



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 11, 2021 – 07:13 PM EDT

PDB ID : 2GA9
Title : Crystal Structure of the Heterodimeric Vaccinia Virus Polyadenylate Polymerase with Bound ATP-gamma-S
Authors : Moure, C.M.; Bowman, B.R.; Gershon, P.D.; Quiocho, F.A.
Deposited on : 2006-03-08
Resolution : 2.30 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)
Xtrriage (Phenix) : 1.13
EDS : 2.23.2
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) : 2.23.2

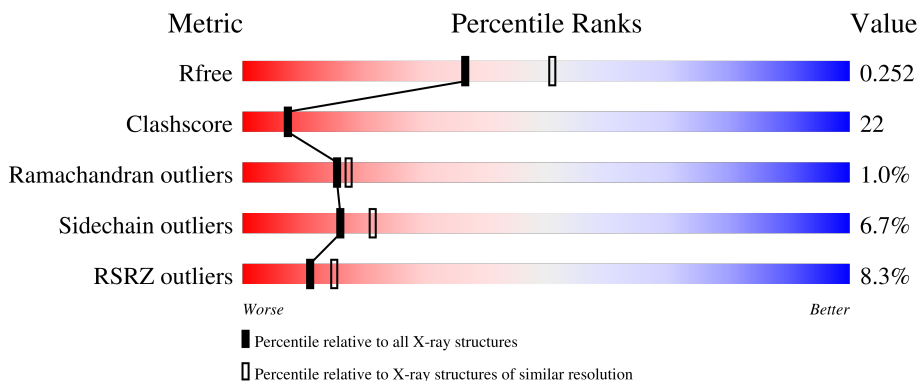
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (2.30-2.30)

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	297	
2	D	469	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	AGS	D	483	-	-	X	-

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 6333 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 Cap-specific mRNA (nucleoside-2'-O-)-methyltransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	288	2382	1552	394	424	12	0	0	0

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	140	ALA	ARG	engineered mutation	UNP P07617
A	142	ALA	LYS	engineered mutation	UNP P07617
A	143	ALA	ARG	engineered mutation	UNP P07617

- Molecule 2 is a protein called Poly(A) polymerase catalytic subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	D	445	3627	2318	605	680	24	0	0	0

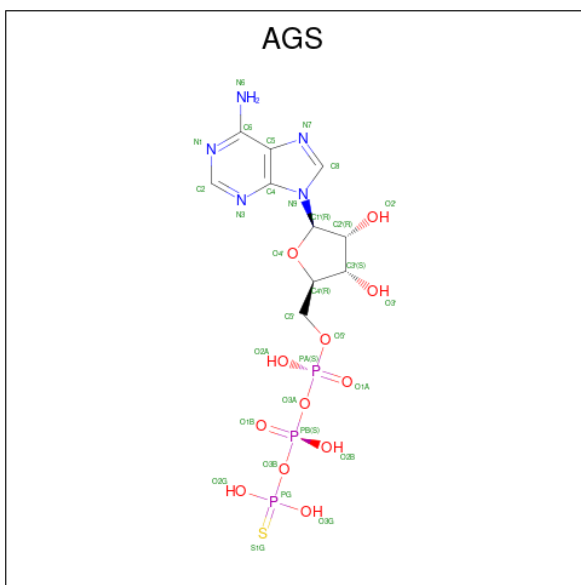
There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	36	SER	LEU	variant	UNP P23371

- Molecule 3 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	D	2	Total	Ca	0	0
			2	2		

- Molecule 4 is PHOSPHOTHIOPHOSPHORIC ACID-ADENYLATE ESTER (three-letter code: AGS) (formula: C₁₀H₁₆N₅O₁₂P₃S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	
			Total	C	N	O	P			S
4	D	1	31	10	5	12	3	1	0	0
4	D	1	31	10	5	12	3	1	0	0

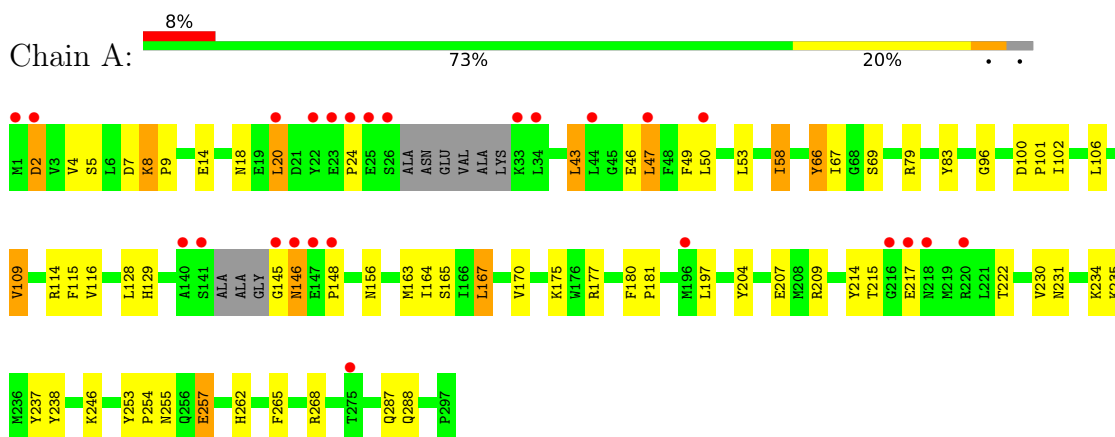
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
5	A	120	120	120	0	0
5	D	140	140	140	0	0

