



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 8, 2020 – 12:38 PM BST

PDB ID : 3GXD
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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.13.1
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.13.1

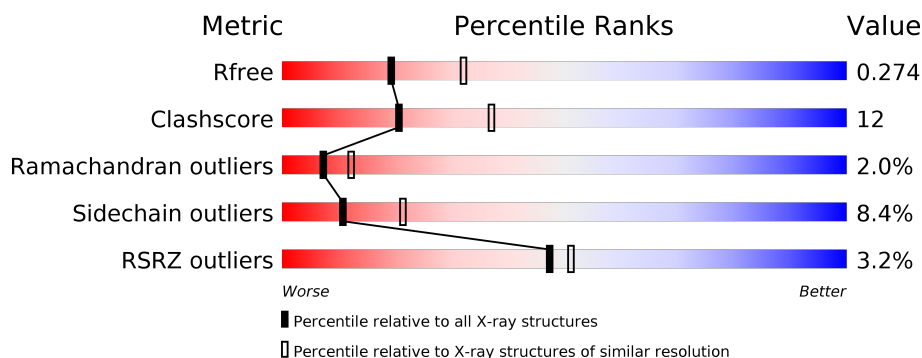
1 Overall quality at a glance

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}	130704	4661 (2.50-2.50)
Clashscore	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)
RSRZ outliers	127900	4559 (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 on 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	<div> <div>3%</div> <div> <div></div> <div>72%</div> <div>24%</div> <div>• •</div> </div> </div>
1	B	497	<div> <div>4%</div> <div> <div></div> <div>73%</div> <div>23%</div> <div>• •</div> </div> </div>
1	C	497	<div> <div>2%</div> <div> <div></div> <div>75%</div> <div>21%</div> <div>• •</div> </div> </div>
1	D	497	<div> <div>4%</div> <div> <div></div> <div>69%</div> <div>25%</div> <div>5%</div> </div> </div>

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 crite-

ria:

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.

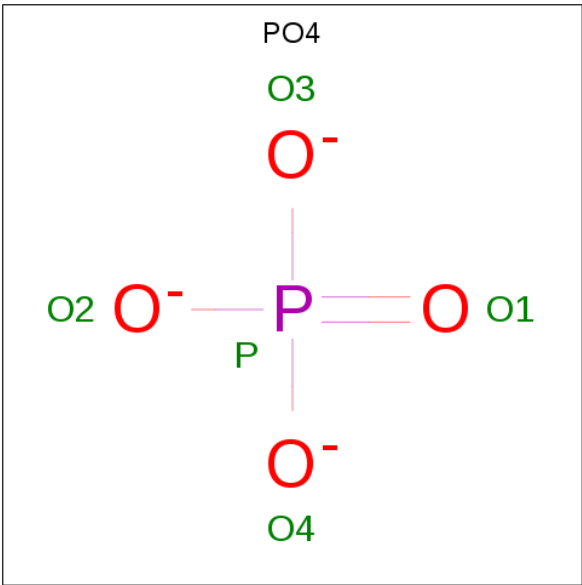
- Molecule 1 is a protein called Glucosylceramidase.

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 (three-letter code: 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		
2	A	1	Total	O	P	0	0
			5	4	1		

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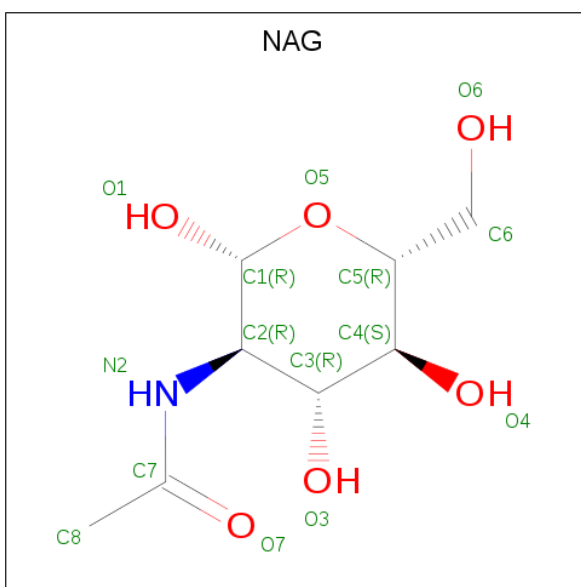
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	P	0	0
			5	4	1		
2	A	1	Total	O	P	0	0
			5	4	1		
2	B	1	Total	O	P	0	0
			5	4	1		
2	B	1	Total	O	P	0	0
			5	4	1		
2	B	1	Total	O	P	0	0
			5	4	1		
2	B	1	Total	O	P	0	0
			5	4	1		
2	B	1	Total	O	P	0	0
			5	4	1		
2	B	1	Total	O	P	0	0
			5	4	1		
2	B	1	Total	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 (three-letter code: 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		

