



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 10:15 AM UTC

PDB ID : 3CEM / pdb_00003cem
Title : Human glycogen phosphorylase (tense state) in complex with the allosteric inhibitor AVE9423
Authors : Wendt, K.U.; Dreyer, M.K.; Anderka, O.; Klabunde, T.; Loenze, P.; Defossa, E.; Schmoll, D.
Deposited on : 2008-02-29
Resolution : 2.47 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
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
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

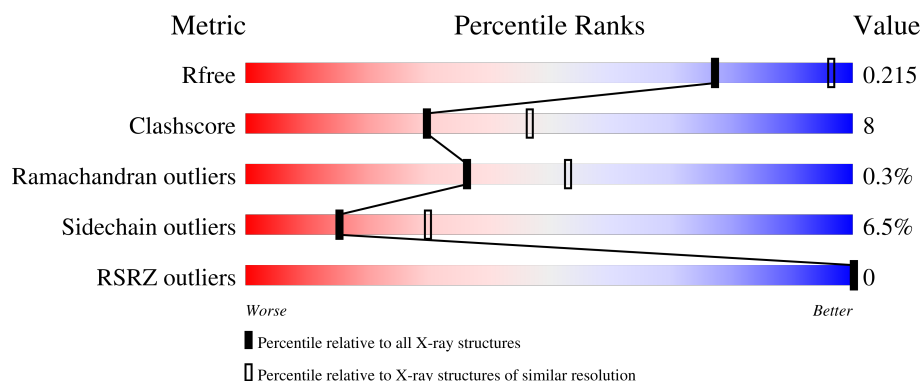
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.47 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	7589 (2.50-2.46)
Clashscore	190562	8295 (2.50-2.46)
Ramachandran outliers	187476	8164 (2.50-2.46)
Sidechain outliers	187428	8166 (2.50-2.46)
RSRZ outliers	180081	7593 (2.50-2.46)

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	809	 77% 19% ..
1	B	809	 75% 21% ..

2 Entry composition [i](#)

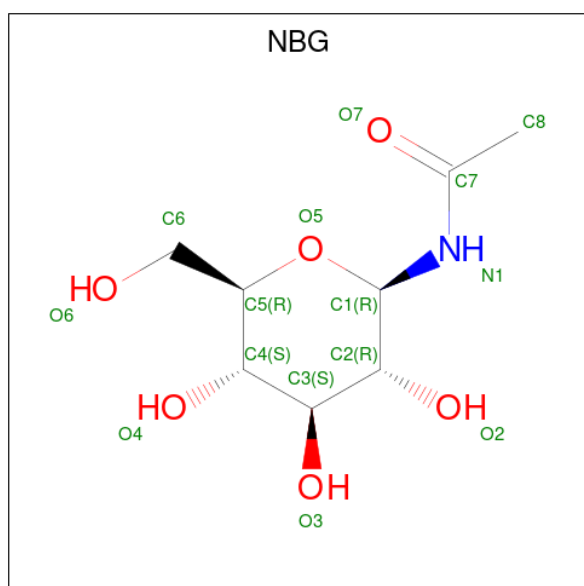
There are 5 unique types of molecules in this entry. The entry contains 13570 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Glycogen phosphorylase, liver form.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	794	Total	C	N	O	S	0	1	0
			6460	4150	1097	1184	29			
1	B	794	Total	C	N	O	S	0	3	0
			6479	4161	1101	1188	29			

- Molecule 2 is N-acetyl-beta-D-glucopyranosylamine (CCD ID: NBG) (formula: $C_8H_{15}NO_6$).



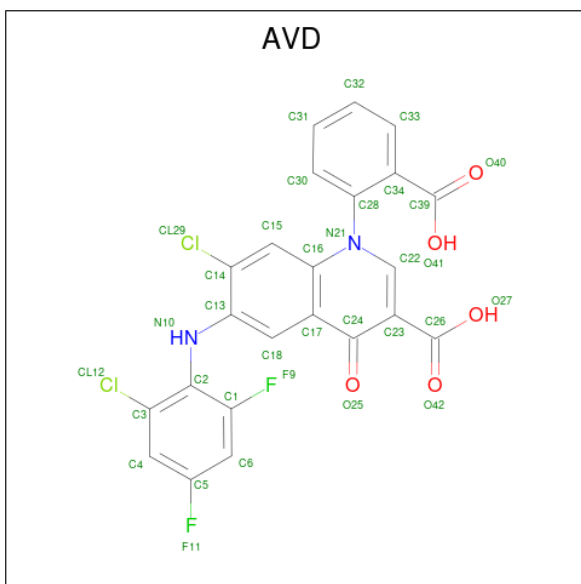
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			15	8	1	6		
2	B	1	Total	C	N	O	0	0
			15	8	1	6		

- Molecule 3 is PYRIDOXAL-5'-PHOSPHATE (CCD ID: PLP) (formula: $C_8H_{10}NO_6P$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			16	8	1	6	1		
3	B	1	Total	C	N	O	P	0	0
			16	8	1	6	1		

- Molecule 4 is 1-(2-carboxyphenyl)-7-chloro-6-[(2-chloro-4,6-difluorophenyl)amino]-4-oxo-1,4-dihydroquinoline-3-carboxylic acid (CCD ID: AVD) (formula: $C_{23}H_{12}Cl_2F_2N_2O_5$).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
4	A	1	Total	C	Cl	F	N	O	0	0
			34	23	2	2	2	5		

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Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
4	B	1	Total	C	Cl	F	N	O	0	0
			34	23	2	2	2	5		

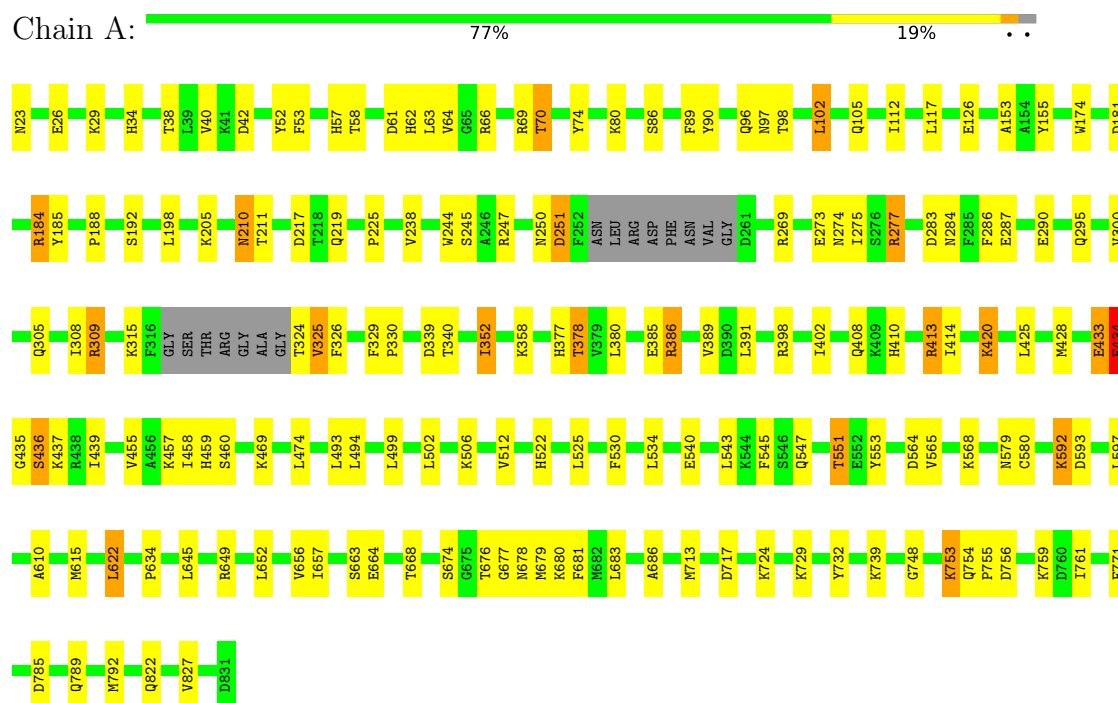
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	274	Total	O	0	0
			274	274		
5	B	227	Total	O	0	0
			227	227		

