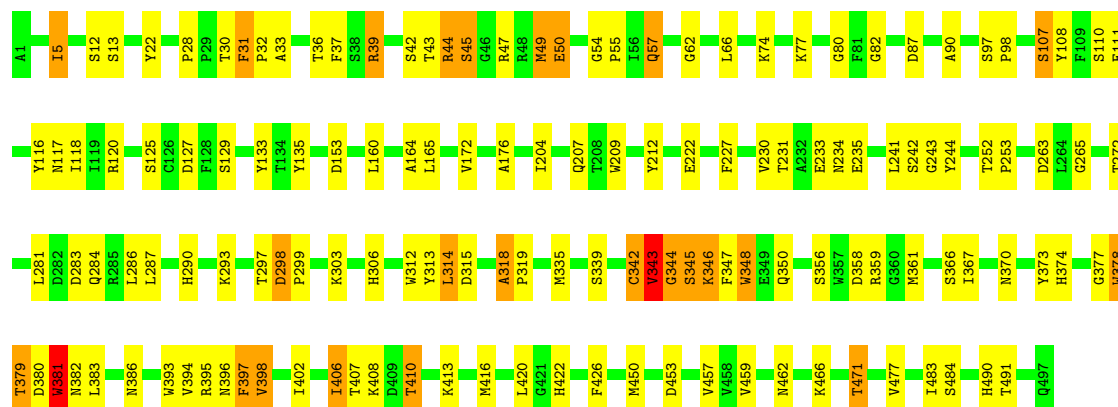


• Molecule 1: Glucosylceramidase



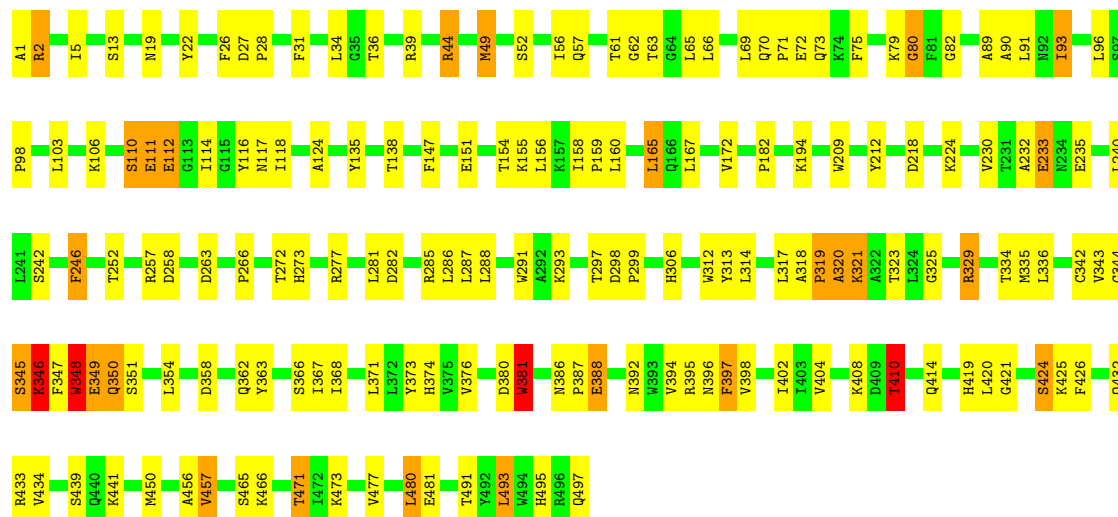
• Molecule 1: Glucosylceramidase

Chain C:  71% 24% 5%



• Molecule 1: Glucosylceramidase

Chain D:  66% 28% 5%



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	109.44Å 91.70Å 152.49Å 90.00° 111.04° 90.00°	Depositor
Resolution (Å)	42.14 – 2.50 42.14 – 2.50	Depositor EDS
% Data completeness (in resolution range)	87.7 (42.14-2.50) 87.6 (42.14-2.50)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.34 (at 2.51Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.204 , 0.275 0.205 , 0.274	Depositor DCC
R_{free} test set	4342 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å ²)	49.8	Xtriage
Anisotropy	0.084	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 25.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.450 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	16277	wwPDB-VP
Average B, all atoms (Å ²)	49.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.32% 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, PO4

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	1.06	1/4051 (0.0%)	1.19	18/5523 (0.3%)
1	B	1.06	2/4051 (0.0%)	1.21	20/5523 (0.4%)
1	C	1.07	1/4051 (0.0%)	1.20	20/5523 (0.4%)
1	D	1.09	3/4051 (0.1%)	1.21	17/5523 (0.3%)
All	All	1.07	7/16204 (0.0%)	1.20	75/22092 (0.3%)

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	B	0	1
1	C	0	1
All	All	0	2

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	410	THR	CA-CB	6.64	1.63	1.53
1	A	459	VAL	CA-C	6.15	1.60	1.52
1	D	158	ILE	CA-CB	6.07	1.57	1.54
1	C	343	VAL	CA-CB	5.84	1.62	1.54
1	D	138	THR	CA-CB	5.63	1.62	1.53
1	B	146	ASN	CG-OD1	5.07	1.33	1.23
1	B	86	THR	CA-CB	5.05	1.61	1.53

All (75) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	398	VAL	N-CA-C	9.02	121.91	108.46
1	A	342	CYS	N-CA-C	8.82	123.83	108.75
1	D	80	GLY	N-CA-C	8.80	121.89	110.45
1	D	346	LYS	N-CA-C	-8.04	102.28	113.37
1	D	397	PHE	N-CA-C	7.82	121.26	108.52
1	B	2	ARG	N-CA-C	7.53	118.25	109.60
1	D	348	TRP	CA-C-N	7.28	134.81	121.70
1	D	348	TRP	C-N-CA	7.28	134.81	121.70
1	B	5	ILE	CA-C-N	7.18	127.74	119.99
1	B	5	ILE	C-N-CA	7.18	127.74	119.99
1	D	348	TRP	N-CA-C	7.05	125.81	110.80
1	C	398	VAL	N-CA-C	7.01	120.28	108.86
1	B	451	HIS	CA-C-N	6.87	126.55	119.82
1	B	451	HIS	C-N-CA	6.87	126.55	119.82
1	A	98	PRO	CA-C-N	-6.86	111.50	119.32
1	A	98	PRO	C-N-CA	-6.86	111.50	119.32
1	C	28	PRO	CA-C-N	-6.60	113.84	120.31
1	C	28	PRO	C-N-CA	-6.60	113.84	120.31
1	B	98	PRO	CA-C-N	-6.60	112.02	119.28
1	B	98	PRO	C-N-CA	-6.60	112.02	119.28
1	A	397	PHE	N-CA-C	6.48	124.60	110.80
1	C	397	PHE	N-CA-C	6.42	124.48	110.80
1	A	164	ALA	N-CA-C	-6.41	104.37	111.36
1	A	161	ILE	N-CA-C	6.38	117.12	110.62
1	C	378	TRP	CA-CB-CG	-6.37	101.50	113.60
1	B	350	GLN	N-CA-C	-6.33	97.32	110.80
1	B	80	GLY	N-CA-C	6.30	119.07	110.69
1	D	388	GLU	N-CA-C	-6.24	105.67	113.28
1	B	342	CYS	N-CA-C	6.20	117.96	108.42
1	C	80	GLY	N-CA-C	5.83	118.30	110.43
1	C	345	SER	N-CA-C	5.81	123.18	110.80
1	D	240	LEU	N-CA-C	-5.80	104.75	112.94
1	A	80	GLY	N-CA-C	5.78	117.69	110.29
1	D	13	SER	N-CA-C	5.74	116.12	108.38
1	A	313	TYR	N-CA-C	5.72	122.99	110.80
1	D	456	ALA	N-CA-C	5.71	118.85	109.72
1	B	235	GLU	CB-CA-C	-5.68	107.17	111.20
1	A	331	PHE	CA-C-N	-5.66	114.17	120.45
1	A	331	PHE	C-N-CA	-5.66	114.17	120.45
1	C	298	ASP	CA-C-N	5.65	126.03	119.47
1	C	298	ASP	C-N-CA	5.65	126.03	119.47
1	B	397	PHE	N-CA-C	5.63	118.42	109.24
1	C	265	GLY	CA-C-N	5.58	125.04	119.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	265	GLY	C-N-CA	5.58	125.04	119.24
1	B	252	THR	N-CA-C	-5.54	102.07	110.39
1	A	104	LEU	N-CA-C	-5.53	104.65	111.40
1	C	457	VAL	N-CA-C	5.53	116.70	108.46
1	A	389	GLY	N-CA-C	-5.52	107.15	115.32
1	B	337	PHE	CA-C-N	-5.46	115.74	122.84
1	B	337	PHE	C-N-CA	-5.46	115.74	122.84
1	D	419	HIS	N-CA-C	-5.43	105.39	112.23
1	D	98	PRO	N-CA-C	5.39	117.28	110.70
1	A	306	HIS	N-CA-C	5.35	118.03	111.82
1	B	305	VAL	N-CA-C	5.31	115.84	108.84
1	A	313	TYR	CA-C-N	5.30	131.24	121.70
1	A	313	TYR	C-N-CA	5.30	131.24	121.70
1	D	368	ILE	N-CA-C	-5.29	105.55	110.53
1	D	36	THR	N-CA-C	5.24	118.10	109.72
1	B	217	LEU	N-CA-C	5.23	116.98	111.28
1	D	342	CYS	N-CA-C	5.20	116.43	108.52
1	C	62	GLY	N-CA-C	-5.20	105.09	112.37
1	C	244	TYR	CA-C-N	5.20	124.51	118.85
1	C	244	TYR	C-N-CA	5.20	124.51	118.85
1	C	477	VAL	N-CA-C	5.20	116.48	112.12
1	B	9	PHE	N-CA-C	-5.13	106.33	112.59
1	C	382	ASN	N-CA-C	5.12	117.98	110.30
1	A	396	ASN	N-CA-C	5.11	119.22	112.89
1	B	320	ALA	CA-C-N	5.10	127.07	120.44
1	B	320	ALA	C-N-CA	5.10	127.07	120.44
1	D	252	THR	N-CA-C	-5.07	102.79	110.39
1	C	164	ALA	N-CA-C	-5.05	105.69	111.14
1	D	345	SER	N-CA-C	-5.04	102.81	110.28
1	C	98	PRO	CA-C-N	-5.01	113.49	119.05
1	C	98	PRO	C-N-CA	-5.01	113.49	119.05
1	A	45	SER	N-CA-C	5.00	118.88	112.87

