Full wwPDB X-ray Structure Validation Report ⓘ

Oct 1, 2023 – 11:59 AM EDT

PDB ID	:	4IOV
Title	:	The structure of AAVrh32.33, a Novel Gene Delivery Vector
Authors	:	Mikalism, K.; Nam, H.-J.; Van vilet, K.; Vandenberghe, L.H.; Mays, L.E.; McKenna, R.; Wilson, J.; Agbandje-McKenna, M.
Deposited on	:	2013-01-08
Resolution	:	3.50 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:

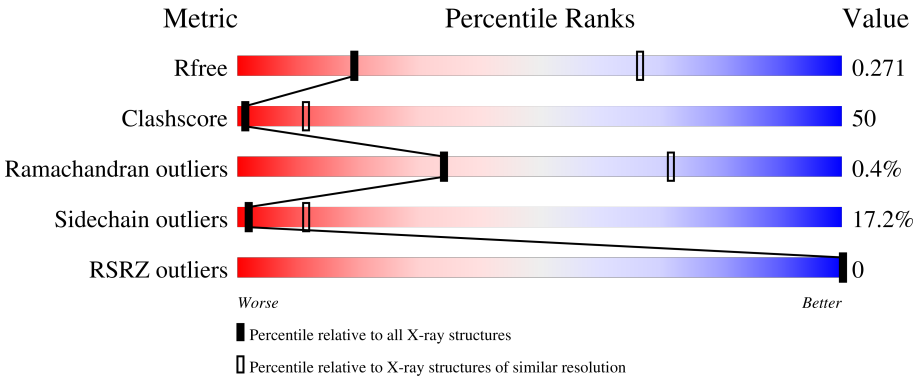
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35.1
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35.1

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 3.50 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	1659 (3.60-3.40)
Clashscore	141614	1036 (3.58-3.42)
Ramachandran outliers	138981	1005 (3.58-3.42)
Sidechain outliers	138945	1006 (3.58-3.42)
RSRZ outliers	127900	1559 (3.60-3.40)

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 <=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	733	31% 32% 8% 29%

2 Entry composition

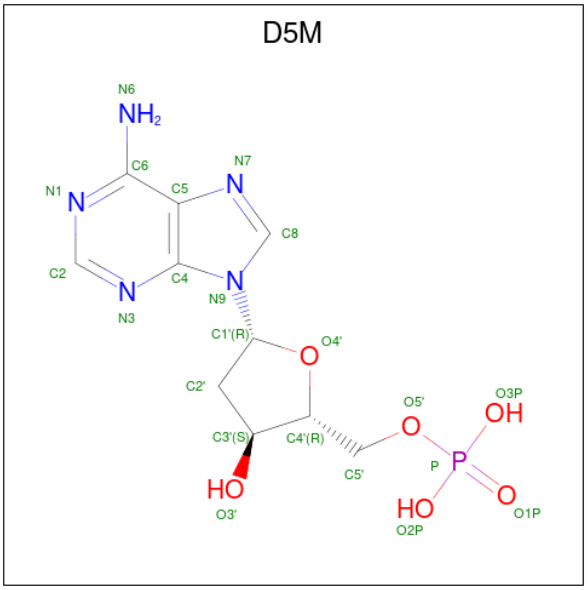
There are 2 unique types of molecules in this entry. The entry contains 4139 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Capsid protein VP1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	520	4117	2604	712	784	17	0	0	0

- Molecule 2 is 2'-DEOXYADENOSINE-5'-MONOPHOSPHATE (three-letter code: D5M) (formula: $C_{10}H_{14}N_5O_6P$).



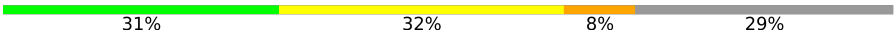
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
2	A	1	22	10	5	6	1	0	0

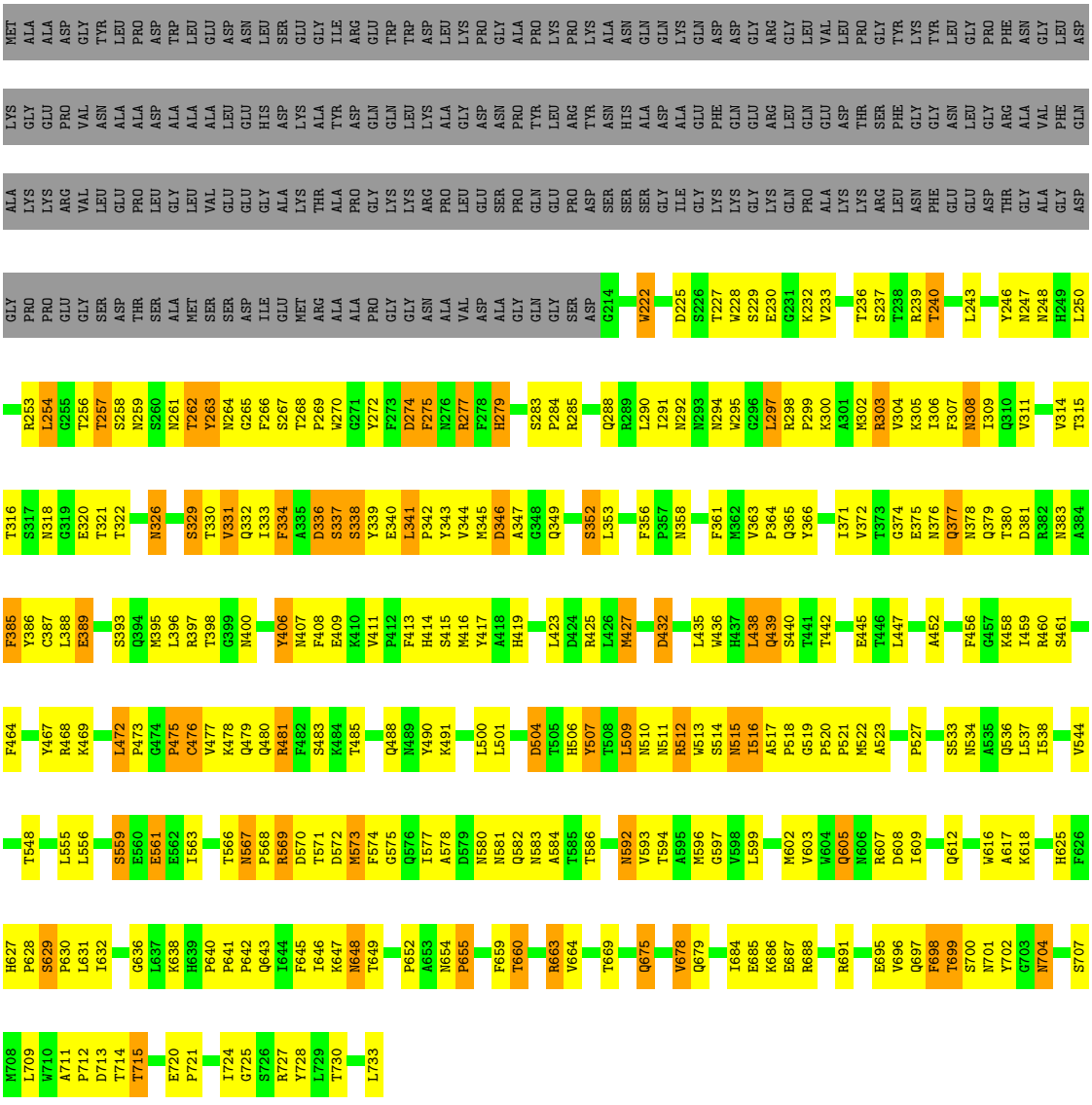
3 Residue-property plots (i)