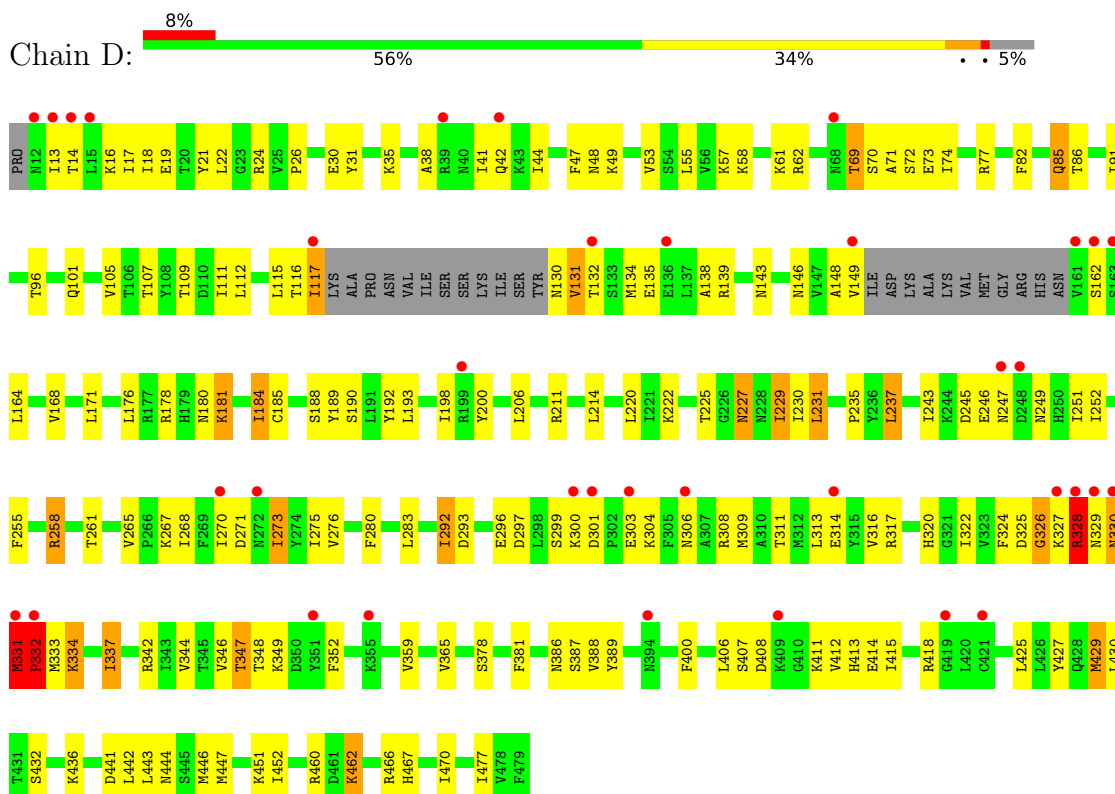
3 Residue-property plots [i](#)

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: Cap-specific mRNA (nucleoside-2'-O-)-methyltransferase



- Molecule 2: Poly(A) polymerase catalytic subunit



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	70.05Å 91.69Å 133.70Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.30 30.17 – 2.31	Depositor EDS
% Data completeness (in resolution range)	93.8 (50.00-2.30) 94.7 (30.17-2.31)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.53 (at 2.31Å)	Xtrriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.222 , 0.260 0.213 , 0.252	Depositor DCC
R_{free} test set	1910 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	28.9	Xtrriage
Anisotropy	0.100	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 47.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	6333	wwPDB-VP
Average B, all atoms (Å ²)	33.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.12% 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 [i](#)

5.1 Standard geometry [i](#)

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

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	0.39	0/2444	0.63	0/3308
2	D	0.39	0/3686	0.66	2/4972 (0.0%)
All	All	0.39	0/6130	0.65	2/8280 (0.0%)

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	A	0	1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
2	D	328	ARG	CA-C-N	-6.52	102.85	117.20
2	D	328	ARG	C-N-CA	5.47	135.38	121.70

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	204	TYR	Sidechain

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen

atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2382	0	2389	53	0
2	D	3627	0	3689	219	0
3	D	2	0	0	0	0
4	D	62	0	24	9	0
5	A	120	0	0	11	0
5	D	140	0	0	20	0
All	All	6333	0	6102	270	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 22.