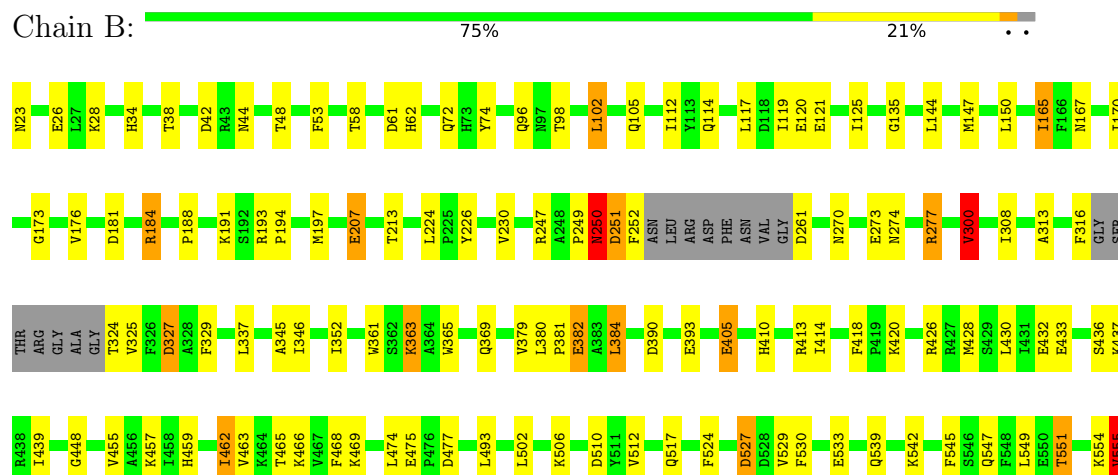
3 Residue-property plots

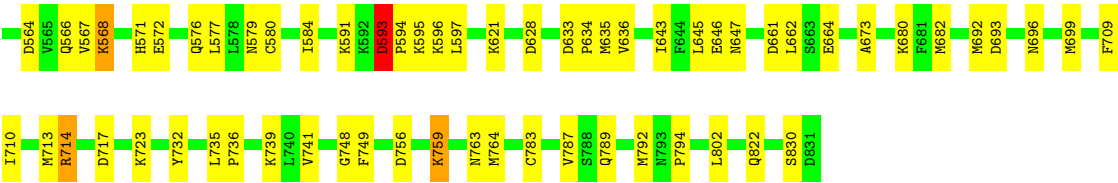
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density.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



- Molecule 1: Glycogen phosphorylase, liver form





4 Data and refinement statistics

Property	Value	Source
Space group	P 31	Depositor
Cell constants a, b, c, α , β , γ	124.38Å 124.38Å 123.43Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	49.39 – 2.47 49.39 – 2.47	Depositor EDS
% Data completeness (in resolution range)	100.0 (49.39-2.47) 99.9 (49.39-2.47)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.45 (at 2.48Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.155 , 0.215 0.156 , 0.215	Depositor DCC
R_{free} test set	5343 reflections (6.97%)	wwPDB-VP
Wilson B-factor (Å ²)	34.6	Xtriage
Anisotropy	0.016	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 18.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.27$	Xtriage
Estimated twinning fraction	0.029 for -h,-k,l 0.095 for h,-h-k,-l 0.037 for -k,-h,-l	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	13570	wwPDB-VP
Average B, all atoms (Å ²)	35.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.32% 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: NBG, AVD, PLP

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	1.14	5/6605 (0.1%)	1.18	17/8931 (0.2%)
1	B	1.12	5/6625 (0.1%)	1.15	13/8958 (0.1%)
All	All	1.13	10/13230 (0.1%)	1.17	30/17889 (0.2%)

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	2

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	300	VAL	CA-CB	6.56	1.62	1.54
1	B	165	ILE	CA-CB	6.07	1.61	1.54
1	A	657	ILE	C-O	-5.96	1.19	1.24
1	A	352	ILE	CA-CB	5.91	1.61	1.54
1	A	656	VAL	CA-CB	5.80	1.62	1.54
1	B	250	ASN	N-CA	-5.39	1.38	1.46
1	B	193	ARG	C-O	5.29	1.30	1.24
1	A	534	LEU	N-CA	-5.19	1.40	1.46
1	A	174	TRP	N-CA	5.15	1.52	1.46
1	B	313	ALA	CA-CB	5.02	1.62	1.53

All (30) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	553	TYR	CA-C-N	-8.98	110.37	122.85

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	553	TYR	C-N-CA	-8.98	110.37	122.85
1	A	377	HIS	CB-CA-C	-6.90	99.85	111.02
1	A	525	LEU	N-CA-C	6.84	119.58	111.71
1	A	309	ARG	CA-CB-CG	6.64	127.38	114.10
1	B	593	ASP	CA-C-N	6.53	126.22	119.82
1	B	593	ASP	C-N-CA	6.53	126.22	119.82
1	B	390	ASP	N-CA-C	6.12	117.95	111.28
1	A	69	ARG	N-CA-C	6.10	118.72	111.71
1	A	676	THR	N-CA-C	-5.97	107.82	114.62
1	A	309	ARG	N-CA-CB	5.85	118.72	110.12
1	A	610	ALA	CA-C-N	5.75	125.60	119.28
1	A	610	ALA	C-N-CA	5.75	125.60	119.28
1	B	555	VAL	N-CA-C	5.66	121.12	109.34
1	A	192	SER	N-CA-CB	-5.58	101.41	109.83
1	A	287	GLU	N-CA-C	-5.40	99.61	108.41
1	A	545	PHE	N-CA-C	5.39	117.23	111.36
1	B	418	PHE	CA-C-N	5.39	125.21	119.28
1	B	418	PHE	C-N-CA	5.39	125.21	119.28
1	B	462	ILE	N-CA-C	5.36	115.99	110.36
1	A	315	LYS	N-CA-C	5.34	119.29	112.34
1	A	677	GLY	N-CA-C	-5.34	106.30	112.50
1	B	273	GLU	CA-CB-CG	-5.33	103.44	114.10
1	B	439	ILE	CB-CA-C	-5.31	104.53	110.96
1	A	283	ASP	N-CA-C	-5.30	100.09	108.73
1	B	135	GLY	N-CA-C	5.23	119.00	112.73
1	A	565	VAL	N-CA-C	5.16	115.40	107.77
1	B	329	PHE	CA-C-N	-5.15	114.40	120.12
1	B	329	PHE	C-N-CA	-5.15	114.40	120.12
1	B	74	TYR	N-CA-C	-5.00	106.02	111.82

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	249	PRO	Peptide
1	B	250	ASN	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	6460	0	6447	108	0
1	B	6479	0	6458	118	0
2	A	15	0	15	0	0
2	B	15	0	14	0	0
3	A	16	0	7	1	0
3	B	16	0	7	2	0
4	A	34	0	10	0	0
4	B	34	0	10	0	0
5	A	274	0	0	17	0
5	B	227	0	0	13	0
All	All	13570	0	12968	220	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 8.