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: Capsid protein VP1

Chain A:





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α, β, γ	246.40Å 247.52Å 250.33Å 70.38° 65.37° 60.17°	Depositor
Resolution (Å)	40.00 – 3.50 31.14 – 3.50	Depositor EDS
% Data completeness (in resolution range)	(Not available) (40.00-3.50) 68.5 (31.14-3.50)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.16	Depositor
$< I/\sigma(I) >$ [1]	1.65 (at 3.47Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.271 , 0.269 0.270 , 0.271	Depositor DCC
R_{free} test set	20013 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å^2)	49.7	Xtriage
Anisotropy	0.473	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.32 , 38.6	EDS
L-test for twinning[2]	$< \|L\| > = 0.47$, $< L^2 > = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.77	EDS
Total number of atoms	4139	wwPDB-VP
Average B, all atoms (Å^2)	41.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.62% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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: D5M

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	0.68	1/4245 (0.0%)	0.84	2/5798 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	628	PRO	C-N	-5.02	1.22	1.34

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	473	PRO	N-CA-C	5.33	125.95	112.10
1	A	452	ALA	N-CA-C	5.16	124.94	111.00

There are no chirality outliers.

There are no planarity outliers.

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	4117	0	3883	398	0
2	A	22	0	12	4	0
All	All	4139	0	3895	398	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 50.