All (270) 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)
2:D:13:ILE:HA	5:D:555:HOH:O	1.28	1.25
2:D:331:MET:HB3	2:D:332:PRO:HD2	1.33	1.09
2:D:325:ASP:OD2	2:D:327:LYS:HB3	1.54	1.05
2:D:283:LEU:HD22	2:D:429:MET:HE2	1.44	0.97
2:D:328:ARG:HG3	2:D:441:ASP:HA	1.50	0.94
1:A:181:PRO:HB3	5:A:375:HOH:O	1.69	0.93
2:D:304:LYS:HG3	2:D:308:ARG:HH21	1.34	0.91
2:D:309:MET:HE2	2:D:313:LEU:HG	1.51	0.90
2:D:413:HIS:HD2	2:D:415:ILE:H	1.17	0.90
2:D:48:ASN:N	4:D:483:AGS:H2	1.89	0.88
2:D:231:LEU:CD2	2:D:243:ILE:HG12	2.04	0.87
2:D:331:MET:O	2:D:332:PRO:C	2.07	0.87
2:D:21:TYR:CZ	2:D:85:GLN:HG2	2.09	0.87
2:D:328:ARG:CG	2:D:441:ASP:HA	2.05	0.85
2:D:229:ILE:HD13	2:D:229:ILE:H	1.42	0.85
2:D:331:MET:HG3	2:D:442:LEU:HA	1.59	0.85
2:D:328:ARG:CB	2:D:441:ASP:HA	2.05	0.84
2:D:333:MET:CE	2:D:348:THR:HG22	2.08	0.83
2:D:184:ILE:HD13	2:D:185:CYS:N	1.92	0.83
2:D:222:LYS:HE2	5:D:595:HOH:O	1.78	0.83
2:D:331:MET:HB3	2:D:332:PRO:CD	2.09	0.82
2:D:444:ASN:HD22	2:D:447:MET:CE	1.93	0.82
2:D:314:GLU:OE2	2:D:317:ARG:NH2	2.14	0.81
2:D:283:LEU:HD22	2:D:429:MET:CE	2.11	0.80
2:D:184:ILE:HD11	2:D:276:VAL:N	1.98	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:328:ARG:HB2	2:D:444:ASN:HB2	1.66	0.78
2:D:70:SER:HB2	2:D:73:GLU:HB2	1.67	0.77
2:D:329:ASN:O	2:D:331:MET:N	2.17	0.77
2:D:328:ARG:HG2	5:D:489:HOH:O	1.84	0.76
2:D:48:ASN:H	4:D:483:AGS:H2	1.50	0.76
2:D:328:ARG:HB3	2:D:441:ASP:HA	1.67	0.76
2:D:444:ASN:HA	2:D:447:MET:HE2	1.67	0.75
2:D:62:ARG:HD3	5:D:588:HOH:O	1.85	0.75
2:D:331:MET:CE	2:D:331:MET:HA	2.17	0.74
2:D:280:PHE:HA	2:D:429:MET:HE1	1.69	0.74
2:D:231:LEU:HD22	2:D:243:ILE:HG12	1.68	0.74
2:D:470:ILE:HG12	2:D:477:ILE:HD12	1.68	0.74
2:D:328:ARG:HG3	2:D:441:ASP:OD1	1.86	0.74
2:D:328:ARG:CG	5:D:489:HOH:O	2.35	0.74
2:D:325:ASP:O	2:D:327:LYS:N	2.21	0.73
2:D:444:ASN:HD22	2:D:447:MET:HE2	1.53	0.73
2:D:337:ILE:HD12	2:D:337:ILE:H	1.52	0.73
1:A:66:TYR:CD1	1:A:69:SER:HB3	2.24	0.72
2:D:130:ASN:HB3	2:D:314:GLU:OE2	1.90	0.72
2:D:333:MET:HE3	2:D:348:THR:HG22	1.70	0.72
2:D:270:ILE:O	2:D:273:ILE:HG23	1.91	0.71
2:D:328:ARG:HG3	2:D:441:ASP:CA	2.20	0.70
2:D:31:TYR:O	2:D:35:LYS:HB2	1.91	0.70
2:D:324:PHE:HA	2:D:444:ASN:HD21	1.57	0.69
2:D:378:SER:HB3	2:D:388:VAL:HG13	1.73	0.69
2:D:227:ASN:OD1	2:D:227:ASN:C	2.30	0.68
2:D:331:MET:HG3	2:D:442:LEU:CA	2.23	0.68
1:A:7:ASP:HB2	1:A:8:LYS:NZ	2.09	0.68
2:D:325:ASP:C	2:D:327:LYS:H	1.95	0.68
2:D:235:PRO:HG3	2:D:466:ARG:O	1.93	0.67
2:D:432:SER:HA	5:D:587:HOH:O	1.93	0.67
2:D:58:LYS:O	2:D:61:LYS:HG3	1.95	0.67
2:D:69:THR:HG22	2:D:73:GLU:OE1	1.95	0.66
2:D:184:ILE:HD12	2:D:276:VAL:HG23	1.78	0.66
1:A:255:ASN:OD1	1:A:257:GLU:HB2	1.96	0.66
2:D:19:GLU:HG3	2:D:24:ARG:O	1.96	0.65
2:D:85:GLN:H	2:D:85:GLN:NE2	1.95	0.65
2:D:143:ASN:O	2:D:451:LYS:HE2	1.96	0.65
2:D:306:ASN:HB2	5:D:622:HOH:O	1.97	0.65
2:D:280:PHE:HA	2:D:429:MET:CE	2.27	0.64
2:D:231:LEU:HD21	2:D:243:ILE:HG12	1.78	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:317:ARG:HH11	2:D:317:ARG:HG2	1.61	0.64
2:D:44:ILE:HD13	2:D:101:GLN:HE21	1.63	0.63
2:D:184:ILE:HD11	2:D:275:ILE:C	2.19	0.62
2:D:109:THR:HG21	4:D:483:AGS:O2A	1.98	0.62
1:A:8:LYS:HD2	1:A:8:LYS:O	1.98	0.62
1:A:53:LEU:HB3	1:A:58:ILE:HG12	1.81	0.62
2:D:258:ARG:HA	5:D:580:HOH:O	2.00	0.62
2:D:444:ASN:ND2	2:D:447:MET:HE2	2.14	0.62
2:D:470:ILE:HG23	2:D:477:ILE:CD1	2.30	0.61
2:D:462:LYS:HD2	5:D:606:HOH:O	1.99	0.60
2:D:408:ASP:HB3	2:D:411:LYS:HD2	1.83	0.60
2:D:316:VAL:CG1	2:D:322:ILE:HD12	2.32	0.60
2:D:297:ASP:HA	2:D:300:LYS:HE3	1.84	0.59
1:A:9:PRO:HG3	1:A:262:HIS:HA	1.84	0.58
1:A:2:ASP:OD1	1:A:246:LYS:HD3	2.04	0.58
2:D:189:TYR:O	2:D:193:LEU:HD23	2.04	0.58
2:D:329:ASN:C	2:D:331:MET:H	2.06	0.58
2:D:325:ASP:C	2:D:447:MET:HE1	2.23	0.58
2:D:229:ILE:H	2:D:229:ILE:CD1	2.15	0.58
2:D:245:ASP:OD1	2:D:249:ASN:HB2	2.03	0.58
2:D:328:ARG:HB3	2:D:441:ASP:CA	2.32	0.58
2:D:328:ARG:NH1	2:D:329:ASN:HD21	2.02	0.58
2:D:314:GLU:CD	2:D:317:ARG:NH2	2.57	0.58
1:A:230:VAL:CG2	5:A:375:HOH:O	2.52	0.57
2:D:14:THR:HG23	2:D:38:ALA:HB2	1.86	0.57
2:D:331:MET:HA	2:D:331:MET:HE1	1.85	0.57
2:D:164:LEU:O	2:D:168:VAL:HG23	2.05	0.57
2:D:309:MET:CE	2:D:313:LEU:HG	2.30	0.57
2:D:171:LEU:HD23	2:D:171:LEU:O	2.03	0.57
2:D:337:ILE:HG23	2:D:344:VAL:HG22	1.86	0.57
2:D:47:PHE:O	2:D:49:LYS:HE3	2.03	0.57
2:D:162:SER:OG	2:D:251:ILE:HD13	2.05	0.57
1:A:215:THR:HG23	2:D:365:VAL:HG22	1.85	0.57
2:D:331:MET:CB	2:D:332:PRO:CD	2.82	0.57
1:A:231:ASN:HD21	1:A:235:LYS:HE3	1.69	0.56
2:D:13:ILE:HD13	5:D:555:HOH:O	2.05	0.56
2:D:436:LYS:HB2	5:D:593:HOH:O	2.06	0.56
2:D:413:HIS:CD2	2:D:415:ILE:H	2.09	0.56
1:A:230:VAL:HG22	5:A:375:HOH:O	2.05	0.56
2:D:109:THR:HG21	4:D:483:AGS:PA	2.46	0.56
2:D:304:LYS:CG	2:D:308:ARG:HH21	2.11	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:132:THR:HA	2:D:135:GLU:HG3	1.87	0.56
2:D:148:ALA:O	2:D:149:VAL:HB	2.06	0.55
1:A:58:ILE:HD12	1:A:170:VAL:HG23	1.88	0.55
2:D:176:LEU:HD13	2:D:273:ILE:HD12	1.88	0.55
2:D:334:LYS:HB3	2:D:347:THR:OG1	2.06	0.55
2:D:337:ILE:HD11	2:D:412:VAL:HG23	1.89	0.55
2:D:211:ARG:NH1	5:D:566:HOH:O	2.39	0.55
2:D:55:LEU:CD2	4:D:483:AGS:S1G	2.95	0.55
2:D:378:SER:HB3	2:D:388:VAL:CG1	2.35	0.55
1:A:96:GLY:HA3	1:A:115:PHE:CE1	2.41	0.54
2:D:348:THR:HB	2:D:352:PHE:HD1	1.72	0.54
2:D:325:ASP:O	2:D:444:ASN:ND2	2.39	0.54
1:A:7:ASP:HB2	1:A:8:LYS:HZ2	1.71	0.54
2:D:320:HIS:HB3	2:D:436:LYS:HD2	1.89	0.54
2:D:359:VAL:CG1	2:D:400:PHE:HB2	2.38	0.54
2:D:444:ASN:HA	2:D:447:MET:CE	2.37	0.54
2:D:18:ILE:HG22	2:D:26:PRO:HG3	1.89	0.54
2:D:303:GLU:HG2	5:D:579:HOH:O	2.08	0.54
1:A:175:LYS:HE3	1:A:207:GLU:OE2	2.08	0.54
2:D:460:ARG:HD2	5:D:512:HOH:O	2.08	0.53
2:D:171:LEU:HD23	2:D:171:LEU:C	2.29	0.53
1:A:102:ILE:HG23	5:A:396:HOH:O	2.08	0.53
2:D:314:GLU:CD	2:D:317:ARG:HH21	2.12	0.53
2:D:116:THR:O	2:D:117:ILE:HG23	2.08	0.53
2:D:444:ASN:HD22	2:D:447:MET:HE1	1.68	0.53
1:A:4:VAL:HG22	1:A:5:SER:N	2.24	0.52
1:A:14:GLU:HG2	1:A:14:GLU:O	2.08	0.52
2:D:229:ILE:HD13	2:D:229:ILE:N	2.19	0.52
1:A:146:ASN:OD1	1:A:146:ASN:N	2.42	0.52