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	349	GLU	Peptide
1	C	344	GLY	Peptide

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3930	0	3843	115	0
1	B	3930	0	3841	103	0
1	C	3930	0	3843	107	0
1	D	3930	0	3841	115	0
2	A	80	0	0	7	0
2	B	50	0	0	6	0
2	C	65	0	0	7	0
2	D	55	0	0	5	0
3	A	14	0	13	1	0
3	B	28	0	26	0	0
3	C	14	0	13	0	0
3	D	28	0	26	0	0
4	A	61	0	0	3	0
4	B	43	0	0	3	0
4	C	59	0	0	3	0
4	D	60	0	0	4	0
All	All	16277	0	15446	422	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 13.

All (422) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:370:ASN:CB	1:C:378:TRP:HH2	1.21	1.48
1:C:370:ASN:HB3	1:C:378:TRP:CH2	1.49	1.47
1:C:370:ASN:CB	1:C:378:TRP:CH2	2.05	1.35
1:D:329:ARG:HG2	1:D:329:ARG:HH11	1.19	1.07
1:C:370:ASN:HB2	1:C:378:TRP:CH2	2.02	0.92
1:C:44:ARG:HD2	2:C:501:PO4:O1	1.70	0.91
1:B:395:ARG:HE	1:C:395:ARG:NH2	1.70	0.89
1:C:117:ASN:HA	1:C:172:VAL:HG22	1.52	0.89
1:D:26:PHE:CZ	1:D:49:MET:HE2	2.08	0.87
1:D:346:LYS:HB3	1:D:349:GLU:HG3	1.56	0.86
1:D:457:VAL:HB	1:D:493:LEU:HD23	1.58	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:5:ILE:HD12	1:B:22:TYR:CE2	2.11	0.85
1:C:380:ASP:OD1	1:C:381:TRP:N	2.10	0.85
1:C:370:ASN:HB3	1:C:378:TRP:HH2	0.66	0.82
1:D:313:TYR:OH	4:D:552:HOH:O	1.98	0.82
1:A:161:ILE:HD13	1:A:225:LEU:HD13	1.62	0.82
1:A:394:VAL:O	1:A:395:ARG:HG3	1.81	0.81
1:C:378:TRP:N	1:C:378:TRP:CD1	2.48	0.81
1:D:345:SER:C	1:D:347:PHE:H	1.86	0.81
1:A:370:ASN:HB3	1:A:378:TRP:HZ2	1.44	0.80
1:B:2:ARG:HD2	2:B:507:PO4:O3	1.82	0.80
1:B:395:ARG:HE	1:C:395:ARG:HH22	1.27	0.79
1:A:44:ARG:HD2	2:A:500:PO4:O2	1.83	0.79
1:A:284:GLN:HG3	1:A:314:LEU:HD12	1.62	0.79
1:A:5:ILE:HD12	1:A:22:TYR:CE2	2.17	0.79
1:A:380:ASP:OD1	1:A:381:TRP:N	2.17	0.77
1:D:80:GLY:HA3	1:D:117:ASN:HD21	1.48	0.77
1:B:285:ARG:HH21	1:B:318:ALA:HB3	1.47	0.77
1:C:284:GLN:HG3	1:C:314:LEU:HD12	1.66	0.77
1:C:370:ASN:CG	1:C:378:TRP:CH2	2.63	0.75
1:B:66:LEU:HD11	1:B:473:LYS:HB2	1.68	0.74
1:D:114:ILE:O	1:D:424:SER:HB2	1.86	0.74
1:D:246:PHE:HD2	1:D:394:VAL:HG11	1.53	0.73
1:D:26:PHE:HZ	1:D:49:MET:HE2	1.54	0.73
1:D:312:TRP:CD1	1:D:314:LEU:HD23	2.24	0.72
1:D:394:VAL:O	1:D:395:ARG:HB2	1.90	0.72
1:A:31:PHE:HB2	1:A:495:HIS:CE1	2.24	0.72
1:A:395:ARG:NH2	1:D:395:ARG:HH11	1.86	0.72
1:B:285:ARG:NH2	1:B:318:ALA:HB3	2.04	0.72
1:D:106:LYS:HG2	1:D:167:LEU:HD22	1.71	0.72
1:B:74:LYS:HB3	1:B:432:GLN:NE2	2.06	0.71
1:D:351:SER:CB	1:D:397:PHE:HB3	2.20	0.71
1:A:341:ALA:HB3	1:A:380:ASP:HA	1.73	0.71
1:D:93:ILE:HD11	1:D:160:LEU:HD22	1.72	0.70
1:D:329:ARG:HH11	1:D:329:ARG:CG	2.01	0.70
1:D:66:LEU:HD11	1:D:473:LYS:HB2	1.72	0.70
1:D:345:SER:C	1:D:347:PHE:N	2.49	0.70
1:A:453:ASP:OD1	1:A:453:ASP:C	2.35	0.70
1:C:377:GLY:C	1:C:378:TRP:CD1	2.70	0.70
1:A:117:ASN:HA	1:A:172:VAL:HG22	1.75	0.68
1:D:334:THR:HG22	4:D:554:HOH:O	1.92	0.68
1:C:312:TRP:HZ2	1:C:378:TRP:CE3	2.11	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:348:TRP:CH2	1:B:242:SER:O	2.46	0.68
1:D:386:ASN:HB2	1:D:387:PRO:CD	2.24	0.67
1:D:312:TRP:HD1	1:D:314:LEU:HD23	1.56	0.67
1:A:161:ILE:HD11	1:A:225:LEU:HD22	1.75	0.67
1:C:370:ASN:HB3	1:C:378:TRP:CZ2	2.24	0.67
1:A:348:TRP:HH2	1:B:242:SER:O	1.78	0.66
1:B:441:LYS:NZ	4:B:549:HOH:O	2.23	0.66
1:A:312:TRP:CZ2	1:A:378:TRP:CD1	2.83	0.66
1:B:307:GLY:HA2	1:B:334:THR:HG22	1.76	0.66
1:B:346:LYS:H	1:B:347:PHE:HA	1.62	0.65
1:D:344:GLY:HA2	1:D:398:VAL:HG12	1.77	0.65
1:D:329:ARG:HG2	1:D:329:ARG:NH1	1.98	0.65
1:C:342:CYS:O	1:C:343:VAL:HG22	1.96	0.65
1:B:246:PHE:HD2	1:B:394:VAL:HG11	1.61	0.64
1:A:176:ALA:HB2	1:A:227:PHE:CE2	2.32	0.64
1:B:467:ASP:OD1	1:B:485:PRO:HA	1.97	0.64
1:A:312:TRP:HZ2	1:A:378:TRP:NE1	1.94	0.64
1:D:246:PHE:CD2	1:D:394:VAL:HG11	2.34	0.63
1:A:370:ASN:HB3	1:A:378:TRP:CZ2	2.31	0.63
1:D:348:TRP:H	1:D:349:GLU:HB2	1.63	0.63
1:A:408:LYS:O	1:A:410:THR:HG23	1.97	0.63
1:A:396:ASN:O	1:A:398:VAL:N	2.30	0.63
1:A:377:GLY:C	1:A:378:TRP:CE3	2.77	0.63
1:C:107:SER:OG	1:C:413:LYS:HE3	1.99	0.63
1:A:406:ILE:HD13	1:A:406:ILE:H	1.64	0.63
1:C:125:SER:HB3	1:C:133:TYR:CE2	2.33	0.62
1:B:155:LYS:NZ	4:B:546:HOH:O	2.16	0.62
1:D:345:SER:HB2	1:D:349:GLU:O	1.99	0.62
1:C:5:ILE:HD12	1:C:22:TYR:CE2	2.34	0.62
1:D:354:LEU:HA	1:D:414:GLN:OE1	1.99	0.62
1:C:207:GLN:NE2	1:C:263:ASP:OD1	2.28	0.62
1:D:56:ILE:HG12	1:D:480:LEU:HD22	1.81	0.62
1:C:312:TRP:CZ2	1:C:378:TRP:CE3	2.87	0.62
1:D:89:ALA:O	1:D:93:ILE:HG23	1.99	0.62
1:B:61:THR:O	1:B:62:GLY:O	2.17	0.61
1:C:39:ARG:HG3	1:C:39:ARG:HH11	1.65	0.61
1:C:344:GLY:HA3	1:C:398:VAL:HA	1.82	0.61
1:D:386:ASN:HB2	1:D:387:PRO:HD2	1.82	0.61
1:D:26:PHE:CG	1:D:425:LYS:HE2	2.35	0.61
1:C:370:ASN:CG	1:C:378:TRP:HH2	1.94	0.61
1:A:31:PHE:HB2	1:A:495:HIS:HE1	1.63	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:26:PHE:CD1	1:D:425:LYS:HE2	2.36	0.61
1:A:82:GLY:HA3	1:A:118:ILE:O	2.01	0.61
1:D:56:ILE:HG21	1:D:477:VAL:HG12	1.82	0.61
1:A:293:LYS:HE2	2:A:505:PO4:O2	2.01	0.60
1:B:319:PRO:O	1:B:320:ALA:HB3	2.00	0.60
1:B:326:GLU:OE1	1:B:329:ARG:HD2	2.01	0.60
1:D:285:ARG:CZ	1:D:318:ALA:HB3	2.31	0.60
1:C:408:LYS:O	1:C:410:THR:HG23	2.01	0.60
1:D:351:SER:OG	1:D:397:PHE:HB3	2.02	0.60
1:A:5:ILE:HD12	1:A:22:TYR:CZ	2.37	0.60
1:D:319:PRO:O	1:D:320:ALA:HB3	2.02	0.60
1:A:120:ARG:HB2	1:A:379:THR:HG21	1.83	0.59
1:A:312:TRP:HZ2	1:A:378:TRP:CD1	2.20	0.59
1:C:312:TRP:HZ2	1:C:378:TRP:CZ3	2.21	0.59
1:D:257:ARG:NH2	1:D:258:ASP:OD2	2.35	0.59
1:D:116:TYR:OH	1:D:420:LEU:HD13	2.03	0.59
1:C:306:HIS:ND1	2:C:504:PO4:O4	2.35	0.59
1:C:314:LEU:O	1:C:315:ASP:HB2	2.02	0.58
1:A:5:ILE:HD13	3:A:513:NAG:H62	1.85	0.58
1:B:451:HIS:HB3	1:B:452:PRO:HD2	1.85	0.58
1:C:176:ALA:HB2	1:C:227:PHE:CE2	2.38	0.58
1:C:74:LYS:NZ	1:C:450:MET:HE1	2.18	0.57
1:A:395:ARG:HH22	1:D:395:ARG:HH11	1.52	0.57
1:D:72:GLU:HB2	4:D:527:HOH:O	2.04	0.57
1:A:365:HIS:HD2	1:A:445:ASP:OD2	1.88	0.57
1:C:31:PHE:CD1	1:C:31:PHE:N	2.73	0.57
1:D:320:ALA:HA	1:D:323:THR:OG1	2.04	0.57
1:A:197:LEU:HD11	1:A:209:TRP:CD1	2.39	0.56
1:C:386:ASN:C	1:C:386:ASN:OD1	2.48	0.56
1:C:453:ASP:OD1	1:C:453:ASP:C	2.46	0.56
1:A:312:TRP:HZ2	1:A:378:TRP:HE1	1.52	0.56
1:B:26:PHE:CG	1:B:425:LYS:HE2	2.40	0.56
1:C:49:MET:HE3	1:C:422:HIS:CE1	2.40	0.56
1:D:345:SER:CB	1:D:349:GLU:O	2.54	0.56
1:D:44:ARG:NH2	2:D:503:PO4:O2	2.38	0.56
1:D:348:TRP:CE3	1:D:349:GLU:HG2	2.41	0.56
1:A:467:ASP:OD1	1:A:485:PRO:HA	2.06	0.55
1:B:26:PHE:CD1	1:B:425:LYS:HE2	2.41	0.55
1:B:462:ASN:HB2	1:B:484:SER:OG	2.06	0.55
1:A:348:TRP:H	1:A:348:TRP:CD1	2.22	0.55