All (398) 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:253:ARG:C	1:A:254:LEU:HD23	1.23	1.51
1:A:253:ARG:O	1:A:254:LEU:CD2	1.90	1.18
1:A:507:TYR:CE2	1:A:514:SER:HB2	1.78	1.17
1:A:253:ARG:C	1:A:254:LEU:CD2	2.15	1.14
1:A:258:SER:O	1:A:262:THR:HG22	1.44	1.14
1:A:253:ARG:O	1:A:254:LEU:HD23	1.43	1.13
1:A:254:LEU:HD23	1:A:254:LEU:N	1.50	1.13
1:A:512:ARG:CB	1:A:512:ARG:HH11	1.64	1.10
1:A:512:ARG:HH11	1:A:512:ARG:HB2	1.17	1.04
1:A:268:THR:HG22	1:A:270:TRP:H	1.15	1.04
1:A:512:ARG:HH11	1:A:512:ARG:CG	1.70	1.04
1:A:257:THR:HG22	1:A:377:GLN:HG3	1.44	1.00
1:A:512:ARG:HB2	1:A:512:ARG:NH1	1.77	0.98
1:A:517:ALA:HB1	1:A:518:PRO:HD2	1.46	0.98
1:A:698:PHE:HB2	1:A:728:TYR:CE2	2.00	0.95
1:A:246:TYR:CE1	1:A:365:GLN:HB2	2.04	0.93
1:A:380:THR:H	1:A:383:ASN:HD22	1.15	0.92
1:A:627:HIS:HA	2:A:801:D5M:H2'1	1.52	0.92
1:A:648:ASN:N	1:A:648:ASN:HD22	1.64	0.92
1:A:687:GLU:HG3	1:A:688:ARG:H	1.35	0.92
1:A:347:ALA:O	1:A:349:GLN:HG3	1.71	0.90
1:A:344:VAL:H	1:A:643:GLN:NE2	1.71	0.89
1:A:344:VAL:H	1:A:643:GLN:HE22	1.19	0.89
1:A:563:ILE:HG22	1:A:567:ASN:OD1	1.73	0.88
1:A:338:SER:HB2	1:A:340:GLU:HG3	1.55	0.88
1:A:277:ARG:HH12	1:A:279:HIS:CE1	1.93	0.87
1:A:577:ILE:HD12	1:A:577:ILE:O	1.74	0.87
1:A:258:SER:O	1:A:262:THR:CG2	2.23	0.86
1:A:507:TYR:CE2	1:A:514:SER:CB	2.58	0.86
1:A:385:PHE:HD1	1:A:386:TYR:N	1.72	0.86
1:A:485:THR:OG1	1:A:488:GLN:HG2	1.75	0.86
1:A:567:ASN:HB2	1:A:568:PRO:HD2	1.59	0.84
1:A:618:LYS:HB2	1:A:640:PRO:HG3	1.58	0.84
1:A:277:ARG:NH1	1:A:279:HIS:CE1	2.45	0.83
1:A:292:ASN:HB3	1:A:697:GLN:HE21	1.42	0.81
1:A:262:THR:HG21	1:A:375:GLU:O	1.80	0.81
1:A:478:LYS:HE2	1:A:571:THR:O	1.79	0.81
1:A:345:MET:H	1:A:643:GLN:HE21	1.29	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:292:ASN:HD22	1:A:697:GLN:CG	1.94	0.80
1:A:292:ASN:HD22	1:A:697:GLN:HG2	1.44	0.80
1:A:415:SER:HB2	1:A:417:TYR:CE1	2.17	0.79
1:A:512:ARG:HH11	1:A:512:ARG:HG3	1.45	0.79
1:A:294:ASN:ND2	1:A:686:LYS:HD3	1.97	0.79
1:A:263:TYR:CD1	1:A:263:TYR:C	2.54	0.79
1:A:599:LEU:H	1:A:602:MET:HE3	1.47	0.79
1:A:713:ASP:OD1	1:A:715:THR:CG2	2.30	0.79
1:A:577:ILE:HD12	1:A:577:ILE:C	2.03	0.78
1:A:344:VAL:HG12	1:A:643:GLN:HE22	1.49	0.78
1:A:376:ASN:HD21	1:A:378:ASN:HD22	1.31	0.78
1:A:605:GLN:HE21	1:A:605:GLN:HA	1.49	0.77
1:A:380:THR:H	1:A:383:ASN:ND2	1.82	0.77
1:A:699:THR:HG23	1:A:699:THR:O	1.82	0.77
1:A:475:PRO:CD	1:A:475:PRO:O	2.30	0.76
1:A:575:GLY:O	1:A:593:VAL:HG12	1.83	0.76
1:A:243:LEU:HG	1:A:648:ASN:HD21	1.51	0.76
1:A:345:MET:H	1:A:643:GLN:NE2	1.82	0.76
1:A:567:ASN:CB	1:A:568:PRO:HD2	2.14	0.76
1:A:385:PHE:HD1	1:A:385:PHE:C	1.88	0.76
1:A:468:ARG:N	1:A:468:ARG:HD2	2.01	0.76
1:A:517:ALA:CB	1:A:518:PRO:HD2	2.15	0.76
1:A:616:TRP:CE2	1:A:641:PRO:HG2	2.20	0.76
1:A:240:THR:HG23	1:A:675:GLN:OE1	1.86	0.75
1:A:517:ALA:HB1	1:A:518:PRO:CD	2.17	0.75
1:A:648:ASN:HD22	1:A:648:ASN:H	1.34	0.75
1:A:713:ASP:OD1	1:A:715:THR:HG23	1.87	0.75
1:A:292:ASN:HD22	1:A:697:GLN:CB	1.99	0.74
1:A:292:ASN:HD21	1:A:698:PHE:H	1.33	0.74
1:A:304:VAL:HG22	1:A:678:VAL:HG22	1.68	0.74
1:A:309:ILE:O	1:A:398:THR:HG23	1.87	0.74
1:A:698:PHE:CZ	1:A:724:ILE:HD13	2.23	0.74
1:A:485:THR:OG1	1:A:488:GLN:CG	2.36	0.73
1:A:346:ASP:OD2	1:A:347:ALA:HB2	1.89	0.73
1:A:648:ASN:N	1:A:648:ASN:ND2	2.38	0.72
1:A:687:GLU:HG3	1:A:688:ARG:N	2.02	0.72
1:A:472:LEU:O	1:A:602:MET:HA	1.90	0.72
1:A:253:ARG:O	1:A:254:LEU:HD22	1.88	0.72
1:A:309:ILE:HG21	1:A:331:VAL:HG11	1.73	0.71
1:A:521:PRO:HG2	1:A:521:PRO:O	1.89	0.71
1:A:346:ASP:OD2	1:A:346:ASP:C	2.29	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:397:ARG:H	1:A:400:ASN:HD22	1.35	0.71
1:A:326:ASN:OD1	1:A:326:ASN:C	2.29	0.71
1:A:385:PHE:C	1:A:385:PHE:CD1	2.61	0.71
1:A:596:MET:HE3	1:A:596:MET:HA	1.72	0.71
1:A:515:ASN:C	1:A:515:ASN:OD1	2.30	0.70
1:A:292:ASN:HD22	1:A:697:GLN:HB3	1.57	0.70
1:A:700:SER:O	1:A:701:ASN:CG	2.30	0.70
1:A:299:PRO:HG2	1:A:408:PHE:HD2	1.57	0.70
1:A:380:THR:N	1:A:383:ASN:HD22	1.89	0.70
1:A:533:SER:H	1:A:536:GLN:NE2	1.88	0.69
1:A:512:ARG:NH1	1:A:512:ARG:HG3	2.02	0.69
1:A:577:ILE:HD13	1:A:578:ALA:O	1.93	0.69
1:A:713:ASP:OD1	1:A:713:ASP:C	2.30	0.69
1:A:285:ARG:HH11	1:A:288:GLN:HE21	1.40	0.69
1:A:701:ASN:C	1:A:701:ASN:OD1	2.30	0.69
1:A:290:LEU:HD21	1:A:297:LEU:HD13	1.75	0.69
1:A:599:LEU:H	1:A:602:MET:CE	2.05	0.68
1:A:599:LEU:N	1:A:602:MET:HE3	2.08	0.68
1:A:292:ASN:ND2	1:A:697:GLN:HB3	2.09	0.68
1:A:344:VAL:HG12	1:A:643:GLN:NE2	2.07	0.68