1:A:253:TYR:OH	1:A:287:GLN:NE2	2.42	0.52
2:D:326:GLY:HA2	2:D:447:MET:HE3	1.92	0.52
2:D:189:TYR:CE2	2:D:193:LEU:HD21	2.45	0.52
2:D:70:SER:HB2	2:D:73:GLU:H	1.75	0.52
2:D:280:PHE:CA	2:D:429:MET:HE1	2.38	0.52
2:D:337:ILE:HG13	2:D:412:VAL:CG2	2.39	0.52
2:D:57:LYS:HE2	2:D:71:ALA:HB1	1.92	0.52
2:D:227:ASN:ND2	2:D:246:GLU:HB2	2.25	0.52
2:D:131:VAL:CG1	2:D:311:THR:HA	2.39	0.52
2:D:146:ASN:HD21	2:D:299:SER:HA	1.75	0.52
2:D:184:ILE:HG22	2:D:206:LEU:HB2	1.92	0.52
2:D:225:THR:HG22	2:D:227:ASN:HB3	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:413:HIS:HE1	2:D:452:ILE:O	1.93	0.51
2:D:261:THR:O	2:D:265:VAL:HG23	2.10	0.51
2:D:327:LYS:O	2:D:328:ARG:HG2	2.11	0.51
1:A:100:ASP:OD1	1:A:101:PRO:HD2	2.11	0.51
1:A:8:LYS:HD2	1:A:8:LYS:C	2.30	0.50
2:D:346:VAL:O	2:D:348:THR:HG23	2.12	0.50
2:D:184:ILE:CD1	2:D:276:VAL:HG23	2.41	0.50
2:D:331:MET:HG3	2:D:442:LEU:N	2.26	0.50
2:D:30:GLU:HG2	2:D:91:ILE:HD11	1.93	0.49
2:D:329:ASN:C	2:D:331:MET:N	2.66	0.49
1:A:7:ASP:HB2	1:A:8:LYS:HZ1	1.76	0.49
2:D:117:ILE:O	2:D:178:ARG:NH2	2.44	0.49
2:D:193:LEU:HD12	2:D:271:ASP:OD1	2.13	0.49
2:D:49:LYS:O	2:D:53:VAL:HG23	2.12	0.49
2:D:325:ASP:C	2:D:327:LYS:N	2.62	0.49
1:A:215:THR:CG2	2:D:365:VAL:HG22	2.43	0.48
2:D:85:GLN:H	2:D:85:GLN:CD	2.16	0.48
2:D:184:ILE:HD13	2:D:185:CYS:O	2.13	0.48
2:D:327:LYS:O	2:D:328:ARG:CG	2.62	0.48
2:D:271:ASP:O	2:D:273:ILE:HG22	2.14	0.48
2:D:206:LEU:HD23	2:D:255:PHE:HB2	1.95	0.48
2:D:381:PHE:CG	2:D:430:LEU:HD13	2.48	0.48
2:D:61:LYS:HZ3	2:D:62:ARG:HG3	1.79	0.48
2:D:188:SER:HB3	2:D:200:TYR:HB3	1.95	0.48
2:D:180:ASN:HB2	2:D:181:LYS:NZ	2.29	0.47
2:D:180:ASN:HB2	2:D:181:LYS:HZ2	1.78	0.47
2:D:268:ILE:HG22	2:D:270:ILE:HG12	1.97	0.47
1:A:43:LEU:C	1:A:43:LEU:HD12	2.34	0.47
2:D:306:ASN:CB	5:D:622:HOH:O	2.60	0.47
1:A:79:ARG:HD3	1:A:79:ARG:C	2.35	0.47
2:D:22:LEU:O	2:D:86:THR:HA	2.15	0.47
2:D:55:LEU:HD22	4:D:483:AGS:S1G	2.54	0.47
2:D:138:ALA:HB3	2:D:306:ASN:OD1	2.15	0.47
2:D:184:ILE:HD12	2:D:276:VAL:CG2	2.44	0.47
1:A:156:ASN:ND2	5:A:397:HOH:O	2.45	0.46
2:D:316:VAL:HG13	2:D:322:ILE:HD12	1.97	0.46
2:D:96:THR:HG23	2:D:477:ILE:HG12	1.95	0.46
2:D:301:ASP:C	2:D:301:ASP:OD1	2.53	0.46
2:D:328:ARG:HG3	5:D:489:HOH:O	2.10	0.46
2:D:48:ASN:H	4:D:483:AGS:C2	2.26	0.46
5:A:409:HOH:O	2:D:258:ARG:HB3	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:16:LYS:HD2	5:D:555:HOH:O	2.15	0.46
2:D:184:ILE:CG2	2:D:206:LEU:HB2	2.46	0.46
2:D:330:ASN:C	2:D:331:MET:O	2.52	0.46
2:D:443:LEU:HD23	2:D:446:MET:HE1	1.98	0.46
2:D:189:TYR:CZ	2:D:193:LEU:HD21	2.51	0.46
2:D:17:ILE:HD13	5:D:558:HOH:O	2.15	0.46
2:D:55:LEU:HD21	4:D:483:AGS:PG	2.56	0.46
2:D:70:SER:O	2:D:74:ILE:HG12	2.16	0.46
2:D:214:LEU:HD22	2:D:243:ILE:HG13	1.98	0.46
2:D:342:ARG:NH1	5:D:520:HOH:O	2.48	0.46
1:A:46:GLU:OE2	1:A:66:TYR:OH	2.25	0.45
2:D:48:ASN:O	4:D:483:AGS:N1	2.49	0.45
2:D:337:ILE:CD1	2:D:412:VAL:HG23	2.45	0.45
2:D:414:GLU:O	2:D:418:ARG:HG3	2.16	0.45
2:D:190:SER:HB2	2:D:275:ILE:HB	1.98	0.45
2:D:252:ILE:HD12	5:D:547:HOH:O	2.16	0.45
2:D:53:VAL:HG12	2:D:57:LYS:HE3	1.98	0.45
1:A:145:GLY:C	1:A:146:ASN:OD1	2.56	0.44
2:D:230:ILE:N	2:D:230:ILE:HD12	2.33	0.44
2:D:225:THR:CG2	2:D:227:ASN:HB3	2.47	0.44
2:D:13:ILE:O	2:D:17:ILE:HG12	2.18	0.44
2:D:237:LEU:HD12	2:D:237:LEU:HA	1.86	0.44
2:D:21:TYR:CE1	2:D:85:GLN:HG2	2.50	0.44
2:D:192:TYR:HA	2:D:198:ILE:HB	1.99	0.44
2:D:328:ARG:HH11	2:D:329:ASN:HD21	1.65	0.44
1:A:18:ASN:HB3	1:A:238:TYR:CE2	2.53	0.43
2:D:283:LEU:HD21	2:D:425:LEU:HB3	1.99	0.43
1:A:177:ARG:HD2	5:A:352:HOH:O	2.17	0.43
2:D:317:ARG:HH11	2:D:317:ARG:CG	2.30	0.43
2:D:112:LEU:HD13	2:D:220:LEU:HD22	2.00	0.43
2:D:69:THR:HG21	2:D:77:ARG:HH22	1.84	0.43
2:D:317:ARG:HG2	2:D:317:ARG:NH1	2.30	0.43
2:D:328:ARG:HA	2:D:328:ARG:HD3	1.27	0.43
2:D:333:MET:O	2:D:334:LYS:C	2.57	0.43
1:A:53:LEU:HD13	1:A:58:ILE:HD11	2.01	0.43
2:D:139:ARG:HG2	2:D:306:ASN:ND2	2.34	0.43
1:A:106:LEU:HB2	1:A:109:VAL:HG22	2.00	0.42
2:D:292:ILE:HG22	2:D:293:ASP:N	2.33	0.42
2:D:107:THR:O	2:D:111:ILE:HG12	2.20	0.42
1:A:164:ILE:HD12	1:A:214:TYR:OH	2.19	0.42
1:A:4:VAL:HG23	5:A:331:HOH:O	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:386:ASN:O	2:D:387:SER:HB2	2.20	0.42
2:D:331:MET:O	2:D:333:MET:N	2.49	0.42
2:D:330:ASN:O	2:D:331:MET:O	2.37	0.42
2:D:408:ASP:CB	2:D:411:LYS:HD2	2.48	0.42
1:A:43:LEU:O	1:A:47:LEU:HB2	2.19	0.42
1:A:235:LYS:HE3	5:A:399:HOH:O	2.20	0.42
1:A:67:ILE:HD12	1:A:116:VAL:HG11	2.02	0.42
2:D:303:GLU:HA	2:D:303:GLU:OE1	2.19	0.42
2:D:388:VAL:CG1	2:D:389:TYR:N	2.82	0.42
1:A:253:TYR:CD2	1:A:254:PRO:HD2	2.55	0.42
2:D:21:TYR:CG	2:D:41:ILE:HG23	2.55	0.42
1:A:20:LEU:HB3	1:A:237:TYR:HD2	1.83	0.41
1:A:100:ASP:HA	1:A:101:PRO:HD3	1.93	0.41
1:A:181:PRO:CB	5:A:375:HOH:O	2.47	0.41
2:D:292:ILE:O	2:D:296:GLU:HG3	2.19	0.41
2:D:348:THR:HB	2:D:352:PHE:CD1	2.53	0.41
1:A:43:LEU:HD12	1:A:43:LEU:O	2.20	0.41
2:D:17:ILE:HD12	2:D:42:GLN:HB2	2.03	0.41
2:D:47:PHE:CD1	2:D:105:VAL:HG13	2.56	0.41
1:A:49:PHE:CZ	1:A:53:LEU:HD11	2.55	0.41
1:A:180:PHE:HA	1:A:181:PRO:HD3	1.91	0.41
2:D:17:ILE:HD11	2:D:42:GLN:OE1	2.20	0.41
2:D:115:LEU:CD1	2:D:171:LEU:HD21	2.51	0.41
2:D:229:ILE:C	2:D:230:ILE:HD12	2.40	0.41
1:A:230:VAL:CG1	1:A:234:LYS:HE2	2.50	0.41
1:A:265:PHE:O	1:A:268:ARG:NH1	2.54	0.41
2:D:148:ALA:O	2:D:149:VAL:CB	2.68	0.41
2:D:331:MET:O	2:D:332:PRO:O	2.37	0.41
2:D:389:TYR:CE2	2:D:427:TYR:HB2	2.56	0.41
1:A:129:HIS:HA	5:A:374:HOH:O	2.20	0.41
2:D:82:PHE:C	2:D:85:GLN:HE22	2.24	0.41
2:D:466:ARG:HG2	2:D:467:HIS:N	2.36	0.41
2:D:181:LYS:HE3	2:D:181:LYS:HA	2.03	0.40
1:A:163:MET:O	1:A:167:LEU:HB2	2.20	0.40
1:A:253:TYR:HE2	1:A:287:GLN:HE22	1.69	0.40
2:D:245:ASP:CG	2:D:249:ASN:HB2	2.42	0.40
2:D:388:VAL:HG13	2:D:389:TYR:N	2.37	0.40
1:A:66:TYR:CG	1:A:69:SER:HB3	2.57	0.40
1:A:79:ARG:O	1:A:83:TYR:HB2	2.21	0.40
2:D:247:ASN:HB2	2:D:249:ASN:ND2	2.36	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	282/297 (95%)	270 (96%)	10 (4%)	2 (1%)	22	26
2	D	439/469 (94%)	413 (94%)	21 (5%)	5 (1%)	14	15
All	All	721/766 (94%)	683 (95%)	31 (4%)	7 (1%)	15	17