1:A:312:TRP:HH2	1:A:367:ILE:HG13	1.72	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:496:ARG:HD3	4:A:557:HOH:O	2.06	0.55
1:A:277:ARG:HD2	1:A:306:HIS:CG	2.41	0.55
1:A:394:VAL:O	1:A:395:ARG:CG	2.54	0.55
1:B:65:LEU:HD12	1:B:440:GLN:HG3	1.90	0.54
1:D:5:ILE:HG12	1:D:22:TYR:CE2	2.41	0.54
1:D:408:LYS:HB2	1:D:410:THR:HG23	1.89	0.54
1:D:39:ARG:O	1:D:39:ARG:HD3	2.06	0.54
1:C:348:TRP:H	1:C:348:TRP:CD1	2.24	0.54
1:B:349:GLU:HA	1:B:350:GLN:HB2	1.89	0.54
1:A:161:ILE:HD13	1:A:225:LEU:CD1	2.35	0.54
1:A:194:LYS:HB2	1:A:242:SER:HA	1.89	0.54
1:D:93:ILE:HD11	1:D:160:LEU:CD2	2.37	0.54
1:A:358:ASP:HA	1:A:361:MET:HE2	1.91	0.53
1:C:370:ASN:CG	1:C:378:TRP:CZ3	2.87	0.53
1:B:47:ARG:HG2	1:B:50:GLU:OE1	2.08	0.53
1:C:373:TYR:O	1:C:374:HIS:HB2	2.08	0.53
1:B:373:TYR:C	1:B:374:HIS:CD2	2.87	0.53
1:D:1:ALA:HB2	1:D:27:ASP:OD1	2.09	0.53
1:C:31:PHE:H	1:C:31:PHE:HD1	1.56	0.53
1:B:44:ARG:HB3	2:B:501:PO4:O2	2.08	0.52
1:B:72:GLU:OE1	1:B:72:GLU:HA	2.03	0.52
1:C:176:ALA:HB3	1:C:230:VAL:HG12	1.91	0.52
1:A:106:LYS:O	1:A:110:SER:HB3	2.08	0.52
1:A:371:LEU:HG	1:A:378:TRP:CH2	2.45	0.52
1:A:303:LYS:NZ	4:A:542:HOH:O	2.43	0.52
1:A:408:LYS:HB3	1:A:410:THR:HG23	1.91	0.52
1:B:87:ASP:OD2	1:B:129:SER:OG	2.24	0.52
1:C:39:ARG:HG3	1:C:39:ARG:NH1	2.25	0.52
1:C:108:TYR:CE1	1:C:402:ILE:HD12	2.45	0.52
1:A:161:ILE:CD1	1:A:225:LEU:HD13	2.36	0.52
1:C:44:ARG:NH1	2:C:501:PO4:O2	2.42	0.52
1:B:349:GLU:HA	1:B:350:GLN:CB	2.40	0.51
1:C:66:LEU:HD13	1:C:471:THR:HB	1.91	0.51
1:C:116:TYR:OH	1:C:420:LEU:HD13	2.10	0.51
1:C:135:TYR:HE2	1:C:153:ASP:OD2	1.93	0.51
1:C:243:GLY:O	1:D:348:TRP:CZ3	2.63	0.51
1:A:312:TRP:C	1:A:315:ASP:OD1	2.54	0.51
1:C:370:ASN:OD1	1:C:378:TRP:CZ3	2.62	0.51
1:A:395:ARG:HD3	1:B:347:PHE:CE2	2.46	0.51
1:B:326:GLU:OE1	1:B:326:GLU:HA	2.09	0.51
1:B:56:ILE:HG12	1:B:480:LEU:HD22	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:293:LYS:O	1:B:297:THR:HG23	2.11	0.51
1:D:80:GLY:HA3	1:D:117:ASN:ND2	2.23	0.51
1:D:321:LYS:O	1:D:325:GLY:HA3	2.10	0.51
1:C:358:ASP:HA	1:C:361:MET:HE2	1.91	0.51
1:D:433:ARG:HG2	1:D:434:VAL:N	2.25	0.51
1:A:243:GLY:O	1:B:348:TRP:NE1	2.44	0.51
1:C:243:GLY:C	1:D:348:TRP:CZ3	2.89	0.50
1:D:285:ARG:NH2	1:D:318:ALA:HB3	2.26	0.50
1:D:287:LEU:HB3	1:D:291:TRP:CD1	2.47	0.50
1:D:351:SER:HB3	1:D:397:PHE:HB3	1.90	0.50
1:B:65:LEU:HD13	1:B:442:ASN:HB3	1.93	0.50
1:C:408:LYS:HB3	1:C:410:THR:HG23	1.93	0.50
1:A:103:LEU:O	1:A:107:SER:HB2	2.12	0.50
1:B:312:TRP:HD1	1:B:314:LEU:CD1	2.24	0.50
1:B:439:SER:OG	1:B:440:GLN:HG2	2.12	0.50
1:D:69:LEU:O	1:D:71:PRO:HD3	2.12	0.50
1:D:346:LYS:CB	1:D:349:GLU:HG3	2.35	0.50
1:A:378:TRP:CE3	1:A:378:TRP:N	2.80	0.50
1:C:293:LYS:O	1:C:297:THR:HG23	2.11	0.50
1:C:370:ASN:OD1	1:C:378:TRP:CH2	2.64	0.50
1:A:127:ASP:OD1	1:A:127:ASP:N	2.43	0.50
1:B:386:ASN:HB2	1:B:387:PRO:CD	2.42	0.50
1:D:293:LYS:O	1:D:297:THR:HG23	2.12	0.50
1:C:235:GLU:HA	1:C:283:ASP:OD2	2.12	0.49
1:C:39:ARG:HH11	1:C:39:ARG:CG	2.25	0.49
1:A:234:ASN:O	1:A:235:GLU:C	2.54	0.49
1:C:312:TRP:CZ2	1:C:378:TRP:CZ3	3.00	0.49
1:C:359:ARG:CB	1:C:416:MET:HE2	2.42	0.49
1:D:363:TYR:O	1:D:367:ILE:HG13	2.13	0.49
1:D:381:TRP:CE3	1:D:381:TRP:HA	2.47	0.49
1:B:300:GLU:OE1	1:B:300:GLU:HA	2.13	0.49
1:C:359:ARG:HB3	1:C:416:MET:HE2	1.94	0.49
1:A:221:ALA:O	1:A:224:LYS:N	2.40	0.49
1:B:446:ALA:HA	1:B:459:VAL:O	2.12	0.49
1:D:312:TRP:HD1	1:D:314:LEU:CD2	2.24	0.49
1:D:209:TRP:O	1:D:212:TYR:HB3	2.13	0.49
1:D:298:ASP:OD1	1:D:298:ASP:C	2.56	0.49
1:B:351:SER:CB	1:B:397:PHE:HB3	2.43	0.48
1:A:280:MET:HG2	1:A:305:VAL:HG11	1.95	0.48
1:C:283:ASP:HB3	1:C:287:LEU:HD12	1.96	0.48
1:A:42:SER:HA	1:A:47:ARG:O	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:209:TRP:O	1:B:212:TYR:HB3	2.13	0.48
1:A:39:ARG:HG3	1:A:39:ARG:HH11	1.77	0.48
1:A:343:VAL:HG12	1:A:363:TYR:HE1	1.77	0.48
1:B:341:ALA:O	1:B:342:CYS:HB3	2.13	0.48
1:D:319:PRO:O	1:D:320:ALA:CB	2.61	0.48
1:C:298:ASP:HA	1:C:299:PRO:HD2	1.74	0.48
1:C:312:TRP:HH2	1:C:367:ILE:HG13	1.78	0.48
1:A:277:ARG:HH21	2:A:502:PO4:P	2.37	0.48
1:A:395:ARG:HH22	1:D:395:ARG:NH1	2.12	0.48
1:B:346:LYS:N	1:B:347:PHE:HA	2.29	0.48
1:A:92:ASN:ND2	1:A:385:LEU:HA	2.29	0.47
1:D:44:ARG:HH22	2:D:503:PO4:P	2.36	0.47
1:C:30:THR:OG1	4:C:551:HOH:O	2.20	0.47
1:D:19:ASN:O	1:D:103:LEU:HD12	2.14	0.47
1:D:65:LEU:HD12	1:D:66:LEU:H	1.79	0.47
1:A:191:VAL:O	1:A:247:GLN:HA	2.13	0.47
1:A:481:GLU:HA	1:A:481:GLU:OE1	2.15	0.47
1:B:392:ASN:OD1	1:B:395:ARG:N	2.47	0.47
2:D:508:PO4:P	4:D:542:HOH:O	2.73	0.47
1:A:165:LEU:HD22	1:A:172:VAL:HB	1.97	0.47
1:B:70:GLN:C	1:B:72:GLU:H	2.22	0.47
1:A:238:ALA:HB1	1:A:244:TYR:CE2	2.50	0.47
1:B:211:ARG:HD2	4:B:539:HOH:O	2.14	0.47
1:A:368:ILE:HG21	1:A:445:ASP:HB3	1.97	0.47
1:B:329:ARG:HH22	2:B:504:PO4:P	2.38	0.47
1:C:13:SER:HB2	1:C:44:ARG:HG2	1.96	0.47
1:B:49:MET:HE1	1:B:426:PHE:CE1	2.50	0.47
1:A:39:ARG:HG3	1:A:39:ARG:NH1	2.30	0.46
1:A:399:ASP:CG	1:A:416:MET:HE1	2.40	0.46
1:B:483:ILE:O	1:B:490:HIS:HE1	1.98	0.46
1:C:49:MET:HE2	1:C:49:MET:HB3	1.74	0.46
1:C:234:ASN:O	1:C:235:GLU:C	2.57	0.46
1:A:106:LYS:HG2	1:A:167:LEU:HD22	1.96	0.46
1:C:82:GLY:HA3	1:C:118:ILE:O	2.15	0.46
1:D:233:GLU:O	1:D:282:ASP:HB3	2.16	0.46
1:B:70:GLN:C	1:B:72:GLU:N	2.73	0.46
1:D:159:PRO:HG3	2:D:505:PO4:O4	2.15	0.46
1:B:277:ARG:HH11	1:B:306:HIS:CG	2.33	0.46
1:B:298:ASP:OD1	1:B:300:GLU:HB2	2.16	0.46
1:B:496:ARG:O	1:B:497:GLN:HB3	2.16	0.46
1:C:406:ILE:HG12	1:C:407:THR:N	2.31	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:406:ILE:HD13	1:A:406:ILE:N	2.31	0.46
1:B:31:PHE:HB2	1:B:495:HIS:CE1	2.51	0.46
1:B:277:ARG:NH1	1:B:306:HIS:CE1	2.83	0.46
1:C:348:TRP:CH2	1:D:242:SER:O	2.69	0.46
1:A:49:MET:HE2	1:A:49:MET:HB3	1.61	0.45
1:A:319:PRO:HD3	1:B:286:LEU:HD21	1.99	0.45
1:A:346:LYS:HZ1	1:A:362:GLN:HE22	1.63	0.45
1:B:159:PRO:HA	2:B:499:PO4:O2	2.16	0.45
1:B:349:GLU:CA	1:B:350:GLN:HB2	2.46	0.45
1:B:246:PHE:CD2	1:B:394:VAL:HG11	2.48	0.45
1:B:296:LEU:HD23	1:B:296:LEU:HA	1.80	0.45
1:B:3:PRO:O	1:B:22:TYR:OH	2.30	0.45
1:A:316:PHE:CD1	1:A:317:LEU:HD13	2.51	0.45
1:C:252:THR:HB	1:C:253:PRO:HD2	1.97	0.45
1:D:421:GLY:HA2	1:D:424:SER:OG	2.16	0.45
1:A:386:ASN:OD1	1:A:386:ASN:C	2.59	0.45
1:B:96:LEU:HD21	1:B:404:VAL:HG13	1.98	0.45
1:B:319:PRO:O	1:B:320:ALA:CB	2.62	0.45
1:C:36:THR:HG23	1:C:54:GLY:O	2.16	0.45
1:D:218:ASP:OD1	1:D:273:HIS:NE2	2.50	0.45
1:B:4:CYS:HA	1:B:24:ASP:HB3	1.99	0.45
1:B:237:SER:OG	1:B:283:ASP:OD2	2.29	0.45
1:B:287:LEU:HB3	1:B:291:TRP:CD1	2.52	0.45
1:C:43:THR:HB	4:C:552:HOH:O	2.15	0.45