1:A:374:GLY:H	1:A:510:ASN:HD21	1.39	0.68
1:A:516:ILE:HG22	1:A:516:ILE:O	1.93	0.68
1:A:292:ASN:HD21	1:A:698:PHE:N	1.92	0.68
1:A:572:ASP:OD1	1:A:573:MET:N	2.27	0.68
1:A:432:ASP:OD2	1:A:460:ARG:HD2	1.94	0.68
1:A:518:PRO:HG3	1:A:537:LEU:HD21	1.75	0.68
1:A:533:SER:H	1:A:536:GLN:HE21	1.42	0.68
1:A:274:ASP:O	1:A:352:SER:HA	1.93	0.68
1:A:377:GLN:NE2	1:A:378:ASN:N	2.42	0.68
1:A:385:PHE:CD1	1:A:386:TYR:N	2.60	0.68
1:A:520:PRO:O	1:A:522:MET:HG3	1.93	0.67
1:A:346:ASP:OD2	1:A:347:ALA:N	2.28	0.67
1:A:459:ILE:CD1	1:A:468:ARG:HD3	2.25	0.67
1:A:475:PRO:O	1:A:475:PRO:CG	2.42	0.67
1:A:336:ASP:CG	1:A:336:ASP:O	2.34	0.66
1:A:377:GLN:NE2	1:A:377:GLN:C	2.48	0.66
1:A:704:ASN:N	1:A:704:ASN:HD22	1.93	0.66
1:A:246:TYR:CD1	1:A:365:GLN:HB2	2.30	0.66
1:A:334:PHE:CE1	1:A:645:PHE:HB2	2.30	0.66
1:A:380:THR:HG22	1:A:381:ASP:H	1.61	0.66
1:A:516:ILE:HG23	1:A:517:ALA:O	1.96	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:406:TYR:CE2	1:A:408:PHE:CD1	2.84	0.66
1:A:580:ASN:OD1	1:A:581:ASN:N	2.29	0.65
1:A:397:ARG:N	1:A:400:ASN:HD22	1.93	0.65
1:A:277:ARG:NH1	1:A:279:HIS:NE2	2.45	0.65
1:A:308:ASN:N	1:A:308:ASN:HD22	1.95	0.65
1:A:341:LEU:HD21	1:A:388:LEU:HD13	1.78	0.65
1:A:713:ASP:OD1	1:A:715:THR:N	2.30	0.65
1:A:654:ASN:OD1	1:A:655:PRO:N	2.30	0.64
1:A:447:LEU:O	1:A:447:LEU:HD12	1.95	0.64
1:A:344:VAL:N	1:A:643:GLN:HE22	1.93	0.64
1:A:699:THR:O	1:A:699:THR:CG2	2.45	0.64
1:A:406:TYR:HE2	1:A:408:PHE:CD1	2.16	0.64
1:A:222:TRP:HD1	1:A:222:TRP:O	1.81	0.63
1:A:222:TRP:O	1:A:222:TRP:CD1	2.52	0.63
1:A:608:ASP:OD1	1:A:609:ILE:N	2.32	0.62
1:A:294:ASN:OD1	1:A:684:ILE:HD12	1.99	0.62
1:A:257:THR:HG22	1:A:377:GLN:CG	2.24	0.62
1:A:316:THR:HG23	1:A:316:THR:O	1.98	0.62
1:A:713:ASP:OD1	1:A:715:THR:HG22	1.98	0.62
1:A:627:HIS:HA	2:A:801:D5M:C2'	2.26	0.62
1:A:268:THR:HB	1:A:366:TYR:O	1.99	0.62
1:A:222:TRP:CD1	1:A:222:TRP:C	2.73	0.61
1:A:314:VAL:CG1	1:A:669:THR:HB	2.30	0.61
1:A:464:PHE:HA	1:A:467:TYR:CD1	2.35	0.61
1:A:567:ASN:OD1	1:A:567:ASN:N	2.33	0.61
1:A:314:VAL:HG13	1:A:669:THR:HB	1.83	0.61
1:A:517:ALA:O	1:A:518:PRO:C	2.38	0.61
1:A:527:PRO:HG3	1:A:559:SER:HB3	1.82	0.61
1:A:700:SER:OG	1:A:701:ASN:N	2.32	0.61
1:A:475:PRO:O	1:A:475:PRO:HD2	1.99	0.60
1:A:617:ALA:HB3	1:A:630:PRO:HG3	1.82	0.60
1:A:480:GLN:HE21	1:A:481:ARG:H	1.49	0.60
1:A:277:ARG:HH12	1:A:279:HIS:HE1	1.50	0.60
1:A:315:THR:O	1:A:316:THR:HG22	2.02	0.60
1:A:292:ASN:ND2	1:A:697:GLN:HG2	2.17	0.59
1:A:654:ASN:OD1	1:A:655:PRO:HD2	2.01	0.59
1:A:507:TYR:HE2	1:A:514:SER:CB	2.12	0.59
1:A:268:THR:HG23	1:A:269:PRO:HD2	1.85	0.58
1:A:292:ASN:ND2	1:A:698:PHE:H	1.99	0.58
1:A:507:TYR:HD2	1:A:514:SER:O	1.87	0.58
1:A:713:ASP:OD2	1:A:715:THR:CG2	2.51	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:380:THR:HG22	1:A:381:ASP:N	2.17	0.58
1:A:713:ASP:CG	1:A:715:THR:CG2	2.72	0.58
1:A:432:ASP:OD1	1:A:432:ASP:N	2.35	0.58
1:A:654:ASN:OD1	1:A:655:PRO:CD	2.51	0.58
1:A:315:THR:HB	1:A:322:THR:HB	1.86	0.58
1:A:376:ASN:HD21	1:A:378:ASN:ND2	2.00	0.57
1:A:256:THR:HG23	1:A:256:THR:O	2.02	0.57
1:A:533:SER:HB3	1:A:570:ASP:OD2	2.05	0.57
1:A:608:ASP:HB2	1:A:727:ARG:NH1	2.18	0.57
1:A:538:ILE:HD12	1:A:538:ILE:N	2.19	0.57
1:A:406:TYR:CD1	1:A:642:PRO:HD3	2.39	0.57
1:A:517:ALA:CB	1:A:518:PRO:CD	2.81	0.57
1:A:311:VAL:HG11	1:A:329:SER:HB3	1.86	0.57
1:A:285:ARG:HH11	1:A:288:GLN:NE2	2.02	0.56
1:A:229:SER:HB2	1:A:232:LYS:O	2.05	0.56
1:A:292:ASN:HB3	1:A:697:GLN:NE2	2.17	0.56
1:A:285:ARG:NH1	1:A:288:GLN:NE2	2.54	0.56
1:A:345:MET:HE3	1:A:643:GLN:HA	1.86	0.56
1:A:256:THR:HG22	1:A:263:TYR:CE2	2.41	0.55
1:A:515:ASN:OD1	1:A:516:ILE:O	2.24	0.55
1:A:563:ILE:CG2	1:A:567:ASN:OD1	2.52	0.55
1:A:299:PRO:HB2	1:A:408:PHE:CE2	2.41	0.55
1:A:475:PRO:O	1:A:475:PRO:HG2	2.05	0.55
1:A:406:TYR:CE1	1:A:641:PRO:HA	2.42	0.55
1:A:573:MET:SD	1:A:592:ASN:OD1	2.65	0.55
1:A:423:LEU:HD23	1:A:423:LEU:C	2.26	0.55
1:A:507:TYR:CD2	1:A:514:SER:O	2.59	0.55
1:A:510:ASN:O	1:A:511:ASN:HB2	2.05	0.55
1:A:337:SER:O	1:A:339:TYR:CD1	2.60	0.55
1:A:478:LYS:CE	1:A:571:THR:O	2.54	0.55
1:A:599:LEU:N	1:A:602:MET:CE	2.66	0.55
1:A:713:ASP:CG	1:A:715:THR:HG22	2.27	0.55
1:A:275:PHE:CD2	1:A:678:VAL:HG21	2.42	0.55
1:A:577:ILE:CD1	1:A:578:ALA:O	2.55	0.55
1:A:374:GLY:N	1:A:510:ASN:HD21	2.03	0.54
1:A:577:ILE:HD12	1:A:578:ALA:C	2.27	0.54
1:A:257:THR:O	1:A:257:THR:OG1	2.23	0.54
1:A:519:GLY:O	1:A:520:PRO:C	2.45	0.54
1:A:356:PHE:HE2	1:A:358:ASN:HB3	1.71	0.54