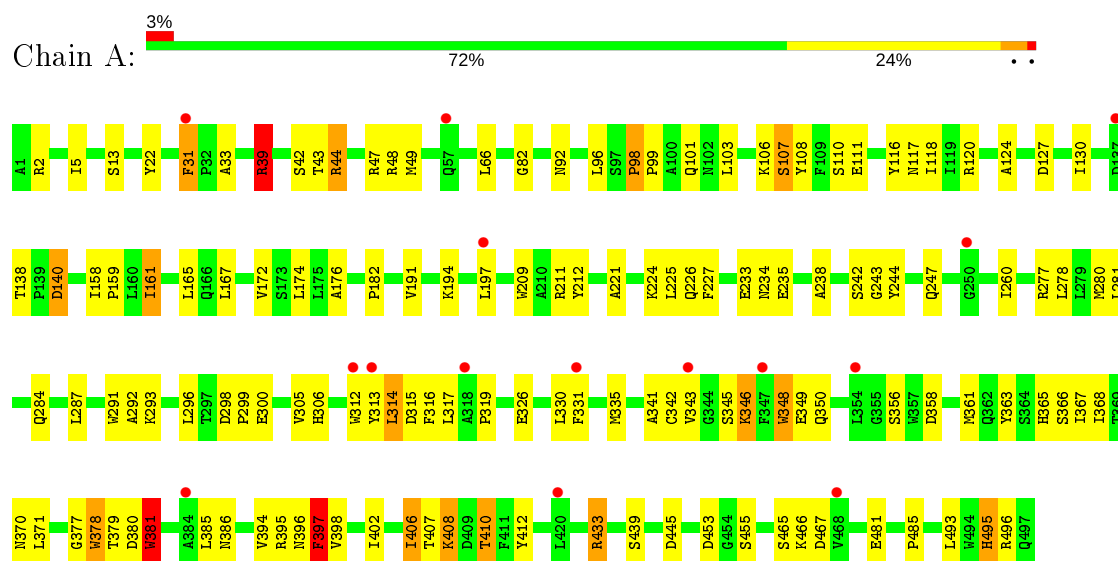
- Molecule 4 is water.

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		

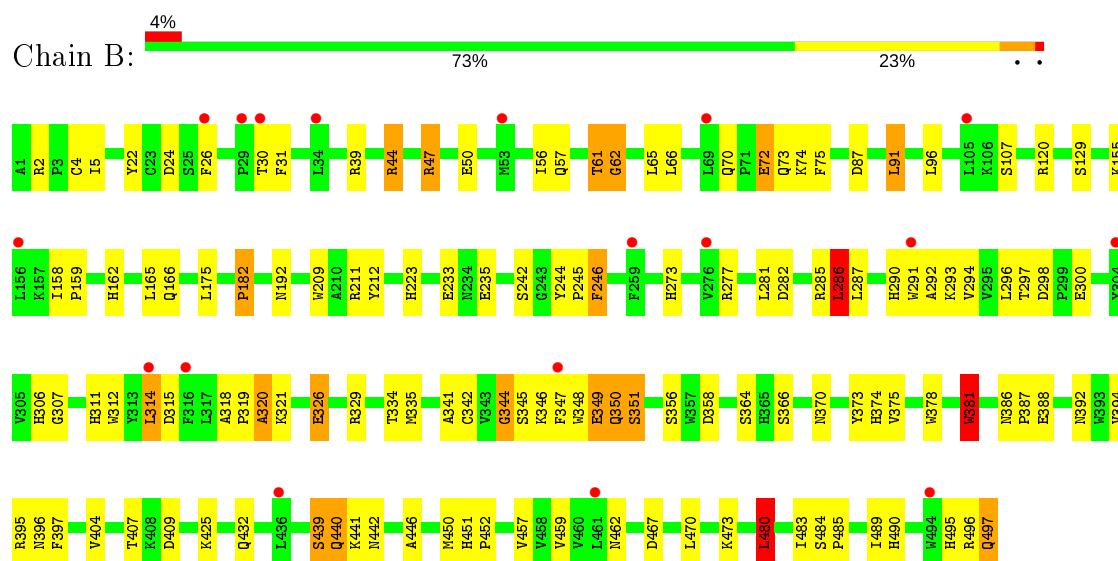
3 Residue-property plots

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.