1:C:348:TRP:CD1	1:C:348:TRP:N	2.83	0.45
1:D:350:GLN:CD	1:D:350:GLN:H	2.24	0.45
1:B:70:GLN:O	1:B:72:GLU:N	2.50	0.45
1:C:12:SER:OG	2:C:500:PO4:O3	2.34	0.45
1:A:277:ARG:HD3	4:A:515:HOH:O	2.17	0.44
1:B:285:ARG:CZ	1:B:318:ALA:HB3	2.47	0.44
1:C:47:ARG:HD3	1:C:50:GLU:OE1	2.17	0.44
1:D:135:TYR:O	1:D:147:PHE:HA	2.17	0.44
1:D:277:ARG:NH1	1:D:306:HIS:CE1	2.85	0.44
1:B:381:TRP:HA	1:B:381:TRP:CE3	2.52	0.44
1:D:471:THR:HG23	1:D:481:GLU:HG2	1.99	0.44
1:A:98:PRO:O	1:A:99:PRO:C	2.57	0.44
1:A:465:SER:OG	1:A:466:LYS:HD2	2.18	0.44
1:D:392:ASN:OD1	1:D:394:VAL:HG12	2.17	0.44
1:D:263:ASP:O	1:D:266:PRO:HD2	2.17	0.44
1:D:66:LEU:HB3	1:D:439:SER:HB3	1.98	0.44
1:C:32:PRO:HB2	1:C:36:THR:HB	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:344:GLY:H	1:C:398:VAL:HG12	1.83	0.44
1:A:43:THR:O	1:A:48:ARG:NH1	2.41	0.44
1:A:256:GLN:CD	1:A:291:TRP:HZ3	2.26	0.44
1:A:406:ILE:HG12	1:A:407:THR:N	2.33	0.44
1:C:37:PHE:CD1	1:C:37:PHE:C	2.96	0.44
1:C:462:ASN:HB2	1:C:484:SER:OG	2.18	0.44
1:D:348:TRP:N	1:D:349:GLU:HB2	2.30	0.44
1:A:82:GLY:HA2	1:A:116:TYR:CD1	2.53	0.44
1:A:158:ILE:HB	1:A:159:PRO:HD3	2.00	0.44
1:C:5:ILE:HD12	1:C:22:TYR:CZ	2.53	0.44
1:C:396:ASN:O	1:C:398:VAL:N	2.45	0.44
1:D:408:LYS:CB	1:D:410:THR:HG23	2.48	0.44
1:A:66:LEU:HB3	1:A:439:SER:HB3	2.00	0.43
1:A:260:ILE:HG12	1:A:278:LEU:HD21	2.00	0.43
1:C:120:ARG:HD2	1:C:379:THR:HG21	2.00	0.43
1:A:348:TRP:CG	1:B:245:PRO:HG3	2.53	0.43
1:A:346:LYS:O	1:A:349:GLU:HB2	2.18	0.43
1:C:55:PRO:HB2	1:C:57:GLN:HG3	2.00	0.43
1:B:451:HIS:HB3	1:B:452:PRO:CD	2.49	0.43
1:D:39:ARG:HD3	1:D:39:ARG:C	2.43	0.43
1:B:158:ILE:HB	1:B:159:PRO:HD3	2.00	0.43
1:C:74:LYS:HZ1	1:C:450:MET:HE1	1.82	0.43
1:D:75:PHE:O	1:D:432:GLN:NE2	2.38	0.43
1:B:312:TRP:CD1	1:B:314:LEU:HD13	2.53	0.43
1:B:345:SER:HA	1:B:349:GLU:O	2.19	0.43
1:C:44:ARG:HH11	2:C:501:PO4:P	2.42	0.43
1:D:165:LEU:HD22	1:D:172:VAL:HB	2.01	0.43
1:A:313:TYR:N	1:A:315:ASP:OD1	2.52	0.43
1:B:244:TYR:HA	1:B:245:PRO:HD3	1.84	0.43
1:B:346:LYS:HB2	1:B:349:GLU:H	1.84	0.43
1:C:127:ASP:HA	1:C:393:TRP:CD1	2.54	0.43
1:C:129:SER:HB3	4:C:546:HOH:O	2.18	0.43
1:A:108:TYR:CE1	1:A:402:ILE:HD12	2.54	0.43
1:A:130:ILE:HD11	1:D:151:GLU:HB2	2.01	0.43
1:B:192:ASN:HB2	1:B:244:TYR:O	2.19	0.43
1:B:349:GLU:HA	1:B:350:GLN:CG	2.49	0.43
1:C:42:SER:HA	1:C:47:ARG:O	2.18	0.43
1:C:242:SER:O	1:D:348:TRP:HH2	2.02	0.43
1:A:402:ILE:HA	1:A:412:TYR:O	2.19	0.43
1:A:298:ASP:HA	1:A:299:PRO:HD2	1.93	0.42
1:D:96:LEU:HD21	1:D:404:VAL:HG13	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:70:GLN:CD	1:B:437:VAL:HG23	2.44	0.42
1:C:290:HIS:ND1	2:C:505:PO4:O4	2.51	0.42
1:A:395:ARG:NH2	1:D:395:ARG:NH1	2.60	0.42
1:C:426:PHE:CD1	1:C:491:THR:HG21	2.54	0.42
1:D:246:PHE:CE2	1:D:396:ASN:HB2	2.53	0.42
1:D:298:ASP:HA	1:D:299:PRO:HD2	1.69	0.42
1:D:471:THR:HA	1:D:480:LEU:O	2.18	0.42
1:A:370:ASN:CB	1:A:378:TRP:HZ2	2.24	0.42
1:C:377:GLY:C	1:C:378:TRP:CG	2.91	0.42
1:D:426:PHE:CD1	1:D:491:THR:HG21	2.54	0.42
1:B:44:ARG:CD	2:B:501:PO4:O4	2.68	0.42
1:A:277:ARG:NH2	2:A:502:PO4:O1	2.49	0.42
1:A:161:ILE:HD11	1:A:174:LEU:HD11	2.01	0.42
1:D:232:ALA:O	1:D:233:GLU:HB2	2.20	0.42
1:A:44:ARG:CD	2:A:500:PO4:O2	2.61	0.42
1:C:312:TRP:CH2	1:C:367:ILE:HG13	2.54	0.42
1:C:318:ALA:HB3	1:C:319:PRO:HA	2.01	0.42
1:B:290:HIS:O	1:B:294:VAL:HG23	2.19	0.42
1:D:386:ASN:CB	1:D:387:PRO:CD	2.92	0.42
1:C:74:LYS:HZ2	1:C:450:MET:HE1	1.85	0.42
1:A:79:LYS:NZ	2:A:502:PO4:O3	2.53	0.41
1:A:209:TRP:HA	1:A:209:TRP:CE3	2.55	0.41
1:C:209:TRP:CZ3	1:C:212:TYR:CD2	3.08	0.41
1:D:312:TRP:CE3	1:D:312:TRP:HA	2.54	0.41
1:D:371:LEU:HD23	1:D:371:LEU:HA	1.95	0.41
1:A:270:ASN:O	1:A:270:ASN:CG	2.63	0.41
1:D:44:ARG:NH1	2:D:503:PO4:O2	2.53	0.41
1:D:90:ALA:HB1	1:D:156:LEU:HB3	2.02	0.41
1:D:286:LEU:C	1:D:288:LEU:H	2.28	0.41
1:A:96:LEU:O	1:A:101:GLN:NE2	2.48	0.41
1:B:120:ARG:HA	1:B:175:LEU:O	2.20	0.41
1:D:106:LYS:O	1:D:110:SER:HB3	2.20	0.41
1:A:200:GLN:O	1:A:201:PRO:C	2.63	0.41
1:C:393:TRP:CD2	1:C:394:VAL:HG23	2.56	0.41
1:A:209:TRP:CZ3	1:A:212:TYR:CD2	3.09	0.41
1:B:75:PHE:O	1:B:432:GLN:NE2	2.54	0.41
1:B:285:ARG:NE	1:B:318:ALA:HB3	2.36	0.41
1:B:344:GLY:CA	1:B:345:SER:HB3	2.49	0.41
1:C:339:SER:O	1:C:379:THR:HG22	2.20	0.41
1:B:306:HIS:O	1:B:306:HIS:ND1	2.54	0.41
1:B:430:GLY:O	1:B:431:SER:C	2.62	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:45:SER:HB3	2:C:501:PO4:O4	2.20	0.41
1:C:90:ALA:CB	1:C:160:LEU:HD12	2.51	0.41
1:D:28:PRO:HA	1:D:111:GLU:OE1	2.21	0.41
1:A:140:ASP:OD1	1:A:140:ASP:N	2.54	0.41
1:A:326:GLU:HA	1:A:326:GLU:OE1	2.20	0.41
1:A:395:ARG:O	1:A:397:PHE:HD2	2.03	0.41
1:B:162:HIS:CE1	1:B:223:HIS:O	2.74	0.41
1:B:298:ASP:OD1	1:B:298:ASP:C	2.64	0.41
1:C:347:PHE:CD1	1:C:348:TRP:HD1	2.39	0.41
1:C:459:VAL:HA	1:C:490:HIS:O	2.20	0.41
1:A:98:PRO:HB2	1:A:99:PRO:HD3	2.03	0.41
1:A:330:LEU:HB3	1:A:331:PHE:CE1	2.56	0.41
1:A:348:TRP:CB	1:B:245:PRO:HG3	2.51	0.41
1:B:22:TYR:C	1:B:22:TYR:CD2	2.99	0.41
1:B:184:TRP:CD1	1:B:184:TRP:H	2.39	0.41
1:B:263:ASP:C	1:B:266:PRO:HD2	2.46	0.41
1:B:282:ASP:OD1	1:B:311:HIS:NE2	2.46	0.41
1:B:312:TRP:HD1	1:B:314:LEU:HD13	1.85	0.41
1:B:370:ASN:O	1:B:375:VAL:HB	2.21	0.41
1:C:252:THR:O	1:C:253:PRO:C	2.64	0.41
1:C:383:LEU:HA	1:C:383:LEU:HD23	1.83	0.41
1:D:362:GLN:O	1:D:366:SER:HB3	2.20	0.41
1:D:380:ASP:OD1	1:D:381:TRP:N	2.54	0.41
1:A:44:ARG:HH11	2:A:500:PO4:P	2.43	0.41
1:A:243:GLY:O	1:B:348:TRP:CD1	2.74	0.41
1:D:82:GLY:HA3	1:D:118:ILE:HB	2.03	0.41
1:A:292:ALA:HB1	1:A:296:LEU:HD12	2.02	0.40
1:D:89:ALA:O	1:D:90:ALA:C	2.63	0.40
1:B:97:SER:O	1:B:98:PRO:C	2.62	0.40
1:B:292:ALA:O	1:B:296:LEU:HB2	2.21	0.40
1:C:342:CYS:C	1:C:343:VAL:HG22	2.47	0.40
1:D:70:GLN:O	1:D:72:GLU:N	2.54	0.40
1:D:112:GLU:H	1:D:112:GLU:HG3	1.59	0.40
1:D:263:ASP:C	1:D:266:PRO:HD2	2.46	0.40
1:D:347:PHE:O	1:D:348:TRP:HB3	2.21	0.40
1:B:273:HIS:ND1	2:B:506:PO4:O2	2.36	0.40
1:C:87:ASP:HB2	1:C:129:SER:HA	2.03	0.40
1:C:393:TRP:O	1:C:393:TRP:CE3	2.74	0.40
1:A:287:LEU:HB3	1:A:291:TRP:CD1	2.55	0.40
1:C:312:TRP:CZ2	1:C:378:TRP:HE3	2.37	0.40
1:D:336:LEU:O	1:D:376:VAL:HG22	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:373:TYR:C	1:D:374:HIS:CG	2.98	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	495/497 (100%)	446 (90%)	41 (8%)	8 (2%)	7	14
1	B	495/497 (100%)	456 (92%)	30 (6%)	9 (2%)	6	12
1	C	495/497 (100%)	452 (91%)	31 (6%)	12 (2%)	4	8
1	D	495/497 (100%)	432 (87%)	52 (10%)	11 (2%)	5	9
All	All	1980/1988 (100%)	1786 (90%)	154 (8%)	40 (2%)	6	10