1:A:272:TYR:O	1:A:364:PRO:HD2	2.07	0.54
1:A:395:MET:C	1:A:396:LEU:HD12	2.28	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:423:LEU:HD23	1:A:423:LEU:O	2.07	0.54
1:A:500:LEU:HD23	1:A:500:LEU:C	2.28	0.54
1:A:299:PRO:HG2	1:A:408:PHE:CD2	2.39	0.54
1:A:629:SER:O	1:A:630:PRO:C	2.45	0.53
1:A:627:HIS:CD2	2:A:801:D5M:H2'2	2.44	0.53
1:A:341:LEU:HD12	1:A:342:PRO:HD2	1.90	0.53
1:A:691:ARG:HH11	1:A:730:THR:HG21	1.72	0.53
1:A:292:ASN:ND2	1:A:697:GLN:CB	2.67	0.53
1:A:243:LEU:CG	1:A:648:ASN:HD21	2.19	0.53
1:A:659:PHE:CD1	1:A:660:THR:N	2.77	0.53
1:A:698:PHE:CZ	1:A:724:ILE:CD1	2.90	0.52
1:A:406:TYR:CD2	1:A:407:ASN:N	2.77	0.52
1:A:309:ILE:HG21	1:A:331:VAL:CG1	2.39	0.52
1:A:596:MET:HA	1:A:596:MET:CE	2.38	0.52
1:A:302:MET:CE	1:A:641:PRO:HB3	2.40	0.52
1:A:567:ASN:HB2	1:A:568:PRO:CD	2.37	0.52
1:A:515:ASN:OD1	1:A:516:ILE:N	2.43	0.52
1:A:563:ILE:HD11	1:A:727:ARG:NH1	2.25	0.52
1:A:632:ILE:HG22	1:A:632:ILE:O	2.09	0.52
1:A:353:LEU:HD22	1:A:361:PHE:CZ	2.45	0.52
1:A:304:VAL:HG22	1:A:678:VAL:CG2	2.38	0.52
1:A:599:LEU:HB2	1:A:602:MET:HE3	1.91	0.52
1:A:406:TYR:CD2	1:A:406:TYR:C	2.84	0.51
1:A:483:SER:HB3	1:A:488:GLN:HB2	1.90	0.51
1:A:555:LEU:C	1:A:556:LEU:HD23	2.31	0.51
1:A:432:ASP:HB3	1:A:461:SER:N	2.25	0.51
1:A:577:ILE:C	1:A:577:ILE:CD1	2.74	0.51
1:A:257:THR:CG2	1:A:377:GLN:HG3	2.29	0.51
1:A:261:ASN:O	1:A:262:THR:C	2.48	0.51
1:A:263:TYR:HD1	1:A:264:ASN:N	2.09	0.51
1:A:419:HIS:ND1	1:A:733:LEU:HD12	2.25	0.51
1:A:507:TYR:HD2	1:A:507:TYR:H	1.57	0.51
1:A:225:ASP:N	1:A:236:THR:O	2.42	0.51
1:A:237:SER:HB2	1:A:239:ARG:HH12	1.75	0.51
1:A:583:ASN:HB3	1:A:586:THR:OG1	2.11	0.51
1:A:334:PHE:HB3	1:A:393:SER:CB	2.41	0.50
1:A:299:PRO:CG	1:A:408:PHE:CD2	2.94	0.50
1:A:480:GLN:HG3	1:A:481:ARG:N	2.26	0.50
1:A:582:GLN:OE1	1:A:583:ASN:N	2.44	0.50
1:A:695:GLU:OE1	1:A:730:THR:HG22	2.10	0.50
1:A:523:ALA:HB3	1:A:569:ARG:HA	1.91	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:227:THR:O	1:A:227:THR:OG1	2.30	0.50
1:A:516:ILE:CG2	1:A:517:ALA:O	2.58	0.50
1:A:336:ASP:O	1:A:336:ASP:OD1	2.29	0.50
1:A:701:ASN:OD1	1:A:701:ASN:O	2.30	0.50
1:A:608:ASP:HB2	1:A:727:ARG:HH11	1.75	0.50
1:A:259:ASN:OD1	1:A:259:ASN:O	2.30	0.49
1:A:299:PRO:HB2	1:A:408:PHE:CD2	2.47	0.49
1:A:518:PRO:HB2	1:A:607:ARG:NH2	2.27	0.49
1:A:309:ILE:CG2	1:A:331:VAL:HG11	2.42	0.49
1:A:316:THR:HA	1:A:321:THR:HA	1.94	0.49
1:A:326:ASN:ND2	1:A:329:SER:HB2	2.26	0.49
1:A:700:SER:O	1:A:701:ASN:OD1	2.30	0.49
1:A:459:ILE:HD11	1:A:468:ARG:HD3	1.95	0.49
1:A:406:TYR:CE2	1:A:408:PHE:HD1	2.28	0.49
1:A:346:ASP:OD2	1:A:347:ALA:CB	2.59	0.49
1:A:377:GLN:HE21	1:A:378:ASN:N	2.10	0.49
1:A:396:LEU:HD12	1:A:396:LEU:N	2.27	0.49
1:A:294:ASN:HD21	1:A:686:LYS:HD3	1.74	0.49
1:A:326:ASN:OD1	1:A:326:ASN:O	2.30	0.49
1:A:257:THR:HB	1:A:377:GLN:H	1.78	0.48
1:A:307:PHE:N	1:A:307:PHE:CD1	2.81	0.48
1:A:346:ASP:HB2	1:A:617:ALA:HA	1.95	0.48
1:A:330:THR:O	1:A:330:THR:OG1	2.30	0.48
1:A:563:ILE:HD12	1:A:605:GLN:HB3	1.94	0.48
1:A:268:THR:HG22	1:A:269:PRO:N	2.29	0.48
1:A:345:MET:N	1:A:643:GLN:HE21	2.05	0.48
1:A:501:LEU:O	1:A:501:LEU:HD12	2.14	0.48
1:A:291:ILE:HD11	1:A:698:PHE:HD2	1.78	0.48
1:A:372:VAL:HG13	1:A:372:VAL:O	2.12	0.48
1:A:306:ILE:HD12	1:A:333:ILE:HD13	1.95	0.48
1:A:406:TYR:HD1	1:A:642:PRO:HD3	1.76	0.48
1:A:302:MET:HG2	1:A:303:ARG:N	2.28	0.48
1:A:388:LEU:N	1:A:388:LEU:CD2	2.77	0.47
1:A:432:ASP:CB	1:A:460:ARG:HA	2.44	0.47
1:A:330:THR:HA	1:A:396:LEU:O	2.14	0.47
1:A:537:LEU:C	1:A:538:ILE:HD12	2.35	0.47
1:A:599:LEU:CB	1:A:602:MET:HE3	2.44	0.47
1:A:247:ASN:O	1:A:248:ASN:C	2.52	0.47
1:A:388:LEU:N	1:A:388:LEU:HD22	2.29	0.47
1:A:356:PHE:CE2	1:A:358:ASN:HB3	2.50	0.47
1:A:298:ARG:NE	1:A:413:PHE:CE1	2.82	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:388:LEU:CD2	1:A:388:LEU:H	2.28	0.47
1:A:460:ARG:HG3	1:A:460:ARG:HH11	1.80	0.47
1:A:507:TYR:CD2	1:A:514:SER:HB2	2.45	0.47
1:A:711:ALA:HB1	1:A:712:PRO:HD2	1.96	0.47
1:A:570:ASP:OD1	1:A:571:THR:HG23	2.15	0.47
1:A:687:GLU:O	1:A:688:ARG:HB2	2.15	0.47
1:A:285:ARG:O	1:A:288:GLN:HB3	2.15	0.47
1:A:258:SER:C	1:A:262:THR:HG22	2.29	0.47
1:A:506:HIS:CD2	1:A:513:TRP:CD1	3.03	0.47
1:A:616:TRP:CZ2	1:A:641:PRO:HG2	2.49	0.47
1:A:236:THR:OG1	1:A:679:GLN:HG3	2.15	0.46
1:A:263:TYR:C	1:A:263:TYR:HD1	2.14	0.46
1:A:500:LEU:HD21	1:A:504:ASP:OD2	2.16	0.46
1:A:567:ASN:CB	1:A:568:PRO:CD	2.90	0.46
1:A:685:GLU:HG3	1:A:685:GLU:O	2.15	0.46