All (220) 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:A:547:GLN:O	1:A:551:THR:HG23	1.57	1.02
1:B:250:ASN:HA	1:B:251:ASP:OD2	1.61	1.00
1:B:96:GLN:HE21	1:B:105:GLN:HE22	0.94	0.94
1:A:615:MET:HE1	1:A:761:ILE:HG12	1.51	0.91
1:B:361:TRP:CH2	1:B:405:GLU:HG2	2.06	0.90
1:A:66:ARG:O	1:A:70:THR:HG23	1.72	0.89
1:A:305:GLN:HG3	5:A:863:HOH:O	1.74	0.85
1:B:274:ASN:ND2	1:B:277:ARG:HH11	1.74	0.85
1:B:96:GLN:HE21	1:B:105:GLN:NE2	1.76	0.83
1:A:184:ARG:HH11	1:A:184:ARG:HG3	1.44	0.81
1:A:96:GLN:HE21	1:A:105:GLN:HE22	1.26	0.81
1:A:198:LEU:HD22	1:A:305:GLN:NE2	1.95	0.81
1:B:251:ASP:HB3	1:B:252:PHE:HA	1.62	0.81
1:B:96:GLN:NE2	1:B:105:GLN:HE22	1.79	0.79
1:B:714:ARG:HH11	1:B:714:ARG:HG2	1.48	0.78
1:A:290:GLU:HG3	1:A:391:LEU:HD11	1.66	0.78
1:B:756:ASP:HB2	5:B:1031:HOH:O	1.84	0.78
1:A:66:ARG:O	1:A:70:THR:CG2	2.32	0.77
1:A:634:PRO:HA	5:A:905:HOH:O	1.86	0.75
1:B:830:SER:HB3	5:B:1019:HOH:O	1.87	0.74
1:A:34:HIS:HD2	1:A:38:THR:OG1	1.71	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:70:THR:HG21	1:A:238:VAL:H	1.52	0.73
1:A:324:THR:N	1:A:325:VAL:HB	2.04	0.72
1:A:251:ASP:N	1:A:251:ASP:OD1	2.23	0.72
1:B:274:ASN:HD22	1:B:277:ARG:HH11	1.35	0.71
1:A:386:ARG:HH11	1:A:386:ARG:HB2	1.56	0.70
1:A:274:ASN:ND2	1:A:277:ARG:HH11	1.91	0.69
1:B:170:ILE:HG12	1:B:646:GLU:HG2	1.74	0.68
1:B:251:ASP:CB	1:B:252:PHE:HA	2.22	0.68
3:B:832:PLP:O4A	3:B:832:PLP:H5A1	1.94	0.67
1:B:455:VAL:H	1:B:459:HIS:HD2	1.43	0.67
1:B:591:LYS:HZ2	1:B:635:MET:HG3	1.59	0.67
1:A:184:ARG:NH2	1:B:250:ASN:HB3	2.10	0.66
1:A:324:THR:HA	1:A:326:PHE:H	1.58	0.66
1:B:436:SER:O	1:B:437:LYS:HB2	1.94	0.66
1:A:615:MET:CE	1:A:761:ILE:HG12	2.25	0.66
1:A:80:LYS:HB3	1:A:827:VAL:HG12	1.78	0.65
1:B:527:ASP:OD2	1:B:529:VAL:HB	1.97	0.64
1:A:437:LYS:HD2	5:A:1057:HOH:O	1.97	0.64
1:A:184:ARG:HG3	1:A:184:ARG:NH1	2.12	0.64
1:B:316:PHE:C	5:B:971:HOH:O	2.40	0.64
1:B:547:GLN:O	1:B:551:THR:HG23	1.97	0.64
1:B:181:ASP:OD2	1:B:184:ARG:HG3	1.97	0.63
1:B:633:ASP:OD2	1:B:635:MET:HB2	1.99	0.63
1:A:181:ASP:OD2	1:A:184:ARG:NH1	2.32	0.62
1:B:250:ASN:CA	1:B:251:ASP:OD2	2.43	0.62
1:B:224:LEU:HD23	1:B:247[A]:ARG:HE	1.65	0.62
1:B:436:SER:HA	5:B:1028:HOH:O	1.99	0.62
1:B:477:ASP:HB2	5:B:901:HOH:O	2.00	0.61
1:B:324:THR:HA	1:B:327:ASP:OD1	2.01	0.61
1:B:584:ILE:HG22	1:B:741:VAL:HG22	1.82	0.61
1:B:34:HIS:HD2	1:B:38:THR:OG1	1.84	0.61
1:B:34:HIS:HE1	1:B:61:ASP:OD2	1.83	0.61
1:A:274:ASN:HD22	1:A:277:ARG:HH11	1.49	0.60
1:B:591:LYS:NZ	1:B:635:MET:HG3	2.15	0.60
1:B:361:TRP:CZ3	1:B:405:GLU:HG2	2.36	0.60
1:B:662:LEU:HD22	1:B:787:VAL:HG11	1.84	0.60
1:A:184:ARG:HD2	1:A:185:TYR:CZ	2.38	0.59
1:B:542:LYS:NZ	1:B:661:ASP:OD2	2.26	0.59
1:B:207:GLU:HG3	5:B:859:HOH:O	2.03	0.59
1:A:597:LEU:HA	5:A:984:HOH:O	2.03	0.59
1:A:455:VAL:HG23	1:A:674:SER:HB2	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:274:ASN:HD22	1:B:277:ARG:HD2	1.67	0.59
1:A:29:LYS:HE2	5:A:1046:HOH:O	2.02	0.58
1:A:592:LYS:HD2	1:A:592:LYS:O	2.04	0.58
1:A:732:TYR:CE1	1:A:739:LYS:HG3	2.39	0.58
1:B:579:ASN:C	1:B:579:ASN:HD22	2.12	0.57
1:B:226:TYR:OH	1:B:247[A]:ARG:NH2	2.37	0.57
1:B:23:ASN:HD22	1:B:26[A]:GLU:HG2	1.69	0.56
1:B:42:ASP:HB3	5:B:1056:HOH:O	2.04	0.56
1:A:274:ASN:HD22	1:A:277:ARG:HD2	1.71	0.56
1:B:759:LYS:O	1:B:763:ASN:HB2	2.06	0.56
1:A:286:PHE:CD1	1:A:385:GLU:HG2	2.41	0.55
1:B:197:MET:HE3	1:B:224:LEU:HB2	1.89	0.55
1:A:785:ASP:O	1:A:789:GLN:HG3	2.06	0.54
1:B:566:GLN:HE22	1:B:576:GLN:HA	1.71	0.54
1:B:714:ARG:HH11	1:B:714:ARG:CG	2.17	0.54
1:A:522:HIS:CD2	5:A:860:HOH:O	2.60	0.54
1:A:34:HIS:HE1	1:A:61:ASP:OD2	1.91	0.54
1:A:580:CYS:SG	1:A:622:LEU:HD13	2.48	0.53
1:A:339:ASP:OD1	1:A:340:THR:N	2.38	0.53
1:A:42:ASP:HB2	5:A:910:HOH:O	2.07	0.53
1:A:184:ARG:HA	1:B:247[B]:ARG:NH1	2.24	0.53
1:A:398:ARG:O	1:A:402:ILE:HG13	2.09	0.53
1:B:593:ASP:C	1:B:595:LYS:H	2.15	0.53
5:A:1016:HOH:O	1:B:250:ASN:HB3	2.08	0.53
1:B:713:MET:HB3	1:B:717:ASP:HB2	1.90	0.52
1:A:247[B]:ARG:NH2	1:B:184:ARG:HG2	2.25	0.52
1:B:48:THR:HG22	1:B:125:ILE:HG13	1.92	0.52
1:A:275:ILE:O	1:A:295:GLN:HG2	2.09	0.52
1:B:554:LYS:HG3	1:B:555:VAL:H	1.75	0.51
1:A:455:VAL:H	1:A:459:HIS:HD2	1.59	0.51
1:B:261:ASP:HB3	5:B:1058:HOH:O	2.10	0.51
1:B:361:TRP:CH2	1:B:405:GLU:CG	2.87	0.51
1:A:414:ILE:HG22	1:A:425:LEU:HD23	1.93	0.51
1:A:420:LYS:O	1:A:420:LYS:HG2	2.11	0.51
1:A:74:TYR:CZ	1:A:153:ALA:HA	2.46	0.50
1:A:579:ASN:C	1:A:579:ASN:HD22	2.20	0.50
1:A:680:LYS:NZ	3:A:832:PLP:O3	2.43	0.50
1:A:494:LEU:C	1:A:494:LEU:HD23	2.37	0.50
1:A:210:ASN:C	1:A:210:ASN:HD22	2.19	0.50
5:A:1016:HOH:O	1:B:250:ASN:CB	2.60	0.50
1:A:789:GLN:HA	1:A:792:MET:HE3	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:408:GLN:HG3	5:A:1064:HOH:O	2.12	0.49
1:A:324:THR:N	1:A:325:VAL:CB	2.73	0.49
1:B:300:VAL:HG13	1:B:345:ALA:HA	1.95	0.49
1:B:692:MET:HG2	1:B:710:ILE:HG21	1.94	0.49
1:A:185:TYR:CD2	1:B:194:PRO:HB3	2.48	0.49
1:A:410:HIS:HD2	1:A:413:ARG:HH11	1.60	0.49
1:A:436:SER:HB3	5:A:990:HOH:O	2.12	0.49
1:A:678:ASN:OD1	1:A:679:MET:N	2.45	0.49