All (40) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	33	ALA
1	A	345	SER
1	A	397	PHE
1	B	233	GLU
1	C	314	LEU
1	C	318	ALA
1	C	397	PHE
1	D	62	GLY
1	D	348	TRP
1	D	381	TRP
1	A	346	LYS
1	A	381	TRP
1	B	62	GLY
1	B	320	ALA

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Mol	Chain	Res	Type
1	B	344	GLY
1	B	381	TRP
1	C	33	ALA
1	C	313	TYR
1	C	346	LYS
1	C	381	TRP
1	D	63	THR
1	D	233	GLU
1	D	320	ALA
1	A	124	ALA
1	C	345	SER
1	D	124	ALA
1	B	73	GLN
1	C	45	SER
1	D	2	ARG
1	A	281	LEU
1	B	281	LEU
1	C	233	GLU
1	C	281	LEU
1	C	343	VAL
1	D	281	LEU
1	D	349	GLU
1	A	233	GLU
1	B	409	ASP
1	B	182	PRO
1	D	319	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	A	424/424 (100%)	388 (92%)	36 (8%)	10	22
1	B	424/424 (100%)	382 (90%)	42 (10%)	7	16
1	C	424/424 (100%)	389 (92%)	35 (8%)	10	22
1	D	424/424 (100%)	376 (89%)	48 (11%)	5	12