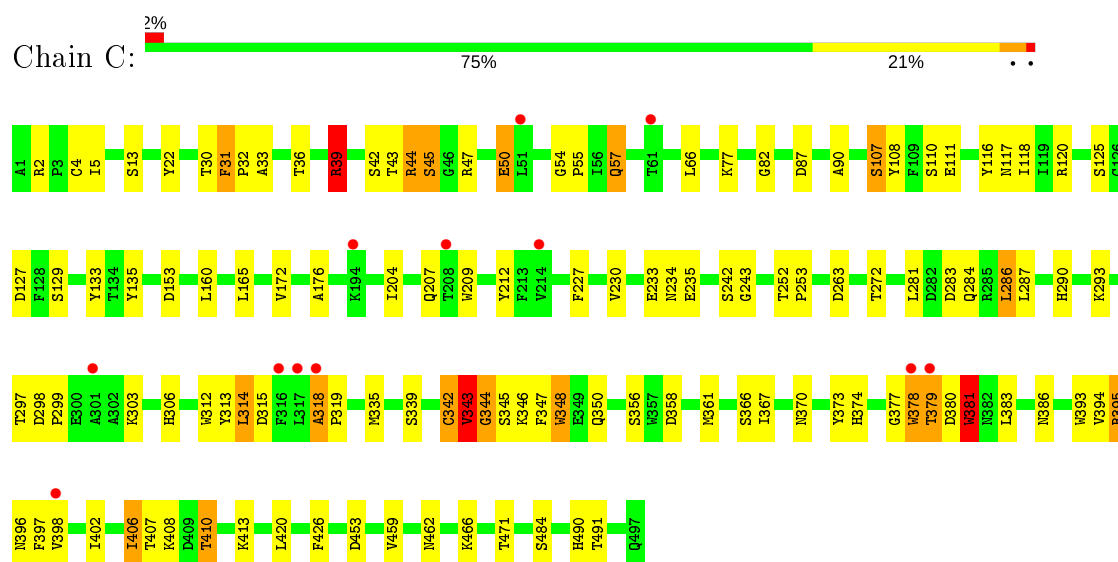
• Molecule 1: Glucosylceramidase



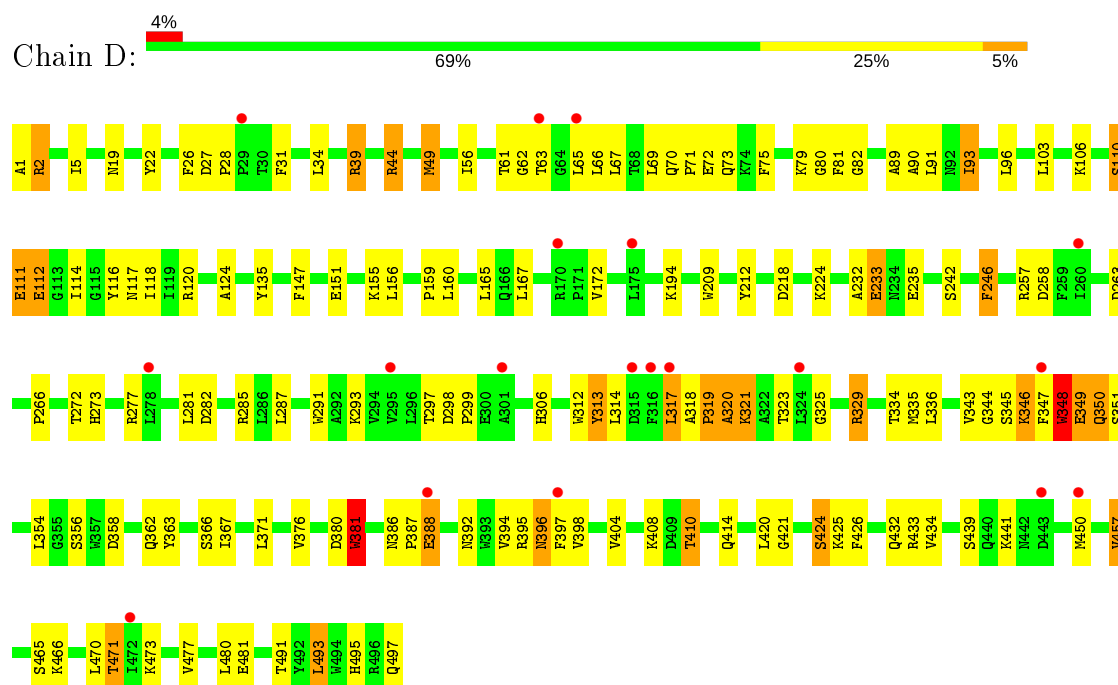
• Molecule 1: Glucosylceramidase



• Molecule 1: Glucosylceramidase



• Molecule 1: Glucosylceramidase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	109.44 Å 91.70 Å 152.49 Å 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 2.51 Å)	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 , 19.7	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	0.95	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: PO4, 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	0.89	1/4051 (0.0%)	0.90	4/5523 (0.1%)
1	B	0.89	0/4051	0.88	4/5523 (0.1%)
1	C	0.88	1/4051 (0.0%)	0.90	3/5523 (0.1%)
1	D	0.92	2/4051 (0.0%)	0.89	5/5523 (0.1%)
All	All	0.90	4/16204 (0.0%)	0.89	16/22092 (0.1%)

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 (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	378	TRP	CB-CG	-7.87	1.36	1.50
1	A	378	TRP	CB-CG	-7.80	1.36	1.50
1	D	388	GLU	CG-CD	5.86	1.60	1.51
1	D	81	PHE	CE1-CZ	5.32	1.47	1.37

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	120	ARG	NE-CZ-NH2	-7.55	116.53	120.30
1	B	286	LEU	CA-CB-CG	-7.09	98.99	115.30
1	A	433	ARG	NE-CZ-NH2	-6.67	116.96	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	378	TRP	CA-CB-CG	-6.42	101.50	113.70
1	C	39	ARG	NE-CZ-NH1	5.71	123.15	120.30
1	B	480	LEU	CA-CB-CG	5.71	128.43	115.30
1	C	286	LEU	CA-CB-CG	5.50	127.96	115.30
1	D	348	TRP	N-CA-C	5.49	125.81	111.00
1	A	39	ARG	NE-CZ-NH2	-5.46	117.57	120.30
1	A	39	ARG	NE-CZ-NH1	5.38	122.99	120.30
1	D	67	LEU	CA-CB-CG	5.26	127.40	115.30
1	D	348	TRP	C-N-CA	5.24	134.81	121.70
1	B	350	GLN	N-CA-C	-5.07	97.32	111.00
1	B	91	LEU	CB-CG-CD1	-5.05	102.42	111.00
1	A	397	PHE	N-CA-C	5.04	124.60	111.00
1	D	317	LEU	CA-CB-CG	5.01	126.83	115.30

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	106	0
1	B	3930	0	3841	93	0
1	C	3930	0	3843	96	0
1	D	3930	0	3841	109	0
2	A	80	0	0	6	0
2	B	50	0	0	6	0
2	C	65	0	0	6	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

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	A	61	0	0	2	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	386	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 12.

