



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 09:49 PM UTC

PDB ID : 2VWB / pdb_00002vwb
Title : Structure of the archaeal Kae1-Bud32 fusion protein MJ1130: a model for the eukaryotic EKC-KEOPS subcomplex involved in transcription and telomere homeostasis.
Authors : Hecker, A.; Lopreiato, R.; Graille, M.; Collinet, B.; Forterre, P.; Domenico, L.; van Tilbeurgh, H.
Deposited on : 2008-06-20
Resolution : 3.05 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](#) ①) 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

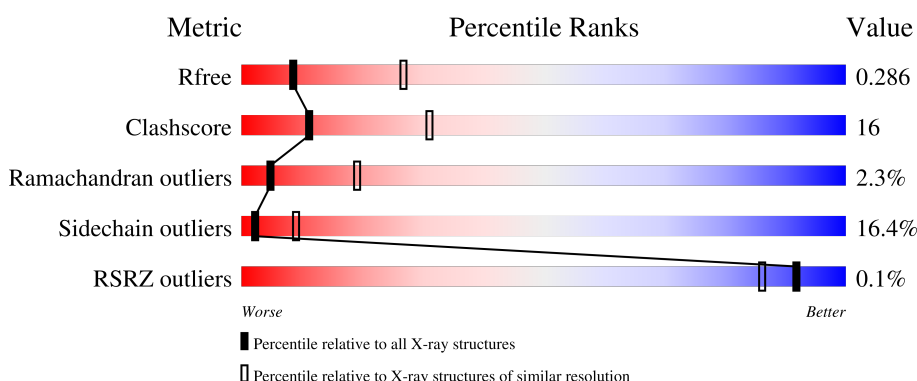
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.05 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	2469 (3.10-3.02)
Clashscore	190562	2569 (3.10-3.02)
Ramachandran outliers	187476	2424 (3.10-3.02)
Sidechain outliers	187428	2423 (3.10-3.02)
RSRZ outliers	180081	2469 (3.10-3.02)

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	535	 59% 30% 7% ..
1	B	535	 54% 34% 6% 5%

2 Entry composition [i](#)

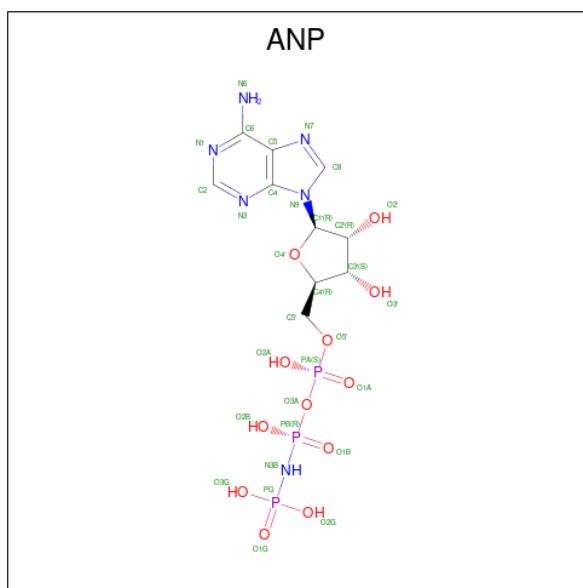
There are 2 unique types of molecules in this entry. The entry contains 8210 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 PUTATIVE O-SIALOGLYCOPROTEIN ENDOPEPTIDASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	519	Total	C	N	O	S	0	0	0
			4125	2636	698	770	21			
1	B	507	Total	C	N	O	S	0	0	0
			4023	2568	680	754	21			

- Molecule 2 is PHOSPHOAMINOPHOSPHONIC ACID-ADENYLATE ESTER (CCD ID: ANP) (formula: $C_{10}H_{17}N_6O_{12}P_3$).