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	1696/1696 (100%)	1535 (90%)	161 (10%)	8 17

All (161) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	ARG
1	A	5	ILE
1	A	13	SER
1	A	31	PHE
1	A	39	ARG
1	A	44	ARG
1	A	49	MET
1	A	98	PRO
1	A	107	SER
1	A	111	GLU
1	A	127	ASP
1	A	138	THR
1	A	156	LEU
1	A	161	ILE
1	A	169	GLN
1	A	182	PRO
1	A	200	GLN
1	A	211	ARG
1	A	226	GLN
1	A	291	TRP
1	A	293	LYS
1	A	300	GLU
1	A	314	LEU
1	A	335	MET
1	A	342	CYS
1	A	345	SER
1	A	350	GLN
1	A	356	SER
1	A	370	ASN
1	A	381	TRP
1	A	406	ILE
1	A	408	LYS
1	A	410	THR
1	A	455	SER
1	A	457	VAL
1	A	493	LEU
1	B	5	ILE

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Mol	Chain	Res	Type
1	B	30	THR
1	B	34	LEU
1	B	44	ARG
1	B	47	ARG
1	B	57	GLN
1	B	61	THR
1	B	72	GLU
1	B	91	LEU
1	B	165	LEU
1	B	166	GLN
1	B	182	PRO
1	B	194	LYS
1	B	235	GLU
1	B	246	PHE
1	B	262	ARG
1	B	286	LEU
1	B	314	LEU
1	B	315	ASP
1	B	321	LYS
1	B	326	GLU
1	B	335	MET
1	B	351	SER
1	B	356	SER
1	B	358	ASP
1	B	364	SER
1	B	366	SER
1	B	368	ILE
1	B	381	TRP
1	B	388	GLU
1	B	396	ASN
1	B	407	THR
1	B	439	SER
1	B	440	GLN
1	B	447	VAL
1	B	450	MET
1	B	457	VAL
1	B	470	LEU
1	B	480	LEU
1	B	489	ILE
1	B	493	LEU
1	B	497	GLN
1	C	5	ILE