1:A:377:GLN:C	1:A:377:GLN:CD	2.74	0.46
1:A:435:LEU:HD12	1:A:468:ARG:HG3	1.98	0.46
1:A:640:PRO:O	1:A:641:PRO:C	2.51	0.46
1:A:702:TYR:CG	1:A:709:LEU:HD12	2.51	0.46
1:A:374:GLY:H	1:A:510:ASN:ND2	2.10	0.46
1:A:713:ASP:CG	1:A:715:THR:HG23	2.36	0.46
1:A:336:ASP:OD1	1:A:339:TYR:N	2.48	0.46
1:A:396:LEU:N	1:A:396:LEU:CD1	2.79	0.46
1:A:423:LEU:C	1:A:423:LEU:CD2	2.85	0.45
1:A:696:VAL:HG23	1:A:728:TYR:O	2.16	0.45
1:A:425:ARG:HA	1:A:427:MET:HE3	1.97	0.45
1:A:490:TYR:CD1	1:A:491:LYS:N	2.84	0.45
1:A:520:PRO:O	1:A:521:PRO:C	2.53	0.45
1:A:521:PRO:O	1:A:521:PRO:CG	2.55	0.45
1:A:295:TRP:O	1:A:416:MET:HB2	2.16	0.45
1:A:700:SER:HB2	1:A:702:TYR:CD2	2.51	0.45
1:A:605:GLN:HA	1:A:605:GLN:NE2	2.26	0.45
1:A:268:THR:CG2	1:A:269:PRO:N	2.80	0.45
1:A:379:GLN:HA	1:A:383:ASN:ND2	2.32	0.45
1:A:228:TRP:CE2	1:A:233:VAL:HG21	2.53	0.45
1:A:603:VAL:HG23	1:A:603:VAL:O	2.17	0.44
1:A:304:VAL:HG12	1:A:305:LYS:N	2.32	0.44
1:A:724:ILE:HG22	1:A:725:GLY:O	2.17	0.44
1:A:256:THR:O	1:A:256:THR:CG2	2.65	0.44
1:A:425:ARG:HE	1:A:425:ARG:HB3	1.46	0.44
1:A:577:ILE:CD1	1:A:578:ALA:C	2.86	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:263:TYR:CD1	1:A:263:TYR:O	2.71	0.43
1:A:297:LEU:HG	1:A:298:ARG:N	2.33	0.43
1:A:376:ASN:OD1	1:A:377:GLN:N	2.51	0.43
1:A:432:ASP:HB2	1:A:459:ILE:O	2.19	0.43
1:A:258:SER:O	1:A:262:THR:N	2.51	0.43
1:A:283:SER:O	1:A:284:PRO:C	2.56	0.43
1:A:333:ILE:HG12	1:A:646:ILE:HG13	2.01	0.43
1:A:377:GLN:C	1:A:377:GLN:HE21	2.22	0.43
1:A:308:ASN:N	1:A:308:ASN:ND2	2.64	0.43
1:A:636:GLY:H	2:A:801:D5M:HN62	1.67	0.43
1:A:387:CYS:SG	1:A:389:GLU:HG2	2.59	0.43
1:A:713:ASP:OD2	1:A:715:THR:HG22	2.19	0.43
1:A:338:SER:HB2	1:A:340:GLU:CG	2.36	0.43
1:A:343:TYR:CE1	1:A:643:GLN:HG3	2.54	0.43
1:A:409:GLU:H	1:A:409:GLU:HG2	1.54	0.43
1:A:512:ARG:CB	1:A:512:ARG:NH1	2.43	0.43
1:A:698:PHE:CE2	1:A:724:ILE:HD13	2.54	0.43
1:A:512:ARG:CG	1:A:512:ARG:NH1	2.41	0.42
1:A:561:GLU:H	1:A:561:GLU:HG3	1.52	0.42
1:A:583:ASN:OD1	1:A:584:ALA:N	2.52	0.42
1:A:698:PHE:HB2	1:A:728:TYR:CZ	2.49	0.42
1:A:229:SER:HB2	1:A:232:LYS:H	1.84	0.42
1:A:555:LEU:O	1:A:556:LEU:HD23	2.19	0.42
1:A:438:LEU:HD12	1:A:439:GLN:N	2.34	0.42
1:A:438:LEU:HB2	1:A:456:PHE:CE1	2.54	0.42
1:A:277:ARG:NH1	1:A:277:ARG:HG3	2.34	0.42
1:A:372:VAL:HG11	1:A:512:ARG:HE	1.84	0.42
1:A:599:LEU:HG	1:A:602:MET:CE	2.49	0.42
1:A:663:ARG:HD2	1:A:664:VAL:O	2.19	0.42
1:A:691:ARG:NH1	1:A:730:THR:HG21	2.33	0.42
1:A:460:ARG:HG3	1:A:460:ARG:NH1	2.34	0.42
1:A:268:THR:HG23	1:A:269:PRO:CD	2.50	0.42
1:A:277:ARG:HH11	1:A:277:ARG:CG	2.32	0.42
1:A:330:THR:O	1:A:649:THR:HB	2.19	0.42
1:A:371:ILE:O	1:A:371:ILE:HG23	2.18	0.42
1:A:425:ARG:HB3	1:A:427:MET:HE1	2.01	0.42
1:A:521:PRO:C	1:A:522:MET:HG3	2.39	0.42
1:A:582:GLN:OE1	1:A:582:GLN:C	2.57	0.42
1:A:298:ARG:CZ	1:A:413:PHE:HE1	2.32	0.42
1:A:509:LEU:O	1:A:512:ARG:NH1	2.53	0.42
1:A:574:PHE:HB3	1:A:593:VAL:HG13	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:605:GLN:HE21	1:A:605:GLN:CA	2.22	0.42
1:A:333:ILE:HG23	1:A:645:PHE:O	2.19	0.42
1:A:265:GLY:C	1:A:266:PHE:CD1	2.93	0.42
1:A:575:GLY:C	1:A:593:VAL:HG12	2.40	0.42
1:A:300:LYS:O	1:A:408:PHE:HB2	2.20	0.42
1:A:485:THR:OG1	1:A:488:GLN:HG3	2.16	0.42
1:A:291:ILE:HD11	1:A:698:PHE:CD2	2.54	0.41
1:A:302:MET:CG	1:A:303:ARG:N	2.83	0.41
1:A:414:HIS:CD2	1:A:609:ILE:HG12	2.55	0.41
1:A:478:LYS:HG3	1:A:479:GLN:N	2.35	0.41
1:A:654:ASN:HA	1:A:655:PRO:HD3	1.83	0.41
1:A:332:GLN:NE2	1:A:649:THR:OG1	2.34	0.41
1:A:376:ASN:ND2	1:A:378:ASN:HD22	2.08	0.41
1:A:419:HIS:ND1	1:A:733:LEU:CD1	2.83	0.41
1:A:247:ASN:N	1:A:247:ASN:ND2	2.69	0.41
1:A:436:TRP:CE2	1:A:458:LYS:HB2	2.55	0.41
1:A:438:LEU:HD12	1:A:438:LEU:C	2.41	0.41
1:A:254:LEU:HD11	1:A:267:SER:HB3	2.03	0.41
1:A:533:SER:OG	1:A:534:ASN:N	2.53	0.41
1:A:268:THR:HA	1:A:269:PRO:HD3	1.85	0.41
1:A:596:MET:HE2	1:A:597:GLY:N	2.35	0.41
1:A:334:PHE:HE1	1:A:645:PHE:HB2	1.81	0.41
1:A:678:VAL:O	1:A:678:VAL:HG12	2.21	0.41
1:A:720:GLU:HA	1:A:721:PRO:HD3	1.73	0.41
1:A:326:ASN:CG	1:A:329:SER:HB2	2.41	0.41
1:A:476:CYS:SG	1:A:477:VAL:N	2.86	0.41
1:A:363:VAL:HA	1:A:364:PRO:HD3	1.86	0.40
1:A:254:LEU:HD22	1:A:254:LEU:HA	1.67	0.40
1:A:257:THR:HA	1:A:262:THR:HB	2.03	0.40
1:A:372:VAL:CG1	1:A:512:ARG:HE	2.34	0.40
1:A:696:VAL:CG2	1:A:728:TYR:O	2.69	0.40
1:A:713:ASP:OD1	1:A:714:THR:N	2.55	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	518/733 (71%)	483 (93%)	33 (6%)	2 (0%)	34 72