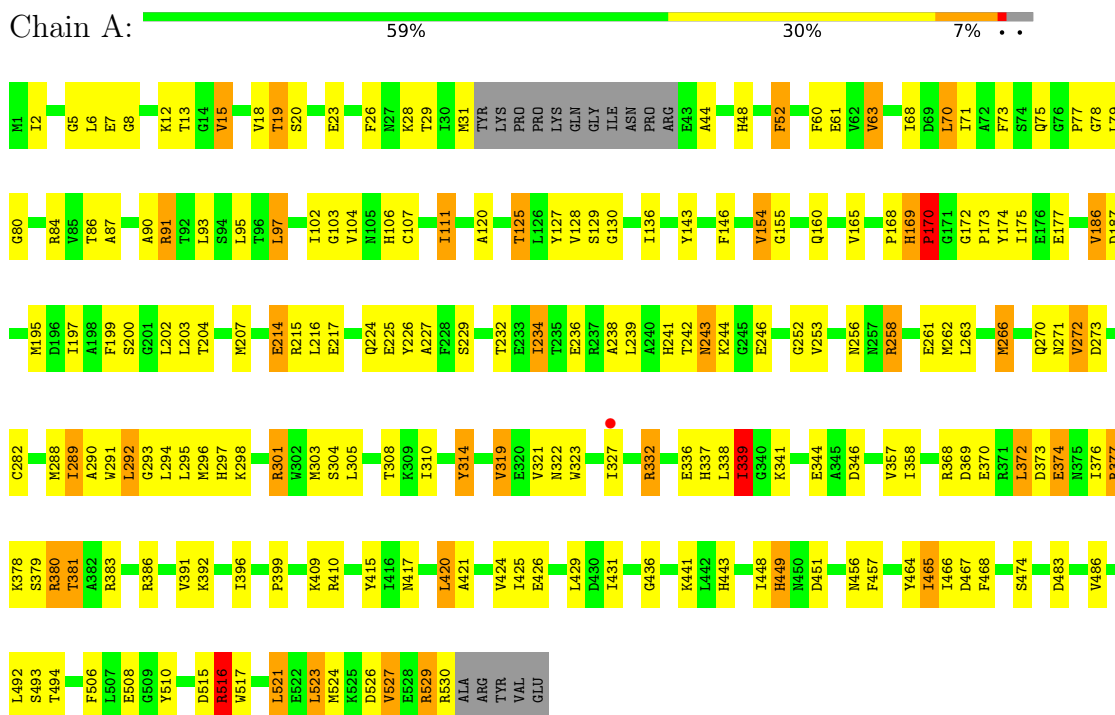


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			31	10	6	12	3		
2	B	1	Total	C	N	O	P	0	0
			31	10	6	12	3		