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	D	330	ASN
2	D	331	MET
2	D	332	PRO
2	D	326	GLY
2	D	334	LYS
1	A	2	ASP
1	A	24	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	266/270 (98%)	246 (92%)	20 (8%)	13	17
2	D	422/443 (95%)	396 (94%)	26 (6%)	18	25
All	All	688/713 (96%)	642 (93%)	46 (7%)	16	21

All (46) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	8	LYS
1	A	20	LEU
1	A	43	LEU
1	A	47	LEU
1	A	50	LEU
1	A	58	ILE
1	A	66	TYR
1	A	109	VAL
1	A	114	ARG
1	A	128	LEU
1	A	146	ASN
1	A	148	PRO
1	A	165	SER
1	A	167	LEU
1	A	197	LEU
1	A	209	ARG
1	A	217	GLU
1	A	222	THR
1	A	257	GLU
1	A	288	GLN
2	D	69	THR
2	D	72	SER
2	D	85	GLN
2	D	117	ILE
2	D	131	VAL
2	D	134	MET
2	D	181	LYS
2	D	184	ILE
2	D	227	ASN
2	D	229	ILE
2	D	231	LEU
2	D	237	LEU
2	D	258	ARG
2	D	267	LYS
2	D	273	ILE
2	D	292	ILE
2	D	328	ARG
2	D	331	MET
2	D	332	PRO
2	D	337	ILE
2	D	347	THR
2	D	349	LYS
2	D	406	LEU

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Mol	Chain	Res	Type
2	D	407	SER
2	D	429	MET
2	D	462	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (20) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	84	ASN
1	A	156	ASN
1	A	160	GLN
1	A	183	GLN
1	A	231	ASN
1	A	287	GLN
1	A	288	GLN
2	D	29	ASN
2	D	32	HIS
2	D	59	ASN
2	D	85	GLN
2	D	87	GLN
2	D	101	GLN
2	D	247	ASN
2	D	249	ASN
2	D	329	ASN
2	D	413	HIS
2	D	428	GLN
2	D	444	ASN
2	D	457	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

Of 4 ligands modelled in this entry, 2 are monoatomic - leaving 2 for Mogul analysis.