1:A:63:LEU:C	1:A:63:LEU:HD12	2.37	0.48
1:A:386:ARG:HB2	1:A:386:ARG:NH1	2.26	0.48
1:A:506:LYS:HG3	1:A:530:PHE:CE1	2.48	0.48
1:B:112:ILE:HG13	1:B:119:ILE:HD13	1.95	0.48
1:A:211:THR:O	1:A:358:LYS:NZ	2.46	0.48
1:A:53:PHE:HE1	1:A:188:PRO:HD3	1.78	0.48
1:B:530:PHE:HE2	1:B:802:LEU:HD13	1.79	0.48
1:B:173:GLY:HA3	5:B:963:HOH:O	2.13	0.48
1:B:346:ILE:HD13	1:B:448:GLY:HA3	1.96	0.48
1:B:732:TYR:CE1	1:B:739:LYS:HG3	2.49	0.47
1:B:506:LYS:HB3	1:B:524:PHE:CZ	2.49	0.47
1:B:510:ASP:HB3	1:B:517:GLN:OE1	2.15	0.47
1:B:680:LYS:NZ	3:B:832:PLP:O3	2.47	0.47
1:A:324:THR:HG21	5:A:1021:HOH:O	2.14	0.47
1:A:308:ILE:HD13	1:A:352:ILE:HG21	1.97	0.47
1:A:386:ARG:HA	1:A:439:ILE:O	2.15	0.47
1:A:753:LYS:O	1:A:754:GLN:HG3	2.14	0.47
1:B:381:PRO:HA	1:B:384:LEU:HD22	1.96	0.47
1:B:571[A]:HIS:ND1	1:B:572:GLU:N	2.62	0.47
1:B:692:MET:HE2	1:B:710:ILE:HG13	1.96	0.47
1:B:379:VAL:CG2	1:B:673:ALA:HB2	2.45	0.47
1:A:460:SER:HB2	5:A:1042:HOH:O	2.15	0.47
1:B:380:LEU:HG	1:B:382:GLU:OE2	2.15	0.47
1:B:591:LYS:HZ2	1:B:635:MET:CG	2.27	0.46
1:A:436:SER:HA	5:A:1018:HOH:O	2.15	0.46
1:B:477:ASP:N	5:B:901:HOH:O	2.47	0.46
1:B:539:GLN:OE1	1:B:539:GLN:HA	2.16	0.46
1:A:668:THR:OG1	1:A:771:PHE:HB3	2.15	0.46
1:A:198:LEU:HD13	1:A:305:GLN:HB3	1.96	0.46
1:A:732:TYR:O	1:A:739:LYS:HB2	2.16	0.46
1:A:58:THR:O	1:A:62:HIS:HD2	1.98	0.46
1:A:410:HIS:HE1	1:A:428:MET:O	1.98	0.46
1:A:681:PHE:HB3	1:A:686:ALA:HB3	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:184:ARG:HH21	1:B:250:ASN:HB3	1.81	0.46
1:B:709:PHE:HB3	1:B:783:CYS:SG	2.56	0.45
1:A:57:HIS:HD2	5:A:1030:HOH:O	1.98	0.45
1:A:378:THR:HB	5:A:1061:HOH:O	2.16	0.45
1:B:58:THR:O	1:B:62:HIS:HD2	1.99	0.45
1:B:26[B]:GLU:OE1	1:B:62:HIS:HE1	2.00	0.45
1:B:593:ASP:O	1:B:595:LYS:N	2.50	0.45
1:A:547:GLN:O	1:A:551:THR:CG2	2.46	0.45
1:A:732:TYR:CZ	1:A:739:LYS:HG3	2.52	0.44
1:B:564:ASP:OD1	1:B:664:GLU:OE2	2.35	0.44
1:B:465:THR:O	1:B:469:LYS:HD3	2.16	0.44
1:B:432:GLU:O	1:B:437:LYS:HA	2.17	0.44
1:A:96:GLN:NE2	1:A:105:GLN:HE22	2.06	0.44
1:B:28:LYS:HE2	1:B:114:GLN:NE2	2.32	0.44
1:A:564:ASP:OD1	1:A:664:GLU:OE2	2.35	0.43
1:A:713:MET:HB3	1:A:717:ASP:HB2	2.00	0.43
1:B:144:LEU:HD23	1:B:147:MET:CE	2.48	0.43
1:A:649:ARG:HH11	1:A:649:ARG:HG2	1.82	0.43
1:A:410:HIS:HD2	1:A:413:ARG:NH1	2.16	0.43
1:B:764:MET:HB3	1:B:764:MET:HE3	1.82	0.43
1:B:732:TYR:CZ	1:B:739:LYS:HG3	2.52	0.43
1:B:365:TRP:CD1	1:B:369:GLN:NE2	2.86	0.43
1:B:635:MET:HA	5:B:992:HOH:O	2.18	0.43
1:A:86:SER:HB3	1:A:89:PHE:CE1	2.54	0.43
1:A:756:ASP:O	1:A:759:LYS:HB2	2.18	0.43
1:B:682:MET:HB2	1:B:699:MET:HE3	2.00	0.43
1:B:735:LEU:HA	1:B:736:PRO:HD2	1.72	0.43
1:B:748:GLY:O	1:B:749:PHE:C	2.61	0.43
1:A:184:ARG:HH11	1:A:184:ARG:CG	2.19	0.42
1:B:577:LEU:O	1:B:580:CYS:HB3	2.18	0.42
1:B:693:ASP:O	1:B:696:ASN:HB2	2.18	0.42
1:A:205:LYS:HB3	1:A:205:LYS:HE2	1.86	0.42
1:B:596:LYS:HG2	1:B:597:LEU:N	2.34	0.42
1:B:545:PHE:CE2	1:B:549:LEU:HD11	2.53	0.42
1:A:225:PRO:HB3	1:A:244:TRP:CZ3	2.55	0.42
1:A:250:ASN:ND2	1:A:269:ARG:HH22	2.18	0.42
1:B:98:THR:HG22	1:B:102:LEU:HD22	2.02	0.42
1:A:184:ARG:HH22	1:B:250:ASN:HB3	1.85	0.42
1:B:112:ILE:HG23	1:B:117:LEU:HB2	2.02	0.42
1:A:23:ASN:ND2	1:A:26:GLU:HG2	2.35	0.42
1:A:247[B]:ARG:HA	1:A:273:GLU:HG2	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:428:MET:HE1	1:A:474:LEU:HD22	2.01	0.42
1:B:361:TRP:CD1	1:B:361:TRP:C	2.97	0.42
1:A:98:THR:HG22	1:A:102:LEU:HD22	2.02	0.41
1:B:270:ASN:ND2	5:B:972:HOH:O	2.52	0.41
1:B:593:ASP:N	1:B:594:PRO:HD3	2.35	0.41
1:A:748:GLY:HA3	1:A:755:PRO:HA	2.02	0.41
1:B:463:VAL:HG13	1:B:468:PHE:CD1	2.55	0.41
1:B:633:ASP:HA	1:B:634:PRO:HD3	1.78	0.41
1:A:80:LYS:HE3	1:A:330:PRO:O	2.21	0.41
1:B:167:ASN:HD22	1:B:647:ASN:HD21	1.68	0.41
1:A:250:ASN:OD1	1:B:184:ARG:NH2	2.53	0.41
1:B:414:ILE:HD13	1:B:428:MET:SD	2.59	0.41
1:B:692:MET:HE2	1:B:710:ILE:HG21	2.03	0.41
1:B:363:LYS:HD3	1:B:363:LYS:O	2.20	0.41
1:A:198:LEU:HD23	1:A:198:LEU:HA	1.84	0.41
1:A:493:LEU:HD21	1:A:512:VAL:HG22	2.03	0.41
1:A:753:LYS:HA	1:A:753:LYS:HD2	1.99	0.41
1:B:593:ASP:C	1:B:595:LYS:N	2.79	0.41
1:A:66:ARG:O	1:A:70:THR:HG22	2.18	0.41
1:B:493:LEU:HD11	1:B:512:VAL:HG22	2.03	0.41
1:B:792:MET:O	1:B:794:PRO:HD3	2.20	0.41
1:B:567:VAL:O	1:B:568:LYS:HB3	2.21	0.40
1:A:97:ASN:ND2	5:A:891:HOH:O	2.54	0.40
1:A:433:GLU:O	1:A:434:GLU:O	2.38	0.40
1:B:42:ASP:HB2	5:B:886:HOH:O	2.20	0.40
1:B:144:LEU:HB3	1:B:230:VAL:HG11	2.04	0.40
1:B:530:PHE:HA	1:B:533:GLU:OE2	2.20	0.40
1:A:52:TYR:CZ	1:A:126:GLU:HB2	2.56	0.40
1:A:112:ILE:HG23	1:A:117:LEU:HB2	2.04	0.40
1:B:53:PHE:HE1	1:B:188:PRO:HD3	1.86	0.40
1:B:308:ILE:HD13	1:B:352:ILE:HG21	2.01	0.40
1:B:363:LYS:HD3	1:B:363:LYS:C	2.46	0.40
1:A:329:PHE:HB3	1:A:330:PRO:HD3	2.04	0.40
1:A:663:SER:HB2	1:A:681:PHE:CG	2.56	0.40
1:B:410:HIS:HE1	1:B:428:MET:O	2.04	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	789/809 (98%)	749 (95%)	37 (5%)	3 (0%)	30	46
1	B	791/809 (98%)	750 (95%)	39 (5%)	2 (0%)	36	53
All	All	1580/1618 (98%)	1499 (95%)	76 (5%)	5 (0%)	36	53