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	655	PRO
1	A	652	PRO

5.3.2 Protein sidechains (i)

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	447/609 (73%)	370 (83%)	77 (17%)	2 11

All (77) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	222	TRP
1	A	230	GLU
1	A	240	THR
1	A	250	LEU
1	A	254	LEU
1	A	257	THR
1	A	262	THR
1	A	263	TYR
1	A	274	ASP
1	A	275	PHE
1	A	277	ARG
1	A	279	HIS
1	A	297	LEU
1	A	303	ARG
1	A	308	ASN

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Mol	Chain	Res	Type
1	A	318	ASN
1	A	320	GLU
1	A	326	ASN
1	A	329	SER
1	A	331	VAL
1	A	334	PHE
1	A	336	ASP
1	A	337	SER
1	A	338	SER
1	A	341	LEU
1	A	346	ASP
1	A	352	SER
1	A	377	GLN
1	A	385	PHE
1	A	389	GLU
1	A	406	TYR
1	A	411	VAL
1	A	427	MET
1	A	432	ASP
1	A	438	LEU
1	A	439	GLN
1	A	440	SER
1	A	442	THR
1	A	445	GLU
1	A	469	LYS
1	A	472	LEU
1	A	475	PRO
1	A	476	CYS
1	A	481	ARG
1	A	504	ASP
1	A	507	TYR
1	A	509	LEU
1	A	512	ARG
1	A	515	ASN
1	A	516	ILE
1	A	544	VAL
1	A	548	THR
1	A	559	SER
1	A	561	GLU
1	A	566	THR
1	A	567	ASN
1	A	569	ARG

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Mol	Chain	Res	Type
1	A	573	MET
1	A	592	ASN
1	A	594	THR
1	A	605	GLN
1	A	612	GLN
1	A	625	HIS
1	A	629	SER
1	A	631	LEU
1	A	638	LYS
1	A	647	LYS
1	A	648	ASN
1	A	660	THR
1	A	663	ARG
1	A	675	GLN
1	A	678	VAL
1	A	698	PHE
1	A	699	THR
1	A	704	ASN
1	A	707	SER
1	A	715	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (22) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	279	HIS
1	A	288	GLN
1	A	292	ASN
1	A	294	ASN
1	A	308	ASN
1	A	365	GLN
1	A	377	GLN
1	A	378	ASN
1	A	383	ASN
1	A	400	ASN
1	A	407	ASN
1	A	480	GLN
1	A	510	ASN
1	A	536	GLN
1	A	583	ASN
1	A	605	GLN
1	A	606	ASN
1	A	627	HIS

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Mol	Chain	Res	Type
1	A	643	GLN
1	A	648	ASN
1	A	697	GLN
1	A	704	ASN

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 monosaccharides in this entry.

5.6 Ligand geometry

1 ligand is modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
2	D5M	A	801	-	22,24,24	0.67	0	24,36,36	1.08	3 (12%)

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	D5M	A	801	-	-	0/6/22/22	0/3/3/3

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	801	D5M	O3P-P-O5'	-2.64	99.70	106.73
2	A	801	D5M	C5-C6-N6	2.36	123.94	120.35
2	A	801	D5M	O2P-P-O1P	2.26	119.52	110.68

There are no chirality outliers.

There are no torsion outliers.

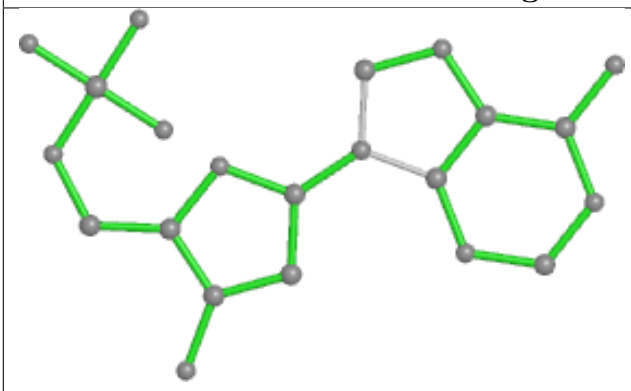
There are no ring outliers.