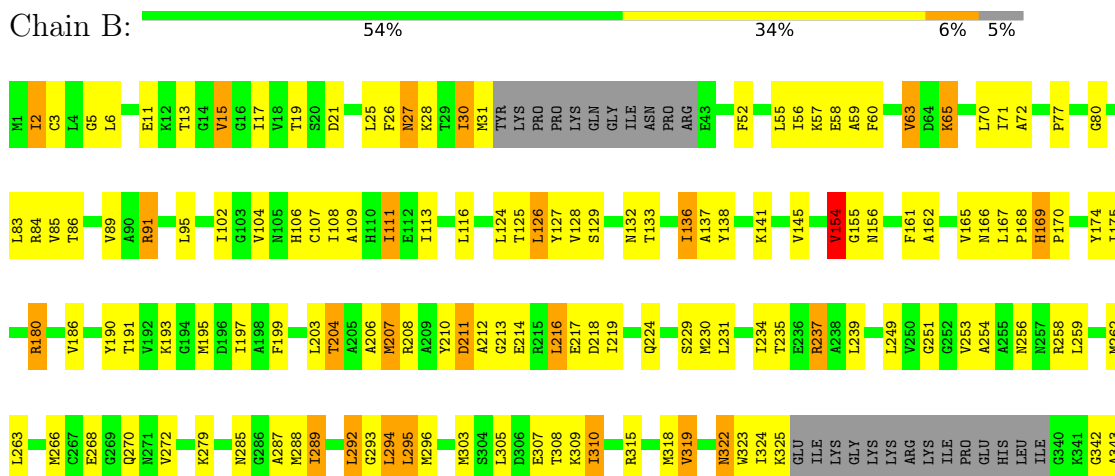
3 Residue-property plots

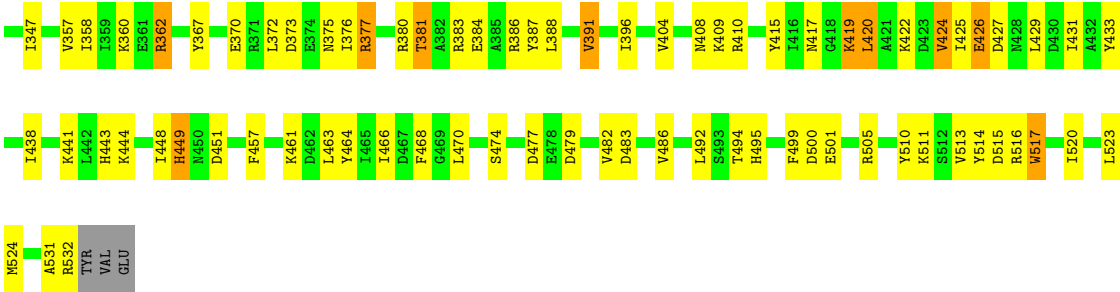
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density.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



• Molecule 1: PUTATIVE O-SIALOGLYCOPROTEIN ENDOPEPTIDASE





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	147.42Å 148.95Å 65.12Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.95 – 3.05 19.95 – 3.05	Depositor EDS
% Data completeness (in resolution range)	94.4 (19.95-3.05) 94.0 (19.95-3.05)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.28 (at 3.04Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.220 , 0.301 0.210 , 0.286	Depositor DCC
R_{free} test set	1319 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	70.9	Xtriage
Anisotropy	0.301	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 26.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.010 for k,h,-l	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	8210	wwPDB-VP
Average B, all atoms (Å ²)	60.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.85% 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: ANP

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	1/4199 (0.0%)	1.01	11/5660 (0.2%)
1	B	0.67	0/4094	1.01	5/5520 (0.1%)
All	All	0.68	1/8293 (0.0%)	1.01	16/11180 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	327	ILE	CA-CB	5.03	1.61	1.54

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	120	ALA	N-CA-C	-6.35	101.13	110.52
1	A	319	VAL	N-CA-C	6.28	116.90	107.80
1	A	424	VAL	CB-CA-C	-5.95	105.08	110.91
1	A	169	HIS	CA-C-N	5.94	127.27	119.84
1	A	169	HIS	C-N-CA	5.94	127.27	119.84
1	B	461	LYS	N-CA-C	-5.85	105.97	113.23
1	A	170	PRO	N-CA-C	-5.85	100.42	112.47
1	A	241	HIS	N-CA-C	-5.73	106.09	112.57
1	B	207	MET	N-CA-C	-5.52	104.90	111.03
1	A	78	GLY	N-CA-C	5.50	118.61	110.42

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	154	VAL	CB-CA-C	-5.36	105.02	112.04
1	A	449	HIS	CA-C-N	-5.31	114.23	122.67
1	A	449	HIS	C-N-CA	-5.31	114.23	122.67
1	B	154	VAL	N-CA-CB	5.28	116.37	110.51
1	B	449	HIS	N-CA-C	-5.28	100.70	109.46
1	B	347	ILE	CB-CA-C	-5.26	105.25	111.09

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	169	HIS	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	4125	0	4181	128	0
1	B	4023	0	4060	141	0
2	A	31	0	13	2	0
2	B	31	0	13	1	0
All	All	8210	0	8267	268	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 16.