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	434	GLU
1	B	555	VAL
1	B	527	ASP
1	A	593	ASP
1	A	435	GLY

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	697/706 (99%)	653 (94%)	44 (6%)	16	31
1	B	699/706 (99%)	652 (93%)	47 (7%)	15	29
All	All	1396/1412 (99%)	1305 (94%)	91 (6%)	15	30

All (91) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	40	VAL

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Mol	Chain	Res	Type
1	A	64	VAL
1	A	70	THR
1	A	90	TYR
1	A	102	LEU
1	A	155	TYR
1	A	184	ARG
1	A	210	ASN
1	A	217	ASP
1	A	219	GLN
1	A	245	SER
1	A	251	ASP
1	A	277	ARG
1	A	284	ASN
1	A	300	VAL
1	A	309	ARG
1	A	325	VAL
1	A	378	THR
1	A	380	LEU
1	A	386	ARG
1	A	389	VAL
1	A	413	ARG
1	A	420	LYS
1	A	433	GLU
1	A	434	GLU
1	A	436	SER
1	A	457	LYS
1	A	458	ILE
1	A	469	LYS
1	A	499	LEU
1	A	502	LEU
1	A	540	GLU
1	A	543	LEU
1	A	551	THR
1	A	568	LYS
1	A	592	LYS
1	A	622	LEU
1	A	645	LEU
1	A	652	LEU
1	A	683	LEU
1	A	724	LYS
1	A	729	LYS
1	A	753	LYS

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Mol	Chain	Res	Type
1	A	822	GLN
1	B	44	ASN
1	B	72	GLN
1	B	102	LEU
1	B	120	GLU
1	B	121	GLU
1	B	150	LEU
1	B	165	ILE
1	B	176	VAL
1	B	184	ARG
1	B	191	LYS
1	B	207	GLU
1	B	213	THR
1	B	251	ASP
1	B	277	ARG
1	B	300	VAL
1	B	325	VAL
1	B	327	ASP
1	B	337	LEU
1	B	363	LYS
1	B	382	GLU
1	B	384	LEU
1	B	393	GLU
1	B	405	GLU
1	B	413	ARG
1	B	420	LYS
1	B	426	ARG
1	B	430	LEU
1	B	433	GLU
1	B	457	LYS
1	B	462	ILE
1	B	466	LYS
1	B	474	LEU
1	B	475	GLU
1	B	502	LEU
1	B	551	THR
1	B	568	LYS
1	B	593	ASP
1	B	621	LYS
1	B	628	ASP
1	B	636	VAL
1	B	643	ILE

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Mol	Chain	Res	Type
1	B	645	LEU
1	B	714	ARG
1	B	723	LYS
1	B	759	LYS
1	B	789	GLN
1	B	822	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (53) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	23	ASN
1	A	34	HIS
1	A	44	ASN
1	A	57	HIS
1	A	62	HIS
1	A	71	GLN
1	A	96	GLN
1	A	97	ASN
1	A	105	GLN
1	A	114	GLN
1	A	167	ASN
1	A	208	HIS
1	A	210	ASN
1	A	239	ASN
1	A	250	ASN
1	A	270	ASN
1	A	274	ASN
1	A	284	ASN
1	A	305	GLN
1	A	369	GLN
1	A	408	GLN
1	A	410	HIS
1	A	459	HIS
1	A	481	ASN
1	A	541	ASN
1	A	566	GLN
1	A	579	ASN
1	A	763	ASN
1	A	768	HIS
1	A	822	GLN
1	B	23	ASN
1	B	32	ASN

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Mol	Chain	Res	Type
1	B	34	HIS
1	B	62	HIS
1	B	105	GLN
1	B	114	GLN
1	B	167	ASN
1	B	239	ASN
1	B	270	ASN
1	B	274	ASN
1	B	284	ASN
1	B	305	GLN
1	B	332	GLN
1	B	369	GLN
1	B	410	HIS
1	B	443	HIS
1	B	459	HIS
1	B	522	HIS
1	B	541	ASN
1	B	566	GLN
1	B	579	ASN
1	B	789	GLN
1	B	826	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