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
4	AGS	D	482	3	26,33,33	1.25	3 (11%)	26,52,52	1.95	5 (19%)
4	AGS	D	483	-	26,33,33	1.37	4 (15%)	26,52,52	2.15	4 (15%)

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
4	AGS	D	482	3	-	3/17/38/38	0/3/3/3
4	AGS	D	483	-	-	3/17/38/38	0/3/3/3

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	D	483	AGS	O4'-C1'	3.28	1.45	1.41
4	D	482	AGS	O4'-C1'	2.69	1.44	1.41
4	D	482	AGS	C8-N7	-2.63	1.30	1.34
4	D	482	AGS	PG-S1G	-2.54	1.85	1.90
4	D	483	AGS	PG-O2G	2.52	1.63	1.54
4	D	483	AGS	C8-N7	-2.46	1.30	1.34
4	D	483	AGS	PG-S1G	-2.06	1.86	1.90

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	483	AGS	O2G-PG-O3B	-8.74	75.46	104.64
4	D	482	AGS	N3-C2-N1	-5.90	119.45	128.68
4	D	482	AGS	PA-O3A-PB	-4.59	117.07	132.83
4	D	483	AGS	N3-C2-N1	-3.52	123.17	128.68

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	482	AGS	O2G-PG-O3B	2.61	113.37	104.64
4	D	482	AGS	C2-N1-C6	2.46	122.97	118.75
4	D	483	AGS	C2-N1-C6	2.43	122.91	118.75
4	D	482	AGS	PA-O5'-C5'	-2.36	107.83	121.68
4	D	483	AGS	PA-O3A-PB	-2.02	125.90	132.83

There are no chirality outliers.

All (6) torsion outliers are listed below:

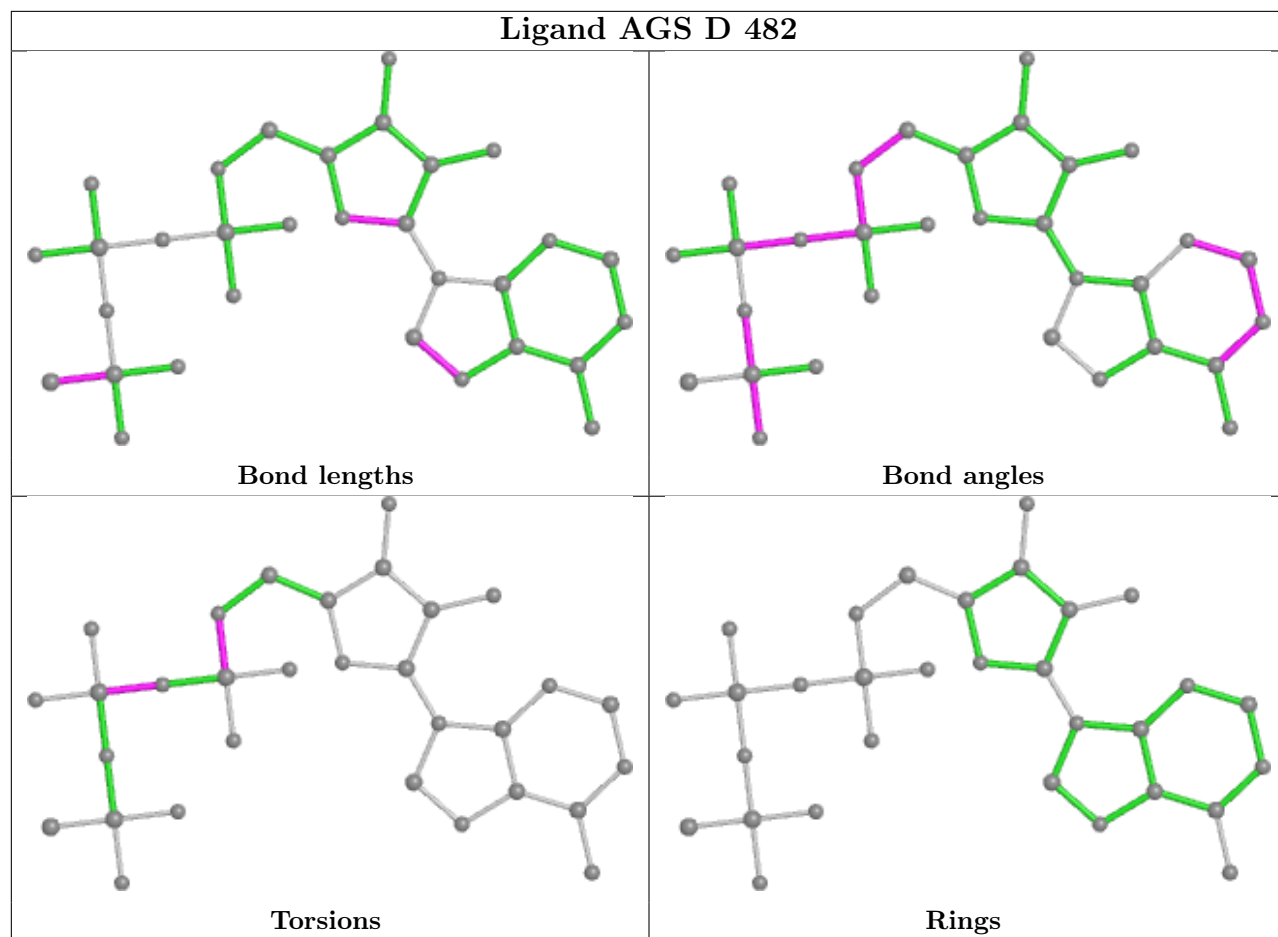
Mol	Chain	Res	Type	Atoms
4	D	482	AGS	C5'-O5'-PA-O3A
4	D	482	AGS	PA-O3A-PB-O1B
4	D	483	AGS	O4'-C4'-C5'-O5'
4	D	483	AGS	PB-O3A-PA-O1A
4	D	482	AGS	C5'-O5'-PA-O2A
4	D	483	AGS	C3'-C4'-C5'-O5'