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Mol	Chain	Res	Type
1	C	31	PHE
1	C	39	ARG
1	C	44	ARG
1	C	49	MET
1	C	50	GLU
1	C	57	GLN
1	C	77	LYS
1	C	97	SER
1	C	107	SER
1	C	110	SER
1	C	111	GLU
1	C	165	LEU
1	C	204	ILE
1	C	222	GLU
1	C	231	THR
1	C	241	LEU
1	C	272	THR
1	C	286	LEU
1	C	303	LYS
1	C	335	MET
1	C	342	CYS
1	C	343	VAL
1	C	346	LYS
1	C	348	TRP
1	C	350	GLN
1	C	356	SER
1	C	366	SER
1	C	379	THR
1	C	381	TRP
1	C	406	ILE
1	C	410	THR
1	C	466	LYS
1	C	471	THR
1	C	483	ILE
1	D	2	ARG
1	D	31	PHE
1	D	34	LEU
1	D	44	ARG
1	D	49	MET
1	D	52	SER
1	D	57	GLN
1	D	61	THR

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Mol	Chain	Res	Type
1	D	73	GLN
1	D	79	LYS
1	D	91	LEU
1	D	93	ILE
1	D	110	SER
1	D	111	GLU
1	D	112	GLU
1	D	154	THR
1	D	155	LYS
1	D	165	LEU
1	D	182	PRO
1	D	194	LYS
1	D	224	LYS
1	D	230	VAL
1	D	235	GLU
1	D	246	PHE
1	D	272	THR
1	D	317	LEU
1	D	321	LYS
1	D	329	ARG
1	D	335	MET
1	D	343	VAL
1	D	346	LYS
1	D	350	GLN
1	D	358	ASP
1	D	381	TRP
1	D	388	GLU
1	D	402	ILE
1	D	410	THR
1	D	424	SER
1	D	441	LYS
1	D	450	MET
1	D	457	VAL
1	D	465	SER
1	D	466	LYS
1	D	471	THR
1	D	480	LEU
1	D	493	LEU
1	D	495	HIS
1	D	497	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (30) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	59	ASN
1	A	60	HIS
1	A	169	GLN
1	A	223	HIS
1	A	362	GLN
1	A	365	HIS
1	A	495	HIS
1	B	57	GLN
1	B	59	ASN
1	B	73	GLN
1	B	162	HIS
1	B	350	GLN
1	B	362	GLN
1	B	374	HIS
1	B	396	ASN
1	B	432	GLN
1	B	495	HIS
1	C	60	HIS
1	C	146	ASN
1	C	200	GLN
1	C	223	HIS
1	C	226	GLN
1	C	365	HIS
1	C	495	HIS
1	D	70	GLN
1	D	143	GLN
1	D	145	HIS
1	D	162	HIS
1	D	440	GLN
1	D	495	HIS

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

56 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$
2	PO4	D	505	-	4,4,4	0.96	0	6,6,6	0.52	0
2	PO4	B	507	-	4,4,4	0.87	0	6,6,6	0.33	0
2	PO4	D	500	-	4,4,4	1.01	0	6,6,6	0.87	0
2	PO4	C	499	-	4,4,4	0.95	0	6,6,6	1.54	2 (33%)
2	PO4	A	511	-	4,4,4	0.86	0	6,6,6	0.70	0
2	PO4	B	503	-	4,4,4	1.12	0	6,6,6	0.81	0
2	PO4	C	504	-	4,4,4	1.04	0	6,6,6	0.65	0
2	PO4	C	502	-	4,4,4	0.85	0	6,6,6	0.86	0
2	PO4	C	505	-	4,4,4	0.97	0	6,6,6	0.75	0
2	PO4	A	500	-	4,4,4	0.88	0	6,6,6	0.63	0
2	PO4	D	499	-	4,4,4	0.94	0	6,6,6	0.92	0
3	NAG	C	510	1	14,14,15	1.01	1 (7%)	17,19,21	1.52	1 (5%)
2	PO4	C	503	-	4,4,4	0.69	0	6,6,6	0.88	0
2	PO4	B	504	-	4,4,4	0.81	0	6,6,6	0.60	0
2	PO4	B	502	-	4,4,4	0.95	0	6,6,6	0.81	0
2	PO4	C	511	-	4,4,4	0.87	0	6,6,6	0.32	0
3	NAG	D	510	1	14,14,15	0.64	0	17,19,21	2.63	2 (11%)
2	PO4	C	507	-	4,4,4	0.82	0	6,6,6	0.67	0
2	PO4	D	501	-	4,4,4	0.49	0	6,6,6	1.14	0
2	PO4	B	506	-	4,4,4	1.01	0	6,6,6	0.66	0
2	PO4	C	509	-	4,4,4	0.93	0	6,6,6	1.06	0
2	PO4	B	498	-	4,4,4	0.79	0	6,6,6	0.67	0
2	PO4	D	504	-	4,4,4	0.92	0	6,6,6	0.45	0
3	NAG	B	508	1	14,14,15	0.80	0	17,19,21	1.88	5 (29%)
2	PO4	A	499	-	4,4,4	1.42	1 (25%)	6,6,6	1.50	1 (16%)
2	PO4	A	506	-	4,4,4	0.91	0	6,6,6	0.75	0
2	PO4	A	501	-	4,4,4	1.02	0	6,6,6	1.02	0
2	PO4	A	504	-	4,4,4	0.66	0	6,6,6	1.25	1 (16%)
2	PO4	A	505	-	4,4,4	0.82	0	6,6,6	0.89	0
2	PO4	D	507	-	4,4,4	0.88	0	6,6,6	0.49	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	PO4	A	503	-	4,4,4	0.97	0	6,6,6	1.51	2 (33%)
2	PO4	A	509	-	4,4,4	0.96	0	6,6,6	0.80	0
2	PO4	B	500	-	4,4,4	1.20	0	6,6,6	0.89	0
2	PO4	D	508	-	4,4,4	0.78	0	6,6,6	0.65	0
2	PO4	A	508	-	4,4,4	0.85	0	6,6,6	0.64	0
2	PO4	C	498	-	4,4,4	0.83	0	6,6,6	0.91	0
3	NAG	B	509	1	14,14,15	0.67	0	17,19,21	2.30	4 (23%)
2	PO4	A	512	-	4,4,4	0.91	0	6,6,6	0.72	0
2	PO4	D	506	-	4,4,4	0.84	0	6,6,6	0.43	0
2	PO4	B	505	-	4,4,4	0.70	0	6,6,6	0.64	0
2	PO4	D	502	-	4,4,4	1.07	0	6,6,6	0.74	0
2	PO4	A	514	-	4,4,4	0.98	0	6,6,6	0.52	0
2	PO4	C	506	-	4,4,4	0.88	0	6,6,6	0.55	0
2	PO4	C	501	-	4,4,4	0.82	0	6,6,6	0.89	0
2	PO4	B	499	-	4,4,4	0.89	0	6,6,6	0.55	0
2	PO4	A	502	-	4,4,4	0.95	0	6,6,6	1.49	2 (33%)
3	NAG	D	509	1	14,14,15	0.67	0	17,19,21	1.71	2 (11%)
2	PO4	C	500	-	4,4,4	1.21	0	6,6,6	1.03	0
2	PO4	B	501	-	4,4,4	1.12	0	6,6,6	1.08	0
3	NAG	A	513	1	14,14,15	0.80	0	17,19,21	1.55	4 (23%)
2	PO4	D	498	-	4,4,4	1.07	0	6,6,6	0.76	0
2	PO4	A	507	-	4,4,4	0.86	0	6,6,6	1.33	0
2	PO4	C	508	-	4,4,4	0.79	0	6,6,6	0.72	0
2	PO4	A	498	-	4,4,4	0.77	0	6,6,6	0.93	0
2	PO4	D	503	-	4,4,4	1.00	0	6,6,6	1.01	0
2	PO4	A	510	-	4,4,4	0.91	0	6,6,6	0.58	0