6 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	NBG	A	1	-	15,15,15	1.55	3 (20%)	21,21,21	1.13	1 (4%)
4	AVD	A	833	-	36,37,37	1.39	5 (13%)	51,55,55	1.75	10 (19%)
3	PLP	B	832	1	16,16,16	1.24	1 (6%)	20,23,23	1.06	2 (10%)
4	AVD	B	833	-	36,37,37	1.73	6 (16%)	51,55,55	1.82	15 (29%)
3	PLP	A	832	1	16,16,16	1.24	2 (12%)	20,23,23	1.04	2 (10%)
2	NBG	B	2	-	15,15,15	1.59	3 (20%)	21,21,21	1.78	5 (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
2	NBG	A	1	-	-	0/6/26/26	0/1/1/1
4	AVD	A	833	-	-	9/20/16/16	0/4/4/4
3	PLP	B	832	1	-	3/8/8/8	0/1/1/1
4	AVD	B	833	-	-	10/20/16/16	0/4/4/4
3	PLP	A	832	1	-	2/8/8/8	0/1/1/1
2	NBG	B	2	-	-	0/6/26/26	0/1/1/1

All (20) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	833	AVD	C23-C26	6.10	1.58	1.48
4	B	833	AVD	C17-C24	-4.14	1.40	1.48
4	A	833	AVD	C23-C26	4.11	1.55	1.48
4	A	833	AVD	C17-C24	-3.80	1.40	1.48
2	A	1	NBG	O5-C1	-2.96	1.39	1.43
4	B	833	AVD	C34-C39	2.86	1.55	1.49
3	B	832	PLP	C2-N1	2.61	1.38	1.33
2	B	2	NBG	O5-C1	-2.61	1.39	1.43
3	A	832	PLP	C2-N1	2.57	1.38	1.33
2	B	2	NBG	O3-C3	-2.53	1.36	1.43
4	A	833	AVD	C34-C39	2.33	1.54	1.49
2	B	2	NBG	O5-C5	-2.31	1.38	1.44

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	833	AVD	C6-C1	2.30	1.41	1.37
2	A	1	NBG	C2-C1	-2.30	1.50	1.53
4	A	833	AVD	C2-N10	-2.27	1.34	1.41
4	B	833	AVD	C2-N10	-2.25	1.34	1.41
4	B	833	AVD	C6-C5	2.21	1.41	1.37
2	A	1	NBG	O5-C5	-2.14	1.39	1.44
4	A	833	AVD	O42-C26	2.07	1.27	1.22
3	A	832	PLP	C6-N1	2.04	1.38	1.34

All (35) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	833	AVD	C17-C24-C23	4.63	121.49	115.64
4	A	833	AVD	C16-C17-C24	-4.50	117.10	121.38
4	A	833	AVD	C17-C24-C23	4.39	121.17	115.64
2	B	2	NBG	O2-C2-C3	-4.19	100.50	110.38
4	B	833	AVD	O42-C26-C23	-3.65	115.11	122.67
4	A	833	AVD	O25-C24-C17	-3.59	115.82	121.57
4	B	833	AVD	O27-C26-C23	3.58	124.07	115.69
4	B	833	AVD	C18-C13-C14	-3.46	114.66	118.21
2	A	1	NBG	O2-C2-C1	-3.40	103.49	109.42
4	B	833	AVD	C13-C14-CL29	3.21	123.00	119.52
4	A	833	AVD	C23-C22-N21	-3.18	120.06	123.81
4	A	833	AVD	C30-C28-N21	3.04	123.93	118.93
4	A	833	AVD	C18-C17-C16	3.03	122.33	118.76
4	B	833	AVD	O25-C24-C17	-3.02	116.74	121.57
4	A	833	AVD	C26-C23-C24	3.00	126.07	121.61
4	A	833	AVD	C22-C23-C26	-2.87	113.71	118.27
4	A	833	AVD	C17-C16-N21	2.86	121.62	119.30
2	B	2	NBG	C1-N1-C7	2.83	126.05	122.51
2	B	2	NBG	C2-C1-N1	-2.62	107.87	111.25
4	B	833	AVD	C15-C16-C17	-2.58	116.50	120.18
4	B	833	AVD	C17-C16-N21	2.57	121.39	119.30
4	A	833	AVD	C33-C34-C28	2.55	121.73	118.81
4	B	833	AVD	C22-C23-C24	-2.48	118.12	119.94
2	B	2	NBG	C3-C4-C5	-2.46	105.77	110.23
2	B	2	NBG	O5-C1-C2	-2.41	107.02	109.72
4	B	833	AVD	F9-C1-C2	2.31	120.03	117.64
3	A	832	PLP	C5-C6-N1	-2.31	120.08	123.83
3	B	832	PLP	C5-C6-N1	-2.29	120.10	123.83
4	B	833	AVD	C15-C14-CL29	-2.25	114.77	118.45
4	B	833	AVD	C18-C17-C16	2.14	121.28	118.76

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	833	AVD	C30-C28-N21	2.11	122.41	118.93
4	B	833	AVD	C16-C17-C24	-2.11	119.37	121.38
4	B	833	AVD	C28-N21-C22	2.10	121.39	118.12
3	B	832	PLP	O4A-C4A-C4	-2.03	119.99	124.80
3	A	832	PLP	O4A-C4A-C4	-2.01	120.03	124.80

There are no chirality outliers.

All (24) torsion outliers are listed below:

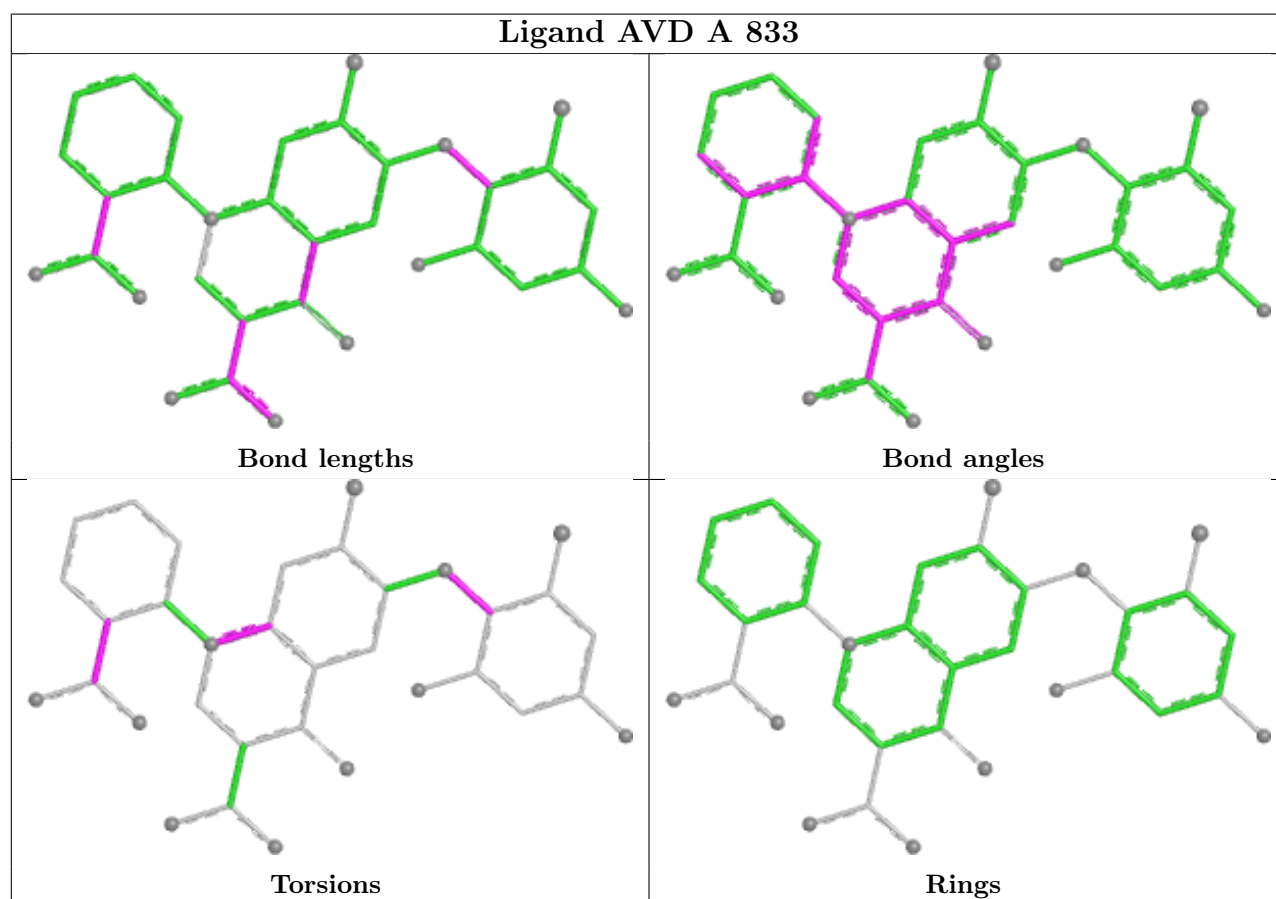
Mol	Chain	Res	Type	Atoms
3	A	832	PLP	C3-C4-C4A-O4A
4	A	833	AVD	C1-C2-N10-C13
4	A	833	AVD	C17-C16-N21-C28
4	A	833	AVD	C15-C16-N21-C28
4	A	833	AVD	C17-C16-N21-C22
4	A	833	AVD	C15-C16-N21-C22
4	B	833	AVD	C1-C2-N10-C13
4	B	833	AVD	C17-C16-N21-C28
4	B	833	AVD	C15-C16-N21-C28
4	B	833	AVD	C17-C16-N21-C22
4	B	833	AVD	C15-C16-N21-C22
3	A	832	PLP	C5-C4-C4A-O4A
3	B	832	PLP	C3-C4-C4A-O4A
3	B	832	PLP	C4-C5-C5A-O4P
4	B	833	AVD	C28-C34-C39-O40
4	B	833	AVD	C28-C34-C39-O41
3	B	832	PLP	C6-C5-C5A-O4P
4	A	833	AVD	C28-C34-C39-O41
4	B	833	AVD	C33-C34-C39-O41
4	A	833	AVD	C28-C34-C39-O40
4	A	833	AVD	C33-C34-C39-O41
4	B	833	AVD	C33-C34-C39-O40
4	B	833	AVD	C30-C28-N21-C22
4	A	833	AVD	C33-C34-C39-O40

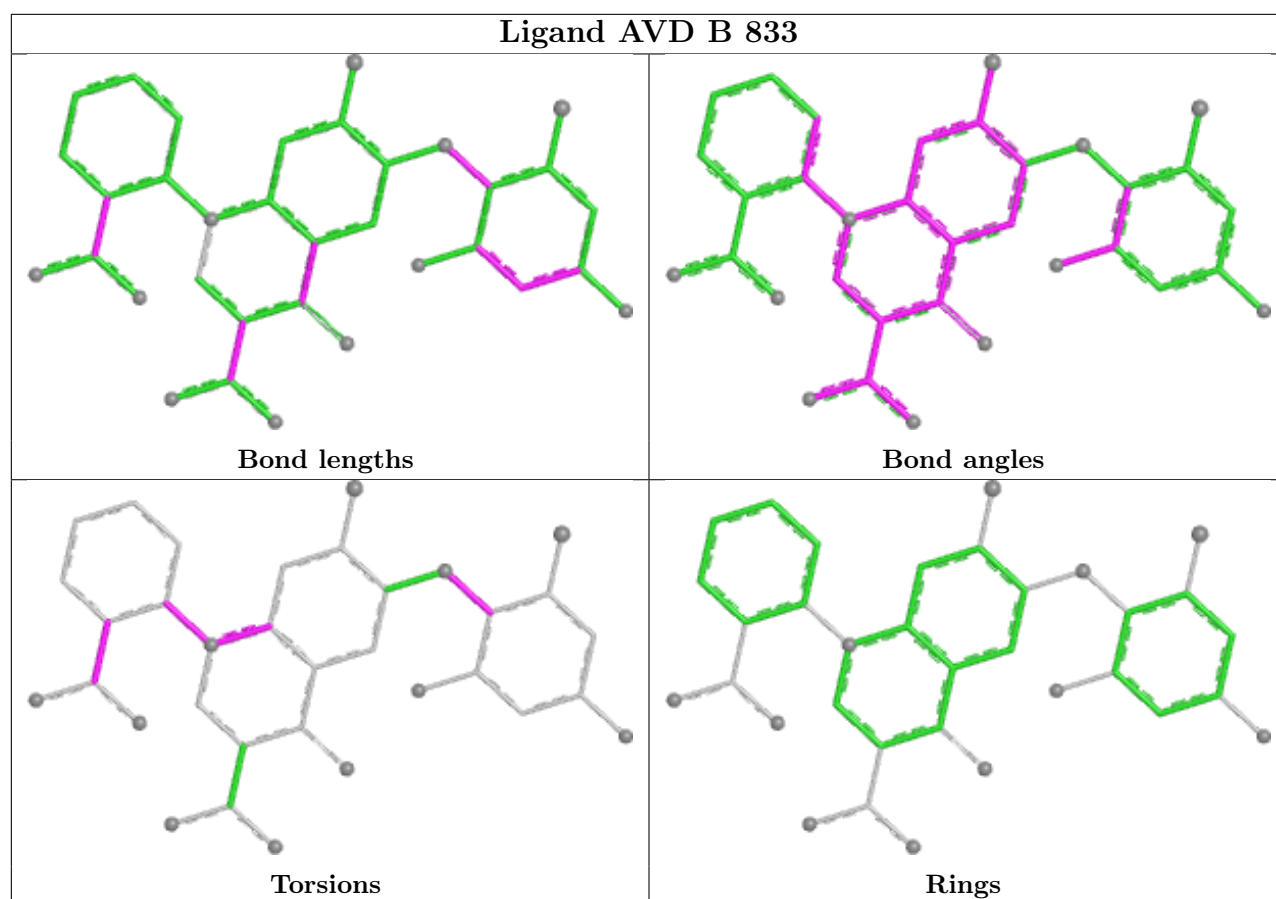
There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	832	PLP	2	0
3	A	832	PLP	1	0

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





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [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	794/809 (98%)	-1.77	0 100 100	14, 32, 56, 72	1 (0%)
1	B	794/809 (98%)	-1.74	0 100 100	14, 34, 61, 75	3 (0%)
All	All	1588/1618 (98%)	-1.75	0 100 100	14, 33, 59, 75	4 (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](#)