All (268) 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:516:ARG:HH11	1:A:516:ARG:HG2	1.13	1.13
1:B:104:VAL:HG13	1:B:292:LEU:HD12	1.34	1.08
1:A:242:THR:HG21	1:A:244:LYS:HG2	1.37	1.06
1:A:242:THR:CG2	1:A:244:LYS:HG2	1.90	1.01
1:A:107:CYS:HG	1:A:127:TYR:HE2	1.09	0.99
1:B:449:HIS:HD2	1:B:451:ASP:H	1.12	0.93

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:108:ILE:HD12	1:B:319:VAL:HG11	1.50	0.91
1:B:229:SER:HA	1:B:262:MET:HE1	1.52	0.90
1:A:516:ARG:HG2	1:A:516:ARG:NH1	1.76	0.88
1:B:108:ILE:CD1	1:B:319:VAL:HG11	2.04	0.87
1:A:229:SER:HA	1:A:262:MET:HE1	1.58	0.85
1:B:107:CYS:HG	1:B:127:TYR:HE2	0.84	0.84
1:B:285:ASN:ND2	1:B:288:MET:H	1.74	0.84
1:A:449:HIS:HE1	1:A:467:ASP:O	1.59	0.84
1:B:107:CYS:SG	1:B:127:TYR:HE2	2.02	0.82
1:B:377:ARG:O	1:B:381:THR:HG23	1.80	0.81
1:A:242:THR:HG21	1:A:244:LYS:CG	2.12	0.79
1:A:104:VAL:HG13	1:A:292:LEU:HD12	1.64	0.79
1:B:104:VAL:HG22	1:B:296:MET:HE1	1.64	0.79
1:B:104:VAL:HG13	1:B:292:LEU:CD1	2.12	0.78
1:B:107:CYS:SG	1:B:127:TYR:CE2	2.75	0.77
1:B:128:VAL:O	1:B:251:GLY:HA3	1.83	0.77
1:B:195:MET:SD	1:B:237:ARG:HD2	2.26	0.76
1:B:449:HIS:CD2	1:B:451:ASP:H	2.02	0.75
1:B:104:VAL:HG22	1:B:296:MET:CE	2.16	0.75
1:A:258:ARG:HH21	1:A:261:GLU:HG2	1.51	0.74
1:A:516:ARG:HH11	1:A:516:ARG:CG	1.96	0.74
1:B:433:TYR:HB2	1:B:505:ARG:HG3	1.70	0.74
1:A:195:MET:O	1:A:234:ILE:HG13	1.88	0.73
1:B:285:ASN:HD21	1:B:288:MET:H	1.37	0.73
1:A:232:THR:OG1	1:A:262:MET:HE2	1.87	0.72
1:A:129:SER:HA	1:A:253:VAL:HG23	1.72	0.72
1:B:104:VAL:CG1	1:B:292:LEU:HD12	2.17	0.72
1:A:87:ALA:HB2	1:A:310:ILE:HD11	1.73	0.71
1:A:336:GLU:O	1:A:338:LEU:N	2.21	0.71
1:B:449:HIS:HD2	1:B:451:ASP:N	1.88	0.71
1:B:477:ASP:OD1	1:B:516:ARG:NH1	2.23	0.70
1:A:449:HIS:HD2	1:A:451:ASP:H	1.39	0.70
1:B:154:VAL:HG13	1:B:199:PHE:CZ	2.27	0.69
1:A:456:ASN:ND2	1:A:467:ASP:HB3	2.08	0.69
1:A:168:PRO:HB2	1:A:174:TYR:CE1	2.28	0.69
1:A:106:HIS:NE2	2:A:1531:ANP:O1G	2.21	0.69
1:B:52:PHE:O	1:B:56:ILE:HG13	1.93	0.68