All (386) 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:HH11	1:D:329:ARG:HG2	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: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
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:CD1	1:C:378:TRP:N	2.48	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:D:345:SER:C	1:D:347:PHE:H	1.86	0.77
1:B:66:LEU:HD11	1:B:473:LYS:HB2	1.68	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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: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: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:A:395:ARG:NH2	1:D:395:ARG:HH11	1.86	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:C:370:ASN:CG	1:C:378:TRP:CH2	2.63	0.70
1:D:329:ARG:CG	1:D:329:ARG:HH11	2.01	0.70
1:D:66:LEU:HD11	1:D:473:LYS:HB2	1.72	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
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:D:345:SER:C	1:D:347:PHE:N	2.49	0.65
1:B:346:LYS:H	1:B:347:PHE:HA	1.62	0.65
1:A:453:ASP:OD1	1:A:453:ASP:C	2.35	0.65
1:C:377:GLY:C	1:C:378:TRP:CD1	2.70	0.65
1:D:344:GLY:HA2	1:D:398:VAL:HG12	1.77	0.65
1:D:329:ARG:NH1	1:D:329:ARG:HG2	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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: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:344:GLY:HA3	1:C:398:VAL:HA	1.82	0.61
1:C:39:ARG:HH11	1:C:39:ARG:HG3	1.65	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:A:31:PHE:HB2	1:A:495:HIS:HE1	1.63	0.61
1:B:319:PRO:O	1:B:320:ALA:HB3	2.00	0.61
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: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:377:GLY:C	1:A:378:TRP:CE3	2.77	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:358:ASP:HA	1:C:361:MET:HE2	1.86	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:N	1:C:31:PHE:CD1	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:370:ASN:CG	1:C:378:TRP:HH2	1.94	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:D:345:SER:CB	1:D:349:GLU:O	2.54	0.56
1:D:348:TRP:CE3	1:D:349:GLU:HG2	2.41	0.56
1:D:44:ARG:NH2	2:D:503:PO4:O2	2.38	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:B:72:GLU:OE1	1:B:72:GLU:HA	2.03	0.55
1:A:312:TRP:HH2	1:A:367:ILE:HG13	1.72	0.55
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:408:LYS:HB2	1:D:410:THR:HG23	1.89	0.54
1:D:5:ILE:HG12	1:D:22:TYR:CE2	2.41	0.54
1:D:39:ARG:O	1:D:39:ARG:HD3	2.06	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: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:D:1:ALA:HB2	1:D:27:ASP:OD1	2.09	0.53
1:C:31:PHE:HD1	1:C:31:PHE:H	1.56	0.53
1:A:358:ASP:HA	1:A:361:MET:HE2	1.91	0.52
1:B:44:ARG:HB3	2:B:501:PO4:O2	2.08	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:408:LYS:HB3	1:A:410:THR:HG23	1.91	0.52
1:B:326:GLU:OE1	1:B:326:GLU:HA	2.09	0.52
1:C:386:ASN:C	1:C:386:ASN:OD1	2.48	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:108:TYR:CE1	1:C:402:ILE:HD12	2.45	0.52
1:C:39:ARG:NH1	1:C:39:ARG:HG3	2.25	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:C:453:ASP:OD1	1:C:453:ASP:C	2.46	0.52
1:D:433:ARG:HG2	1:D:434:VAL:N	2.25	0.52
1:B:349:GLU:HA	1:B:350:GLN:CB	2.40	0.51
1:C:116:TYR:OH	1:C:420:LEU:HD13	2.10	0.51
1:C:66:LEU:HD13	1:C:471:THR:HB	1.91	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: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:293:LYS:O	1:B:297:THR:HG23	2.11	0.51
1:B:56:ILE:HG12	1:B:480:LEU:HD22	1.92	0.51
1:D:321:LYS:O	1:D:325:GLY:HA3	2.10	0.51
1:D:80:GLY:HA3	1:D:117:ASN:ND2	2.23	0.51
1:A:243:GLY:O	1:B:348:TRP:NE1	2.44	0.51
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:346:LYS:CB	1:D:349:GLU:HG3	2.35	0.50
1:D:69:LEU:O	1:D:71:PRO:HD3	2.12	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:N	1:A:127:ASP:OD1	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:C:312:TRP:CZ2	1:C:378:TRP:CZ3	3.00	0.49
1:D:363:TYR:O	1:D:367:ILE:HG13	2.13	0.49
1:D:381:TRP:HA	1:D:381:TRP:CE3	2.47	0.49
1:B:300:GLU:HA	1:B:300:GLU:OE1	2.13	0.49
1:A:221:ALA:O	1:A:224:LYS:N	2.40	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:446:ALA:HA	1:B:459:VAL:O	2.12	0.49
1:C:30:THR:OG1	4:C:551:HOH:O	2.20	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: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:370:ASN:CG	1:C:378:TRP:CZ3	2.87	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
1:B:209:TRP:O	1:B:212:TYR:HB3	2.13	0.48
1:A:343:VAL:HG12	1:A:363:TYR:HE1	1.77	0.48
1:A:39:ARG:HG3	1:A:39:ARG:HH11	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:B:373:TYR:C	1:B:374:HIS:CD2	2.87	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:395:ARG:HH22	1:D:395:ARG:NH1	2.12	0.48