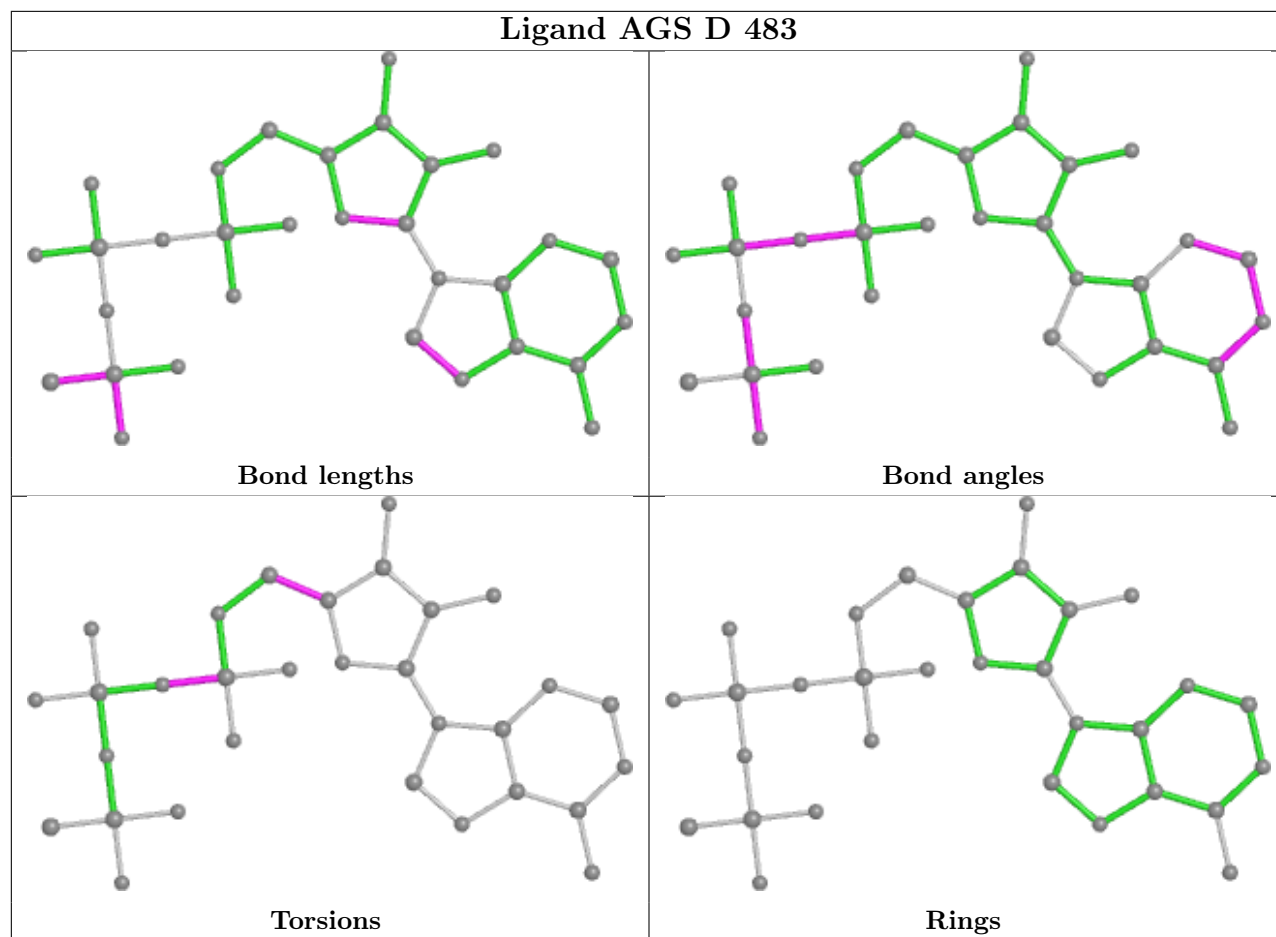
There are no ring outliers.

1 monomer is involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	D	483	AGS	9	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

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	288/297 (96%)	0.41	25 (8%) 10 14	15, 29, 56, 72	0
2	D	445/469 (94%)	0.31	36 (8%) 12 16	17, 33, 55, 66	0
All	All	733/766 (95%)	0.35	61 (8%) 11 15	15, 31, 56, 72	0

All (61) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	24	PRO	7.5
2	D	328	ARG	7.4
1	A	217	GLU	6.1
1	A	141	SER	6.1
2	D	161	VAL	6.1
2	D	327	LYS	5.7
1	A	218	ASN	5.0
2	D	332	PRO	4.6
2	D	199	ARG	4.4
1	A	145	GLY	4.4
2	D	39	ARG	4.3
2	D	132	THR	4.2
1	A	25	GLU	4.2
1	A	1	MET	4.1
1	A	146	ASN	4.1
2	D	12	ASN	4.0
2	D	162	SER	3.8
2	D	331	MET	3.6
2	D	329	ASN	3.6
1	A	147	GLU	3.5
2	D	303	GLU	3.5
1	A	148	PRO	3.3
2	D	300	LYS	3.2
2	D	163	SER	3.2

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Mol	Chain	Res	Type	RSRZ
2	D	394	ASN	3.2
1	A	23	GLU	3.1
2	D	117	ILE	3.1
1	A	26	SER	3.0
2	D	14	THR	3.0
2	D	136	GLU	2.8
1	A	50	LEU	2.8
1	A	2	ASP	2.7
1	A	22	TYR	2.7
2	D	248	ASP	2.6
1	A	220	ARG	2.6
2	D	355	LYS	2.6
2	D	330	ASN	2.5
2	D	42	GLN	2.5
2	D	272	ASN	2.4
2	D	301	ASP	2.4
2	D	68	ASN	2.4
2	D	15	LEU	2.4
2	D	13	ILE	2.3
1	A	47	LEU	2.3
2	D	314	GLU	2.3
1	A	20	LEU	2.3
1	A	196	MET	2.2
1	A	216	GLY	2.2
1	A	34	LEU	2.2
2	D	149	VAL	2.2
2	D	247	ASN	2.2
2	D	270	ILE	2.2
2	D	421	CYS	2.2
2	D	419	GLY	2.2
2	D	409	LYS	2.1
1	A	140	ALA	2.1
2	D	351	TYR	2.0
1	A	44	LEU	2.0
2	D	306	ASN	2.0
1	A	275	THR	2.0
1	A	33	LYS	2.0

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 [i](#)