1:A:336:GLU:C	1:A:338:LEU:H	2.03	0.67
1:B:193:LYS:NZ	1:B:482:VAL:HG21	2.09	0.67
1:B:262:MET:HE3	1:B:367:TYR:CD2	2.29	0.67
1:A:242:THR:HG22	1:A:244:LYS:HG2	1.76	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:204:THR:HA	1:B:207:MET:HE2	1.75	0.67
1:B:77:PRO:HD2	1:B:106:HIS:HB3	1.75	0.66
1:A:243:ASN:HD22	1:A:243:ASN:H	1.44	0.65
1:B:136:ILE:HG22	1:B:145:VAL:HA	1.79	0.65
1:A:373:ASP:O	1:A:377:ARG:HG2	1.97	0.65
1:A:380:ARG:HH21	1:A:380:ARG:CG	2.10	0.65
1:B:91:ARG:NH1	1:B:308:THR:O	2.30	0.65
1:B:17:ILE:HD11	1:B:59:ALA:HB1	1.78	0.64
1:B:95:LEU:HD21	1:B:305:LEU:HD11	1.79	0.64
1:A:107:CYS:SG	1:A:127:TYR:HE2	2.17	0.64
1:B:531:ALA:O	1:B:532:ARG:HB2	1.98	0.63
1:A:457:PHE:CE1	1:A:465:ILE:HG23	2.34	0.63
1:A:372:LEU:HD22	1:A:376:ILE:HD11	1.79	0.62
1:A:172:GLY:O	1:A:175:ILE:HG13	1.99	0.62
1:A:374:GLU:O	1:A:378:LYS:HB2	1.99	0.62
1:B:19:THR:HG22	1:B:21:ASP:H	1.64	0.62
1:B:180:ARG:HB2	1:B:180:ARG:HH11	1.65	0.62
1:B:441:LYS:HG3	1:B:513:VAL:HG11	1.81	0.62
1:A:204:THR:HA	1:A:207:MET:HE3	1.83	0.61
1:A:449:HIS:CE1	1:A:467:ASP:O	2.49	0.61
1:A:271:ASN:HB2	1:B:307:GLU:OE1	2.01	0.61
1:B:169:HIS:O	1:B:169:HIS:ND1	2.33	0.61
1:A:252:GLY:HA3	2:A:1531:ANP:O5'	2.02	0.60
1:B:303:MET:HA	1:B:307:GLU:OE2	2.01	0.60
1:B:408:ASN:HB3	1:B:410:ARG:HE	1.64	0.60
1:A:203:LEU:HG	1:A:207:MET:HE2	1.83	0.59
1:A:232:THR:OG1	1:A:262:MET:CE	2.50	0.59
1:A:246:GLU:HA	1:A:272:VAL:HG23	1.84	0.58
1:B:429:LEU:HD23	1:B:505:ARG:NH2	2.18	0.58
1:A:70:LEU:HD11	1:A:297:HIS:CG	2.39	0.58
1:A:483:ASP:O	1:A:486:VAL:HG22	2.03	0.58
1:A:391:VAL:HG11	1:A:465:ILE:HD11	1.86	0.57
1:A:19:THR:OG1	1:A:23:GLU:HB3	2.04	0.57
1:B:108:ILE:CD1	1:B:319:VAL:CG1	2.78	0.57
1:B:193:LYS:HZ3	1:B:482:VAL:HG21	1.70	0.57
1:B:322:ASN:HD22	1:B:323:TRP:HE3	1.52	0.57
1:B:109:ALA:O	1:B:288:MET:HB2	2.05	0.56
1:B:214:GLU:HB3	1:B:219:ILE:HD11	1.87	0.56
1:A:175:ILE:CD1	1:A:224:GLN:HE21	2.17	0.56
1:A:236:GLU:HG3	1:A:266:MET:HE3	1.87	0.56