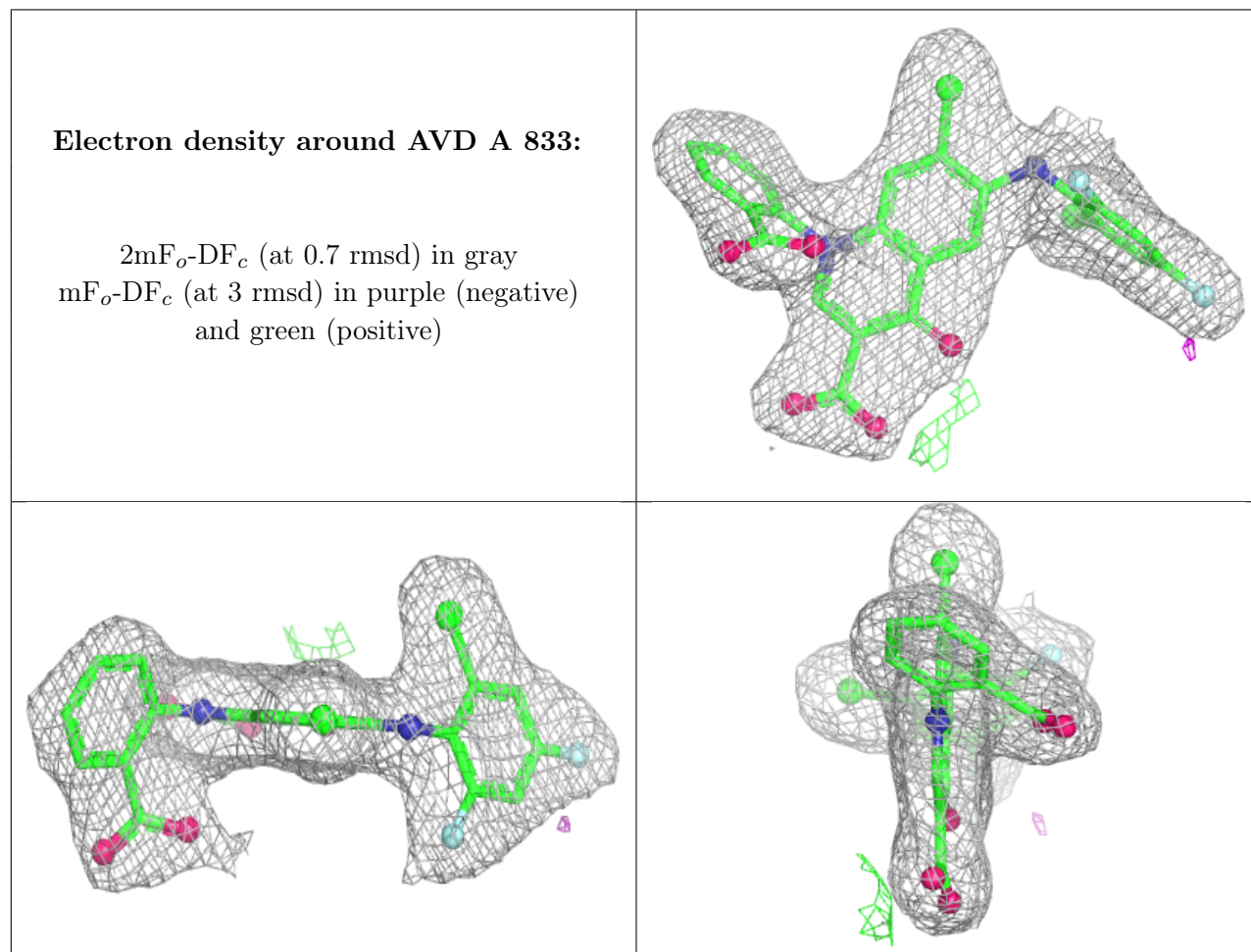
There are no oligosaccharides in this entry.

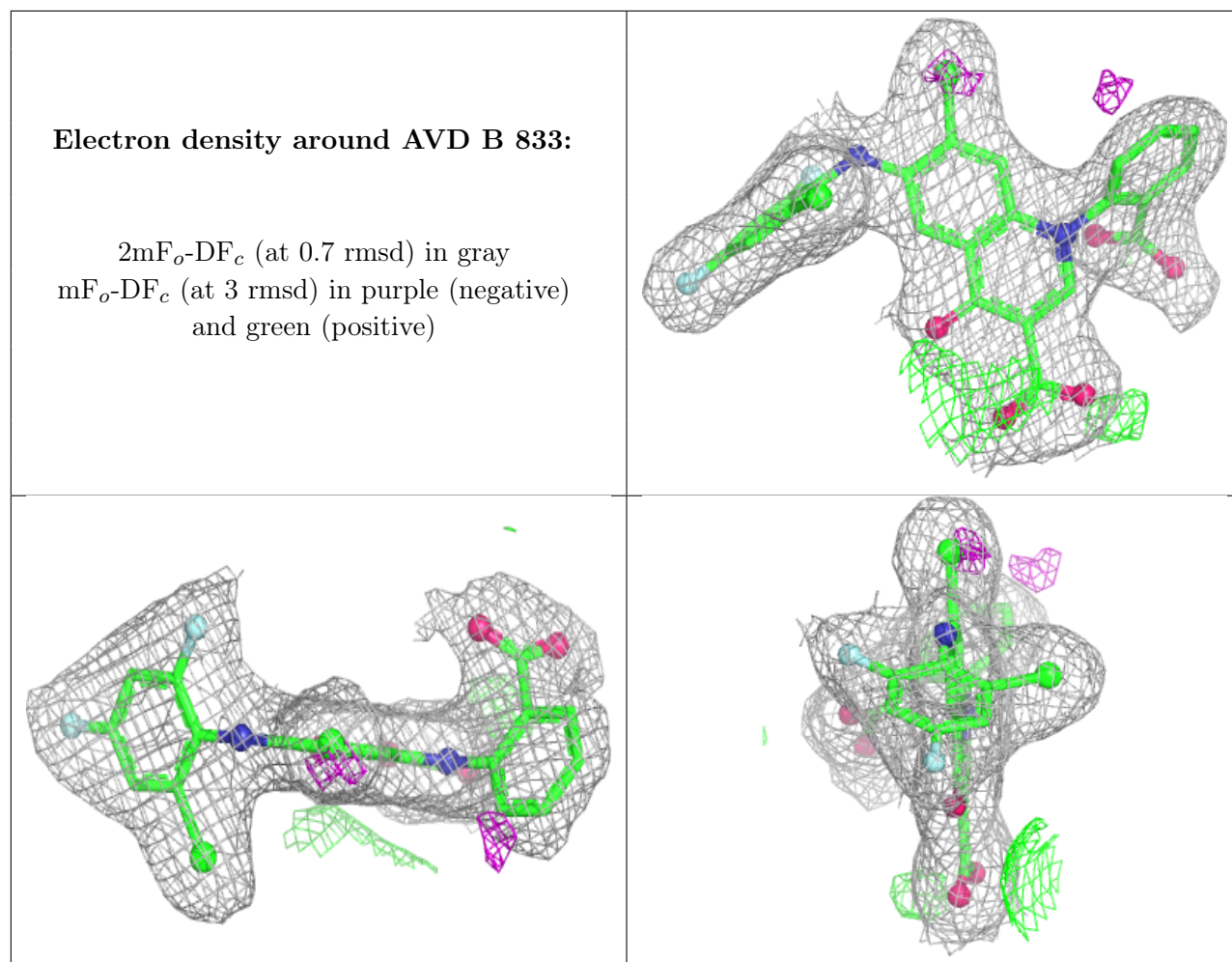
6.4 Ligands [i](#)

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
2	NBG	A	1	15/15	1.00	0.01	18,26,33,33	0
2	NBG	B	2	15/15	1.00	0.02	22,27,33,35	0
3	PLP	A	832	16/16	1.00	0.02	18,23,33,34	0
3	PLP	B	832	16/16	1.00	0.02	19,25,32,33	0
4	AVD	A	833	34/34	1.00	0.02	22,28,37,42	0
4	AVD	B	833	34/34	1.00	0.02	20,29,32,36	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.





6.5 Other polymers [i](#)

There are no such residues in this entry.