1:A:277:ARG:HH21	2:A:502:PO4:P	2.37	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: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: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:A:312:TRP:C	1:A:315:ASP:OD1	2.54	0.46
1:A:39:ARG:NH1	1:A:39:ARG:HG3	2.30	0.46
1:B:483:ILE:O	1:B:490:HIS:HE1	1.98	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:C:243:GLY:C	1:D:348:TRP:CZ3	2.89	0.46
1:D:233:GLU:O	1:D:282:ASP:HB3	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
1:A:406:ILE:HD13	1:A:406:ILE:N	2.31	0.46
1:B:277:ARG:NH1	1:B:306:HIS:CE1	2.83	0.46
1:B:31:PHE:HB2	1:B:495:HIS:CE1	2.51	0.46
1:C:348:TRP:CH2	1:D:242:SER:O	2.69	0.46
1:A:319:PRO:HD3	1:B:286:LEU:HD21	1.99	0.45
1:B:349:GLU:CA	1:B:350:GLN:HB2	2.46	0.45
1:B:159:PRO:HA	2:B:499:PO4:O2	2.16	0.45
1:B:296:LEU:HD23	1:B:296:LEU:HA	1.80	0.45
1:B:246:PHE:CD2	1:B:394:VAL:HG11	2.48	0.45
1:A:234:ASN:O	1:A:235:GLU:C	2.54	0.45
1:C:342:CYS:SG	1:C:343:VAL:N	2.90	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:B:319:PRO:O	1:B:320:ALA:CB	2.62	0.45
1:B:96:LEU:HD21	1:B:404:VAL:HG13	1.98	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:287:LEU:HB3	1:B:291:TRP:CD1	2.52	0.45
1:B:4:CYS:HA	1:B:24:ASP:HB3	1.99	0.45
1:C:348:TRP:CD1	1:C:348:TRP:N	2.83	0.45
1:C:43:THR:HB	4:C:552:HOH:O	2.15	0.45
1:B:70:GLN:O	1:B:72:GLU:N	2.50	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: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:298:ASP:C	1:D:298:ASP:OD1	2.56	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:406:ILE:HG12	1:A:407:THR:N	2.33	0.44
1:A:43:THR:O	1:A:48:ARG:NH1	2.41	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:396:ASN:O	1:C:398:VAL:N	2.45	0.44
1:C:5:ILE:HD12	1:C:22:TYR:CZ	2.53	0.44
1:D:408:LYS:CB	1:D:410:THR:HG23	2.48	0.44
1:A:260:ILE:HG12	1:A:278:LEU:HD21	2.00	0.43
1:A:66:LEU:HB3	1:A:439:SER:HB3	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:B:158:ILE:HB	1:B:159:PRO:HD3	2.00	0.43
1:D:75:PHE:O	1:D:432:GLN:NE2	2.38	0.43
1:A:49:MET:HE2	1:A:49:MET:HB3	1.80	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: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:242:SER:O	1:D:348:TRP:HH2	2.02	0.43
1:C:42:SER:HA	1:C:47:ARG:O	2.18	0.43
1:A:130:ILE:HD11	1:D:151:GLU:HB2	2.01	0.43
1:A:402:ILE:HA	1:A:412:TYR:O	2.19	0.43
1:B:70:GLN:C	1:B:72:GLU:H	2.22	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
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:377:GLY:C	1:C:378:TRP:CG	2.91	0.42
1:C:426:PHE:CD1	1:C:491:THR:HG21	2.54	0.42
1:D:298:ASP:HA	1:D:299:PRO:HD2	1.69	0.42
1:D:246:PHE:CE2	1:D:396:ASN:HB2	2.53	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: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:318:ALA:HB3	1:C:319:PRO:HA	2.01	0.42
1:C:312:TRP:CH2	1:C:367:ILE:HG13	2.54	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:A:209:TRP:HA	1:A:209:TRP:CE3	2.55	0.41
1:B:70:GLN:C	1:B:72:GLU:N	2.73	0.41
1:B:87:ASP:OD2	1:B:129:SER:OG	2.24	0.41
1:C:209:TRP:CZ3	1:C:212:TYR:CD2	3.08	0.41
1:D:312:TRP:HA	1:D:312:TRP:CE3	2.54	0.41
1:D:371:LEU:HA	1:D:371:LEU:HD23	1.95	0.41
1:C:234:ASN:O	1:C:235:GLU:C	2.57	0.41
1:D:90:ALA:HB1	1:D:156:LEU:HB3	2.02	0.41
1:D:44:ARG:NH1	2:D:503:PO4:O2	2.53	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: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: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:B:75:PHE:O	1:B:432:GLN:NE2	2.54	0.41
1:C:339:SER:O	1:C:379:THR:HG22	2.20	0.41
1:B:306:HIS:ND1	1:B:306:HIS:O	2.54	0.41
1:C:90:ALA:CB	1:C:160:LEU:HD12	2.51	0.41
1:C:45:SER:HB3	2:C:501:PO4:O4	2.20	0.41
1:D:26:PHE:CZ	1:D:49:MET:CE	3.03	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:OE1	1:A:326:GLU:HA	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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: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:330:LEU:HB3	1:A:331:PHE:CE1	2.56	0.41
1:A:98:PRO:HB2	1:A:99:PRO:HD3	2.03	0.41
1:A:348:TRP:CB	1:B:245:PRO:HG3	2.51	0.41
1:B:282:ASP:OD1	1:B:311:HIS:NE2	2.46	0.41
1:B:370:ASN:O	1:B:375:VAL:HB	2.21	0.41
1:C:383:LEU:HA	1:C:383:LEU:HD23	1.83	0.41
1:B:312:TRP:HD1	1:B:314:LEU:HD13	1.85	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:243:GLY:O	1:B:348:TRP:CD1	2.74	0.41
1:A:44:ARG:HH11	2:A:500:PO4:P	2.43	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:B:292:ALA:O	1:B:296:LEU:HB2	2.21	0.40
1:D:112:GLU:HG3	1:D:112:GLU:H	1.59	0.40
1:D:347:PHE:O	1:D:348:TRP:HB3	2.21	0.40
1:D:70:GLN:O	1:D:72:GLU:N	2.54	0.40
1:A:386:ASN:OD1	1:A:386:ASN:C	2.59	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:CE3	1:C:393:TRP:O	2.74	0.40
1:D:350:GLN:H	1:D:350:GLN:CD	2.24	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