1:A:165:VAL:HG12	1:A:165:VAL:O	2.05	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:315:ARG:HG3	1:B:318:MET:HE3	1.87	0.56
1:B:322:ASN:ND2	1:B:323:TRP:HE3	2.04	0.55
1:B:373:ASP:O	1:B:377:ARG:HG3	2.06	0.55
1:A:229:SER:CA	1:A:262:MET:HE1	2.33	0.55
1:B:102:ILE:HG22	1:B:303:MET:HG3	1.88	0.55
1:A:52:PHE:CZ	1:A:86:THR:HG23	2.41	0.55
1:A:73:PHE:HZ	1:A:308:THR:HB	1.71	0.55
1:B:415:TYR:HE2	1:B:417:ASN:HD22	1.54	0.55
1:B:391:VAL:HG13	1:B:396:ILE:HB	1.89	0.54
1:B:249:LEU:HD21	1:B:254:ALA:HA	1.90	0.54
1:B:457:PHE:HB3	1:B:463:LEU:HD11	1.89	0.54
1:A:443:HIS:HD2	1:A:510:TYR:OH	1.90	0.54
1:A:288:MET:HG3	1:A:289:ILE:HD12	1.90	0.54
1:B:124:LEU:HA	1:B:137:ALA:HB2	1.90	0.54
1:A:523:LEU:O	1:A:527:VAL:HG23	2.07	0.54
1:B:262:MET:HE3	1:B:367:TYR:HD2	1.71	0.54
1:B:107:CYS:O	1:B:111:ILE:HG23	2.08	0.53
1:A:60:PHE:HA	1:A:63:VAL:O	2.09	0.53
1:B:285:ASN:HD21	1:B:288:MET:N	2.03	0.53
1:B:60:PHE:HA	1:B:63:VAL:O	2.08	0.53
1:B:211:ASP:C	1:B:213:GLY:H	2.16	0.53
1:B:127:TYR:CE2	1:B:132:ASN:ND2	2.77	0.52
1:B:373:ASP:O	1:B:377:ARG:CG	2.57	0.52
1:A:215:ARG:NH1	1:A:217:GLU:HB2	2.24	0.52
1:A:396:ILE:HD11	1:A:441:LYS:HB2	1.92	0.52
1:A:380:ARG:HH21	1:A:380:ARG:HG3	1.74	0.52
1:A:102:ILE:HD11	1:A:293:GLY:HA2	1.92	0.52
1:A:242:THR:O	1:A:332:ARG:NH2	2.43	0.52
1:B:3:CYS:HB3	1:B:294:LEU:HD23	1.92	0.51
1:B:83:LEU:HB3	1:B:310:ILE:HD12	1.92	0.51
1:B:108:ILE:HD11	1:B:319:VAL:CG1	2.39	0.51
1:B:126:LEU:HD13	1:B:235:THR:OG1	2.11	0.51
1:B:443:HIS:HD2	1:B:510:TYR:OH	1.93	0.51
1:B:26:PHE:O	1:B:27:ASN:HB3	2.10	0.51
1:B:420:LEU:HD13	1:B:422:LYS:HB3	1.92	0.51
1:B:168:PRO:HB2	1:B:170:PRO:HD2	1.92	0.51
1:A:336:GLU:C	1:A:338:LEU:N	2.68	0.51
1:B:165:VAL:HG13	1:B:210:TYR:CZ	2.46	0.51
1:B:106:HIS:NE2	2:B:1533:ANP:O1G	2.43	0.50
1:A:95:LEU:C	1:A:97:LEU:H	2.20	0.50
1:B:457:PHE:HA	1:B:464:TYR:O	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:160:GLN:NE2	1:A:203:LEU:HD21	2.27	0.50
1:B:285:ASN:ND2	1:B:288:MET:N	2.52	0.50
1:A:232:THR:HG23	1:A:263:LEU:HD23	1.93	0.50
1:A:44:ALA:O	1:A:48:HIS:HD2	1.95	0.50