1 monomer is involved in 4 short contacts:

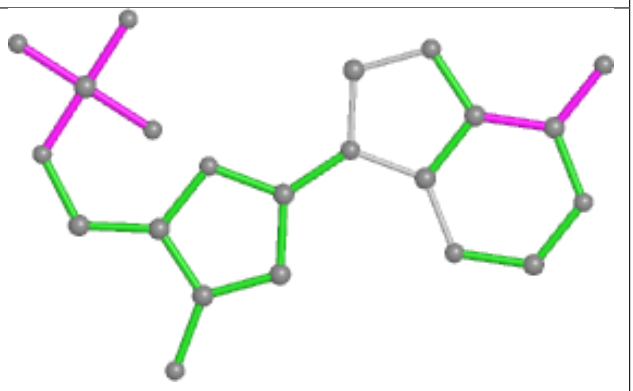
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	801	D5M	4	0

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 then 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.

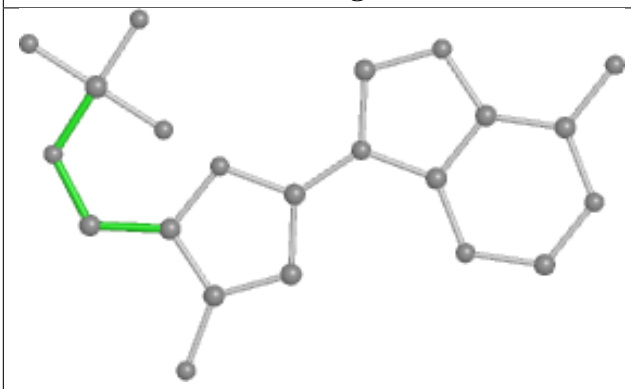
Ligand D5M A 801



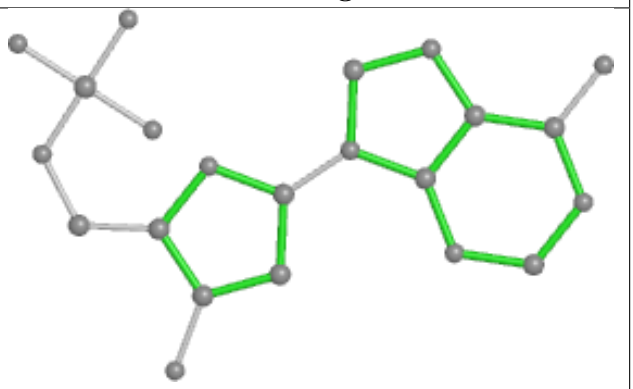
Bond lengths



Bond angles



Torsions



Rings

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, 95^{th} 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	520/733 (70%)	-0.74	0 100 100	21, 41, 58, 92	0

There are no RSRZ outliers to report.

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

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

6.3 Carbohydrates

There are no monosaccharides in this entry.

6.4 Ligands

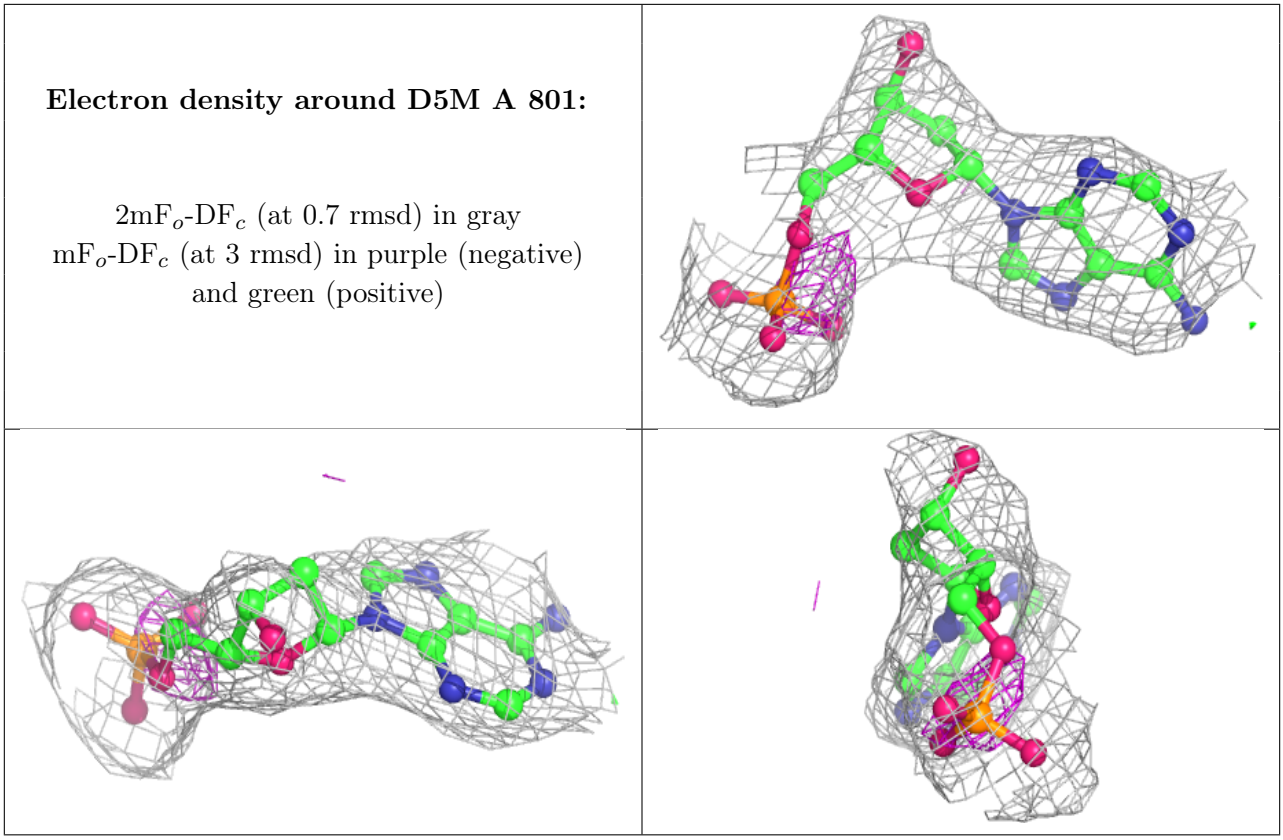
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' 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	D5M	A	801	22/22	0.93	0.17	40,50,73,73	22

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.

Electron density around D5M A 801:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)



6.5 Other polymers (i)

There are no such residues in this entry.