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	495/497 (100%)	446 (90%)	41 (8%)	8 (2%)	9	17
1	B	495/497 (100%)	456 (92%)	30 (6%)	9 (2%)	8	14
1	C	495/497 (100%)	452 (91%)	31 (6%)	12 (2%)	6	9
1	D	495/497 (100%)	432 (87%)	52 (10%)	11 (2%)	6	10
All	All	1980/1988 (100%)	1786 (90%)	154 (8%)	40 (2%)	7	12

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
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

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Mol	Chain	Res	Type
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%)	394 (93%)	30 (7%)	14	28
1	B	424/424 (100%)	386 (91%)	38 (9%)	9	19
1	C	424/424 (100%)	395 (93%)	29 (7%)	16	30
1	D	424/424 (100%)	379 (89%)	45 (11%)	6	13
All	All	1696/1696 (100%)	1554 (92%)	142 (8%)	11	21

All (142) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	ARG
1	A	13	SER
1	A	31	PHE
1	A	39	ARG
1	A	44	ARG
1	A	98	PRO
1	A	107	SER
1	A	111	GLU
1	A	138	THR
1	A	140	ASP
1	A	161	ILE
1	A	182	PRO
1	A	211	ARG
1	A	226	GLN

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Mol	Chain	Res	Type
1	A	300	GLU
1	A	314	LEU
1	A	335	MET
1	A	342	CYS
1	A	348	TRP
1	A	350	GLN
1	A	356	SER
1	A	366	SER
1	A	381	TRP
1	A	406	ILE
1	A	408	LYS
1	A	410	THR
1	A	433	ARG
1	A	455	SER
1	A	493	LEU
1	A	495	HIS
1	B	30	THR
1	B	39	ARG
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	107	SER
1	B	165	LEU
1	B	166	GLN
1	B	182	PRO
1	B	235	GLU
1	B	246	PHE
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	378	TRP

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Mol	Chain	Res	Type
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	450	MET
1	B	457	VAL
1	B	470	LEU
1	B	480	LEU
1	B	489	ILE
1	B	497	GLN
1	C	2	ARG
1	C	4	CYS
1	C	31	PHE
1	C	39	ARG
1	C	44	ARG
1	C	50	GLU
1	C	57	GLN
1	C	77	LYS
1	C	107	SER
1	C	110	SER
1	C	111	GLU
1	C	165	LEU
1	C	204	ILE
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	348	TRP
1	C	350	GLN
1	C	356	SER
1	C	366	SER
1	C	379	THR
1	C	381	TRP
1	C	395	ARG
1	C	406	ILE
1	C	410	THR
1	C	466	LYS
1	D	2	ARG

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Mol	Chain	Res	Type
1	D	31	PHE
1	D	34	LEU
1	D	39	ARG
1	D	44	ARG
1	D	49	MET
1	D	61	THR
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	155	LYS
1	D	194	LYS
1	D	224	LYS
1	D	235	GLU
1	D	246	PHE
1	D	272	THR
1	D	313	TYR
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	356	SER
1	D	358	ASP
1	D	381	TRP
1	D	388	GLU
1	D	396	ASN
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	470	LEU
1	D	471	THR
1	D	493	LEU

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Mol	Chain	Res	Type
1	D	495	HIS
1	D	497	GLN

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

Mol	Chain	Res	Type
1	A	60	HIS
1	A	362	GLN
1	A	365	HIS
1	A	495	HIS
1	B	57	GLN
1	B	162	HIS
1	B	350	GLN
1	B	362	GLN
1	B	374	HIS
1	B	432	GLN
1	B	495	HIS
1	C	60	HIS
1	C	223	HIS
1	C	365	HIS
1	D	60	HIS
1	D	143	GLN
1	D	162	HIS

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

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	C	500	-	4,4,4	1.16	0	6,6,6	1.00	0
2	PO4	D	505	-	4,4,4	0.91	0	6,6,6	0.49	0
3	NAG	D	510	1	14,14,15	0.64	0	17,19,21	2.60	1 (5%)
2	PO4	C	508	-	4,4,4	0.75	0	6,6,6	0.68	0
2	PO4	C	505	-	4,4,4	0.92	0	6,6,6	0.72	0
2	PO4	A	505	-	4,4,4	0.78	0	6,6,6	0.86	0
2	PO4	B	500	-	4,4,4	1.16	0	6,6,6	0.86	0
2	PO4	A	509	-	4,4,4	0.91	0	6,6,6	0.77	0
2	PO4	C	511	-	4,4,4	0.82	0	6,6,6	0.30	0
2	PO4	B	503	-	4,4,4	1.06	0	6,6,6	0.77	0
2	PO4	C	504	-	4,4,4	0.98	0	6,6,6	0.63	0
2	PO4	B	498	-	4,4,4	0.75	0	6,6,6	0.64	0
2	PO4	B	507	-	4,4,4	0.82	0	6,6,6	0.31	0
2	PO4	A	510	-	4,4,4	0.86	0	6,6,6	0.55	0
3	NAG	D	509	1	14,14,15	0.67	0	17,19,21	1.73	2 (11%)
2	PO4	D	498	-	4,4,4	1.02	0	6,6,6	0.72	0
2	PO4	A	506	-	4,4,4	0.86	0	6,6,6	0.72	0
2	PO4	D	507	-	4,4,4	0.83	0	6,6,6	0.46	0
2	PO4	B	501	-	4,4,4	1.07	0	6,6,6	1.03	0
2	PO4	D	508	-	4,4,4	0.73	0	6,6,6	0.62	0
2	PO4	C	502	-	4,4,4	0.80	0	6,6,6	0.83	0
2	PO4	D	504	-	4,4,4	0.87	0	6,6,6	0.43	0
3	NAG	A	513	1	14,14,15	0.79	0	17,19,21	1.55	4 (23%)
2	PO4	C	498	-	4,4,4	0.79	0	6,6,6	0.87	0
2	PO4	A	503	-	4,4,4	0.93	0	6,6,6	1.46	1 (16%)
2	PO4	A	500	-	4,4,4	0.84	0	6,6,6	0.60	0
2	PO4	A	499	-	4,4,4	1.36	0	6,6,6	1.45	1 (16%)
2	PO4	B	505	-	4,4,4	0.66	0	6,6,6	0.61	0
2	PO4	B	502	-	4,4,4	0.90	0	6,6,6	0.77	0
2	PO4	D	502	-	4,4,4	1.02	0	6,6,6	0.71	0
2	PO4	A	501	-	4,4,4	0.97	0	6,6,6	0.98	0
2	PO4	D	501	-	4,4,4	0.47	0	6,6,6	1.09	0
2	PO4	A	512	-	4,4,4	0.86	0	6,6,6	0.69	0
2	PO4	B	499	-	4,4,4	0.84	0	6,6,6	0.52	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	PO4	C	506	-	4,4,4	0.83	0	6,6,6	0.52	0
2	PO4	B	504	-	4,4,4	0.76	0	6,6,6	0.57	0
2	PO4	A	502	-	4,4,4	0.90	0	6,6,6	1.43	2 (33%)
2	PO4	D	500	-	4,4,4	0.97	0	6,6,6	0.84	0
2	PO4	A	507	-	4,4,4	0.81	0	6,6,6	1.29	0
2	PO4	A	498	-	4,4,4	0.73	0	6,6,6	0.88	0
2	PO4	C	499	-	4,4,4	0.91	0	6,6,6	1.48	2 (33%)
2	PO4	A	504	-	4,4,4	0.62	0	6,6,6	1.20	1 (16%)
2	PO4	B	506	-	4,4,4	0.96	0	6,6,6	0.63	0
2	PO4	A	508	-	4,4,4	0.81	0	6,6,6	0.61	0
2	PO4	C	501	-	4,4,4	0.78	0	6,6,6	0.85	0
2	PO4	A	511	-	4,4,4	0.82	0	6,6,6	0.67	0
3	NAG	C	510	1	14,14,15	0.99	0	17,19,21	1.48	1 (5%)
2	PO4	D	503	-	4,4,4	0.95	0	6,6,6	0.97	0
2	PO4	C	509	-	4,4,4	0.88	0	6,6,6	1.02	0
2	PO4	D	499	-	4,4,4	0.90	0	6,6,6	0.89	0
2	PO4	A	514	-	4,4,4	0.93	0	6,6,6	0.49	0
2	PO4	C	503	-	4,4,4	0.65	0	6,6,6	0.84	0
2	PO4	D	506	-	4,4,4	0.80	0	6,6,6	0.40	0
3	NAG	B	508	1	14,14,15	0.79	0	17,19,21	1.88	6 (35%)
2	PO4	C	507	-	4,4,4	0.78	0	6,6,6	0.63	0
3	NAG	B	509	1	14,14,15	0.67	0	17,19,21	2.28	4 (23%)