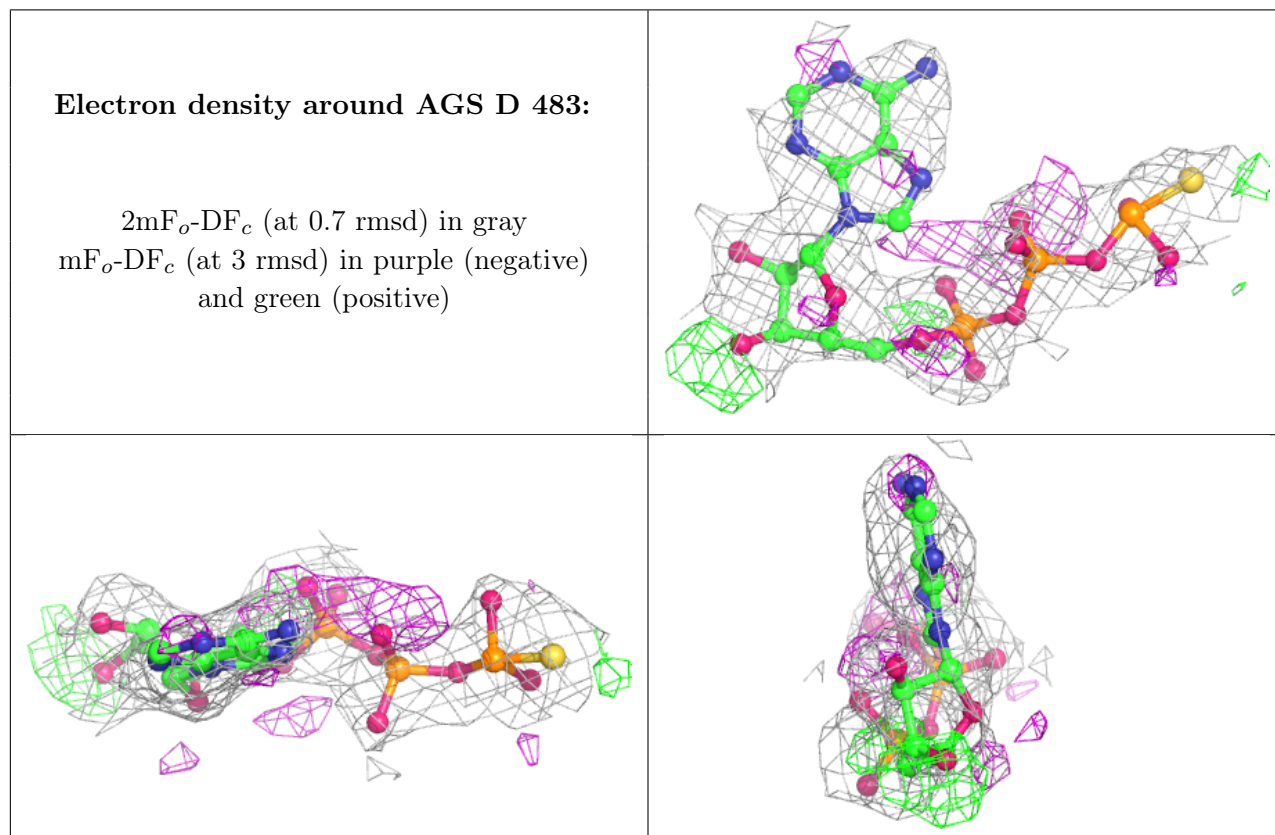
There are no monosaccharides in this entry.

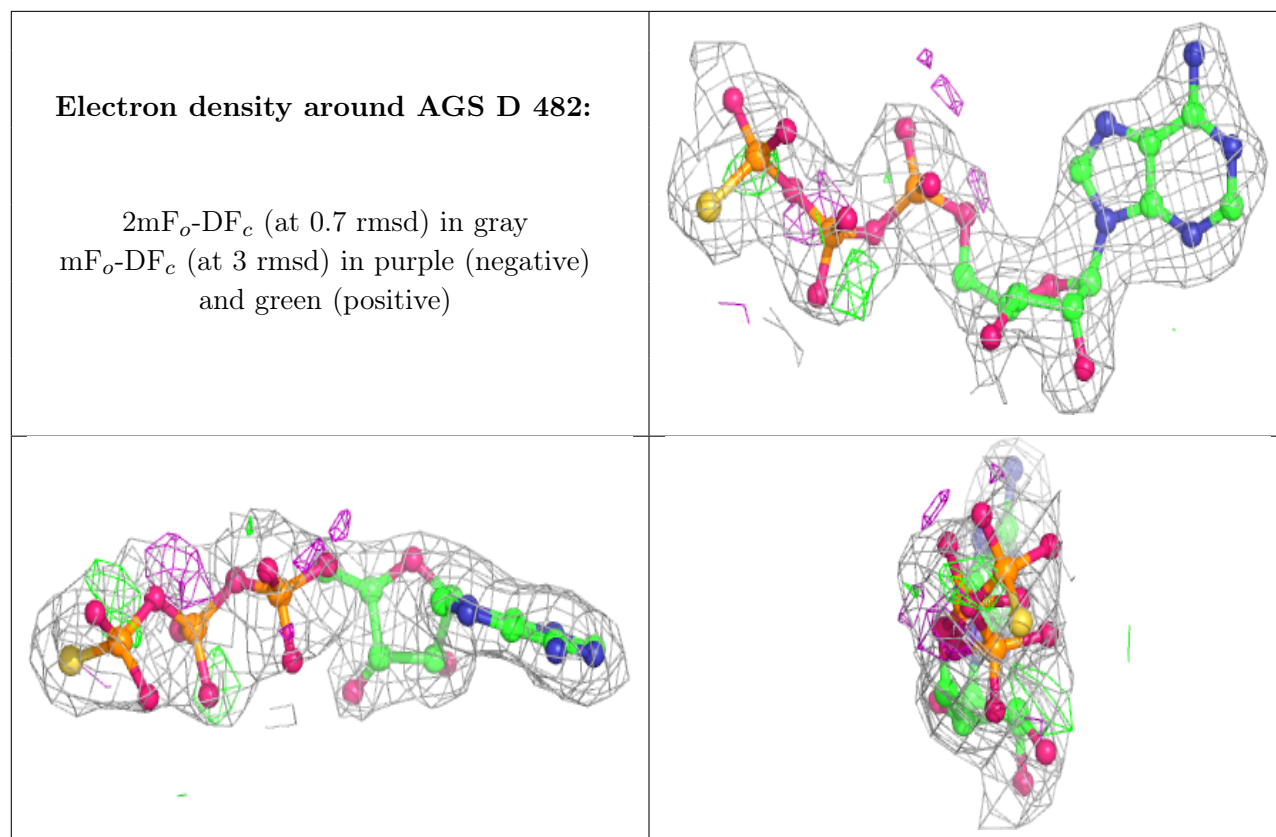
6.4 Ligands [i](#)

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
3	CA	D	481	1/1	0.74	0.21	71,71,71,71	0
4	AGS	D	483	31/31	0.75	0.26	55,63,83,85	0
3	CA	D	480	1/1	0.86	0.07	36,36,36,36	0
4	AGS	D	482	31/31	0.91	0.17	38,46,57,58	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.