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	509	1	-	0/6/23/26	0/1/1/1
3	NAG	A	513	1	-	1/6/23/26	0/1/1/1
3	NAG	B	508	1	-	0/6/23/26	0/1/1/1
3	NAG	C	510	1	-	2/6/23/26	0/1/1/1
3	NAG	B	509	1	-	0/6/23/26	0/1/1/1
3	NAG	D	510	1	1/1/5/7	2/6/23/26	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	510	NAG	C1-C2	2.19	1.55	1.52
2	A	499	PO4	P-O3	-2.04	1.48	1.54

All (26) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	510	NAG	C1-O5-C5	9.89	125.44	112.19
3	B	509	NAG	C1-O5-C5	7.12	121.72	112.19
3	D	509	NAG	C4-C3-C2	4.68	117.88	111.02
3	C	510	NAG	C2-N2-C7	-4.17	117.32	122.90
3	D	509	NAG	C3-C4-C5	3.55	116.67	110.23
3	B	508	NAG	C2-N2-C7	3.50	127.60	122.90
3	B	509	NAG	C4-C3-C2	3.31	115.87	111.02
3	A	513	NAG	C1-O5-C5	3.20	116.47	112.19
3	B	508	NAG	O7-C7-C8	-2.97	116.77	122.05
3	B	508	NAG	C4-C3-C2	2.75	115.05	111.02
2	C	499	PO4	O3-P-O1	-2.72	101.35	110.95
2	A	504	PO4	O4-P-O2	2.65	116.15	107.91
3	A	513	NAG	C4-C3-C2	2.54	114.75	111.02
3	B	509	NAG	C2-N2-C7	-2.54	119.50	122.90
2	A	502	PO4	O4-P-O2	2.53	115.77	107.91
2	A	502	PO4	O2-P-O1	-2.46	102.27	110.95
3	B	509	NAG	O3-C3-C2	-2.38	104.46	109.40
3	B	508	NAG	C1-C2-N2	2.27	114.02	110.43
3	A	513	NAG	O4-C4-C5	2.21	114.76	109.32
3	B	508	NAG	C3-C4-C5	2.19	114.21	110.23
2	A	503	PO4	O3-P-O2	-2.17	101.16	107.91
2	C	499	PO4	O3-P-O2	2.15	114.60	107.91
2	A	499	PO4	O4-P-O3	-2.11	101.35	107.91
3	A	513	NAG	C6-C5-C4	-2.08	107.90	113.02
2	A	503	PO4	O4-P-O3	2.06	114.33	107.91
3	D	510	NAG	O5-C1-C2	2.02	114.41	111.29

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	D	510	NAG	C1

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	D	510	NAG	C4-C5-C6-O6
3	D	510	NAG	O5-C5-C6-O6

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Mol	Chain	Res	Type	Atoms
3	C	510	NAG	O5-C5-C6-O6
3	C	510	NAG	C4-C5-C6-O6
3	A	513	NAG	C4-C5-C6-O6

There are no ring outliers.

16 monomers are involved in 26 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	505	PO4	1	0
2	B	507	PO4	1	0
2	C	504	PO4	1	0
2	C	505	PO4	1	0
2	A	500	PO4	3	0
2	B	504	PO4	1	0
2	B	506	PO4	1	0
2	A	505	PO4	1	0
2	D	508	PO4	1	0
2	C	501	PO4	4	0
2	B	499	PO4	1	0
2	A	502	PO4	3	0
2	C	500	PO4	1	0
2	B	501	PO4	2	0
3	A	513	NAG	1	0
2	D	503	PO4	3	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 [i](#)

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

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	497/497 (100%)	-1.24	0 100 100	30, 46, 67, 76	0
1	B	497/497 (100%)	-1.24	0 100 100	33, 48, 73, 87	0
1	C	497/497 (100%)	-1.25	0 100 100	29, 47, 67, 75	0
1	D	497/497 (100%)	-1.21	0 100 100	34, 47, 72, 88	0
All	All	1988/1988 (100%)	-1.24	0 100 100	29, 47, 69, 88	0

There are no RSRZ outliers to report.

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(Å ²)	Q<0.9
3	NAG	B	508	14/15	0.96	0.05	62,69,73,73	0
2	PO4	D	506	5/5	0.97	0.04	113,113,114,114	0
2	PO4	B	507	5/5	0.97	0.03	102,103,103,104	0
3	NAG	B	509	14/15	0.97	0.05	44,50,53,54	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	NAG	D	510	14/15	0.97	0.05	49,55,57,58	0
2	PO4	A	510	5/5	0.98	0.05	76,76,79,79	0
2	PO4	A	512	5/5	0.98	0.05	101,102,102,103	0
2	PO4	B	505	5/5	0.98	0.04	84,84,87,87	0
2	PO4	B	498	5/5	0.98	0.04	105,106,107,107	0
2	PO4	B	499	5/5	0.98	0.04	80,81,82,83	0
2	PO4	A	498	5/5	0.98	0.06	67,70,71,71	0
2	PO4	C	502	5/5	0.98	0.05	87,87,88,89	0
2	PO4	C	505	5/5	0.98	0.03	99,99,100,100	0
2	PO4	C	508	5/5	0.98	0.04	95,96,96,97	0
2	PO4	C	509	5/5	0.98	0.17	86,86,87,89	0
2	PO4	C	511	5/5	0.98	0.04	92,92,92,93	0
2	PO4	D	503	5/5	0.98	0.03	77,78,82,82	0
2	PO4	D	504	5/5	0.98	0.08	88,89,90,90	0
2	PO4	D	505	5/5	0.98	0.06	80,80,81,81	0
2	PO4	A	506	5/5	0.98	0.08	80,80,82,83	0
2	PO4	D	507	5/5	0.98	0.04	83,83,84,86	0
2	PO4	D	508	5/5	0.98	0.05	84,84,85,86	0
3	NAG	A	513	14/15	0.98	0.05	54,63,64,65	0
2	PO4	A	507	5/5	0.98	0.03	73,74,75,76	0
2	PO4	A	508	5/5	0.98	0.04	119,120,120,120	0
3	NAG	C	510	14/15	0.98	0.04	56,62,68,68	0
3	NAG	D	509	14/15	0.98	0.05	69,73,75,76	0
2	PO4	A	509	5/5	0.98	0.04	101,101,102,102	0
2	PO4	C	503	5/5	0.99	0.06	73,73,75,76	0
2	PO4	C	504	5/5	0.99	0.03	74,76,78,79	0
2	PO4	A	511	5/5	0.99	0.05	123,123,123,124	0
2	PO4	C	506	5/5	0.99	0.04	88,88,89,89	0
2	PO4	C	507	5/5	0.99	0.04	102,103,104,104	0
2	PO4	A	505	5/5	0.99	0.03	86,86,86,87	0
2	PO4	A	514	5/5	0.99	0.03	95,95,95,96	0
2	PO4	B	501	5/5	0.99	0.03	64,67,67,69	0
2	PO4	D	500	5/5	0.99	0.04	59,60,61,62	0
2	PO4	D	501	5/5	0.99	0.04	68,68,71,71	0
2	PO4	D	502	5/5	0.99	0.03	51,54,56,57	0
2	PO4	D	498	5/5	0.99	0.04	78,79,80,81	0
2	PO4	B	502	5/5	0.99	0.03	64,66,67,68	0
2	PO4	B	503	5/5	0.99	0.04	58,60,61,63	0
2	PO4	B	504	5/5	0.99	0.03	75,76,77,80	0
2	PO4	A	501	5/5	0.99	0.05	53,53,56,57	0
2	PO4	A	502	5/5	0.99	0.04	63,64,65,67	0
2	PO4	A	503	5/5	0.99	0.06	59,60,60,63	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	PO4	B	506	5/5	0.99	0.06	75,76,77,77	0
2	PO4	A	500	5/5	0.99	0.02	66,68,69,70	0
2	PO4	C	499	5/5	0.99	0.04	60,60,62,63	0
2	PO4	C	501	5/5	0.99	0.02	54,56,58,60	0
2	PO4	C	498	5/5	0.99	0.05	70,72,72,73	0
2	PO4	A	504	5/5	0.99	0.06	74,74,76,77	0
2	PO4	C	500	5/5	1.00	0.02	37,40,41,45	0
2	PO4	A	499	5/5	1.00	0.02	36,40,41,44	0
2	PO4	B	500	5/5	1.00	0.02	47,47,49,50	0
2	PO4	D	499	5/5	1.00	0.02	42,45,48,50	0

6.5 Other polymers [i](#)

There are no such residues in this entry.