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

There are no bond length outliers.

All (25) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	510	NAG	C1-O5-C5	9.78	125.44	112.19
3	B	509	NAG	C1-O5-C5	7.03	121.72	112.19
3	D	509	NAG	C4-C3-C2	4.68	117.88	111.02
3	C	510	NAG	C2-N2-C7	-3.92	117.32	122.90
3	D	509	NAG	C3-C4-C5	3.60	116.67	110.24
3	B	509	NAG	C4-C3-C2	3.31	115.87	111.02
3	B	508	NAG	C2-N2-C7	3.30	127.60	122.90
3	A	513	NAG	C1-O5-C5	3.16	116.47	112.19
3	B	508	NAG	O7-C7-C8	-2.85	116.77	122.06
3	B	508	NAG	C4-C3-C2	2.75	115.05	111.02
3	B	508	NAG	O5-C5-C6	2.63	111.33	107.20
2	C	499	PO4	O3-P-O1	-2.61	101.35	110.89
2	A	504	PO4	O4-P-O2	2.55	116.15	107.97
3	A	513	NAG	C4-C3-C2	2.54	114.75	111.02
2	A	502	PO4	O4-P-O2	2.43	115.77	107.97
3	B	509	NAG	O3-C3-C2	-2.42	104.46	109.47
3	B	509	NAG	C2-N2-C7	-2.39	119.50	122.90
2	A	502	PO4	O2-P-O1	-2.36	102.27	110.89
3	B	508	NAG	C3-C4-C5	2.23	114.21	110.24
3	A	513	NAG	O4-C4-C5	2.20	114.76	109.30
3	A	513	NAG	C6-C5-C4	-2.18	107.90	113.00
2	A	503	PO4	O3-P-O2	-2.12	101.16	107.97
2	C	499	PO4	O3-P-O2	2.07	114.60	107.97
3	B	508	NAG	C1-C2-N2	2.06	114.02	110.49
2	A	499	PO4	O4-P-O3	-2.06	101.35	107.97

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
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.

15 monomers are involved in 24 short contacts:

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

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	497/497 (100%)	0.38	15 (3%)	50	53	30, 46, 67, 76	0
1	B	497/497 (100%)	0.37	18 (3%)	42	46	33, 48, 73, 87	0
1	C	497/497 (100%)	0.35	12 (2%)	59	62	29, 47, 67, 75	0
1	D	497/497 (100%)	0.41	19 (3%)	40	43	34, 47, 72, 88	0
All	All	1988/1988 (100%)	0.38	64 (3%)	47	51	29, 47, 69, 88	0

All (64) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	317	LEU	12.1
1	C	318	ALA	8.1
1	A	312	TRP	6.1
1	D	317	LEU	5.7
1	A	347	PHE	4.9
1	D	316	PHE	4.7
1	D	347	PHE	4.1
1	C	378	TRP	4.1
1	C	301	ALA	4.0
1	B	291	TRP	3.7
1	A	137	ASP	3.3
1	C	194	LYS	3.2
1	B	34	LEU	3.0
1	C	51	LEU	3.0
1	A	318	ALA	2.9
1	D	301	ALA	2.9
1	A	197	LEU	2.9
1	D	260	ILE	2.8
1	A	313	TYR	2.8
1	A	331	PHE	2.7
1	D	63	THR	2.7

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Mol	Chain	Res	Type	RSRZ
1	A	31	PHE	2.7
1	B	53	MET	2.7
1	D	278	LEU	2.6
1	D	324	LEU	2.6
1	B	105	LEU	2.6
1	A	468	VAL	2.6
1	B	314	LEU	2.6
1	B	347	PHE	2.5
1	B	30	THR	2.5
1	B	494	TRP	2.5
1	D	29	PRO	2.5
1	D	443	ASP	2.4
1	C	61	THR	2.4
1	B	69	LEU	2.4
1	B	436	LEU	2.4
1	D	388	GLU	2.3
1	B	29	PRO	2.3
1	C	316	PHE	2.3
1	B	156	LEU	2.3
1	C	379	THR	2.3
1	C	208	THR	2.3
1	D	295	VAL	2.2
1	C	214	VAL	2.2
1	C	398	VAL	2.2
1	B	316	PHE	2.2
1	A	420	LEU	2.2
1	B	304	TYR	2.2
1	D	170	ARG	2.2
1	D	175	LEU	2.2
1	B	276	VAL	2.1
1	D	315	ASP	2.1
1	D	397	PHE	2.1
1	D	65	LEU	2.1
1	A	384	ALA	2.1
1	D	472	ILE	2.1
1	A	354	LEU	2.1
1	D	450	MET	2.0
1	B	26	PHE	2.0
1	B	259	PHE	2.0
1	A	343	VAL	2.0
1	A	250	GLY	2.0
1	B	461	LEU	2.0

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Mol	Chain	Res	Type	RSRZ
1	A	57	GLN	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 monosaccharides in this entry.

6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	PO4	A	508	5/5	0.77	0.21	119,120,120,120	0
2	PO4	A	506	5/5	0.82	0.20	80,80,82,83	0
3	NAG	B	508	14/15	0.82	0.19	62,69,73,73	0
3	NAG	A	513	14/15	0.86	0.17	54,63,64,65	0
2	PO4	A	512	5/5	0.86	0.15	101,102,102,103	0
2	PO4	B	498	5/5	0.87	0.11	105,106,107,107	0
2	PO4	D	503	5/5	0.87	0.14	77,78,82,82	0
2	PO4	C	508	5/5	0.88	0.20	95,96,96,97	0
2	PO4	D	506	5/5	0.88	0.09	113,113,114,114	0
2	PO4	A	509	5/5	0.88	0.14	101,101,102,102	0
3	NAG	C	510	14/15	0.89	0.14	56,62,68,68	0
2	PO4	A	504	5/5	0.89	0.20	74,74,76,77	0
3	NAG	D	509	14/15	0.89	0.14	69,73,75,76	0
3	NAG	B	509	14/15	0.89	0.20	44,50,53,54	0
2	PO4	A	511	5/5	0.91	0.20	123,123,123,124	0
2	PO4	B	499	5/5	0.91	0.12	80,81,82,83	0
2	PO4	C	509	5/5	0.91	0.31	86,86,87,89	0
2	PO4	A	514	5/5	0.91	0.19	95,95,95,96	0
2	PO4	A	507	5/5	0.91	0.10	73,74,75,76	0
2	PO4	D	507	5/5	0.91	0.16	83,83,84,86	0
3	NAG	D	510	14/15	0.91	0.15	49,55,57,58	0
2	PO4	C	504	5/5	0.92	0.13	74,76,78,79	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	PO4	B	504	5/5	0.92	0.16	75,76,77,80	0
2	PO4	C	506	5/5	0.93	0.12	88,88,89,89	0
2	PO4	C	507	5/5	0.93	0.15	102,103,104,104	0
2	PO4	A	505	5/5	0.93	0.10	86,86,86,87	0
2	PO4	D	504	5/5	0.94	0.27	88,89,90,90	0
2	PO4	A	498	5/5	0.94	0.15	67,70,71,71	0
2	PO4	A	510	5/5	0.94	0.17	76,76,79,79	0
2	PO4	C	502	5/5	0.94	0.12	87,87,88,89	0
2	PO4	B	506	5/5	0.95	0.16	75,76,77,77	0
2	PO4	B	507	5/5	0.95	0.09	102,103,103,104	0
2	PO4	D	501	5/5	0.95	0.10	68,68,71,71	0
2	PO4	C	511	5/5	0.95	0.20	92,92,92,93	0
2	PO4	D	508	5/5	0.95	0.12	84,84,85,86	0
2	PO4	D	505	5/5	0.95	0.15	80,80,81,81	0
2	PO4	C	505	5/5	0.95	0.09	99,99,100,100	0
2	PO4	B	505	5/5	0.95	0.10	84,84,87,87	0
2	PO4	B	502	5/5	0.95	0.12	64,66,67,68	0
2	PO4	D	502	5/5	0.95	0.13	51,54,56,57	0
2	PO4	B	501	5/5	0.96	0.14	64,67,67,69	0
2	PO4	C	498	5/5	0.96	0.11	70,72,72,73	0
2	PO4	B	503	5/5	0.97	0.09	58,60,61,63	0
2	PO4	D	498	5/5	0.97	0.12	78,79,80,81	0
2	PO4	A	503	5/5	0.97	0.14	59,60,60,63	0
2	PO4	C	503	5/5	0.97	0.15	73,73,75,76	0
2	PO4	A	500	5/5	0.97	0.11	66,68,69,70	0
2	PO4	A	501	5/5	0.97	0.15	53,53,56,57	0
2	PO4	C	501	5/5	0.97	0.13	54,56,58,60	0
2	PO4	D	500	5/5	0.97	0.13	59,60,61,62	0
2	PO4	B	500	5/5	0.98	0.14	47,47,49,50	0
2	PO4	A	499	5/5	0.98	0.13	36,40,41,44	0
2	PO4	A	502	5/5	0.98	0.10	63,64,65,67	0
2	PO4	D	499	5/5	0.98	0.15	42,45,48,50	0
2	PO4	C	499	5/5	0.98	0.13	60,60,62,63	0
2	PO4	C	500	5/5	0.99	0.12	37,40,41,45	0

6.5 Other polymers ⓘ

There are no such residues in this entry.