1:A:420:LEU:O	1:A:421:ALA:C	2.55	0.50
1:A:12:LYS:HG3	1:A:31:MET:HG2	1.94	0.49
1:A:338:LEU:HG	1:A:339:ILE:HD12	1.93	0.49
1:A:7:GLU:HB2	1:A:289:ILE:HD13	1.94	0.49
1:B:224:GLN:HE22	1:B:256:ASN:ND2	2.09	0.49
1:A:294:LEU:O	1:A:298:LYS:HB2	2.12	0.49
1:B:292:LEU:HD13	1:B:296:MET:HE2	1.94	0.49
1:A:130:GLY:HA2	1:A:155:GLY:HA3	1.94	0.49
1:A:102:ILE:HG22	1:A:303:MET:HB2	1.94	0.49
1:A:111:ILE:HD11	1:A:143:TYR:OH	2.13	0.49
1:A:73:PHE:CZ	1:A:308:THR:HB	2.48	0.48
1:B:113:ILE:HD13	1:B:288:MET:HA	1.95	0.48
1:B:449:HIS:O	1:B:483:ASP:OD2	2.31	0.48
1:A:77:PRO:HD2	1:A:106:HIS:HB3	1.95	0.48
1:A:199:PHE:O	1:A:200:SER:C	2.55	0.48
1:A:186:VAL:HG11	1:A:214:GLU:HG2	1.95	0.48
1:A:301:ARG:HH12	1:A:322:ASN:ND2	2.11	0.48
1:A:436:GLY:HA2	1:A:506:PHE:CE1	2.49	0.48
1:B:494:THR:C	1:B:495:HIS:CD2	2.92	0.48
1:A:104:VAL:HG13	1:A:292:LEU:CD1	2.40	0.47
1:B:293:GLY:O	1:B:294:LEU:C	2.56	0.47
1:B:126:LEU:HD11	1:B:231:LEU:HD22	1.95	0.47
1:B:448:ILE:HG12	1:B:479:ASP:HB3	1.95	0.47
1:B:190:TYR:CE1	1:B:230:MET:HG3	2.49	0.47
1:B:377:ARG:HB2	1:B:409:LYS:HG2	1.97	0.47
1:A:242:THR:HG22	1:A:243:ASN:N	2.29	0.47
1:A:377:ARG:HB2	1:A:409:LYS:HG2	1.96	0.47
1:A:75:GLN:NE2	1:A:103:GLY:HA3	2.28	0.47
1:A:225:GLU:HB3	1:A:372:LEU:HD12	1.97	0.47
1:A:368:ARG:HG3	1:A:373:ASP:HB2	1.96	0.47
1:B:28:LYS:HD2	1:B:58:GLU:OE1	2.15	0.47
1:B:126:LEU:HD23	1:B:249:LEU:HD13	1.95	0.47
1:B:128:VAL:HG23	1:B:253:VAL:HB	1.96	0.47
1:B:362:ARG:HD2	1:B:381:THR:HG22	1.96	0.47
1:B:5:GLY:HA2	1:B:72:ALA:O	2.15	0.47
1:B:511:LYS:HG2	1:B:517:TRP:CD2	2.50	0.47
1:B:342:GLY:O	1:B:343:ALA:HB3	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:375:ASN:N	1:B:375:ASN:HD22	2.13	0.47
1:A:102:ILE:HD11	1:A:293:GLY:CA	2.45	0.46
1:B:52:PHE:CZ	1:B:86:THR:HG23	2.50	0.46
1:A:170:PRO:O	1:A:173:PRO:HD2	2.15	0.46
1:A:224:GLN:O	1:A:225:GLU:C	2.56	0.46
1:B:91:ARG:HD2	1:B:308:THR:OG1	2.16	0.46
1:B:102:ILE:HD12	1:B:296:MET:HE3	1.97	0.46
1:A:229:SER:HA	1:A:262:MET:CE	2.37	0.46
1:B:203:LEU:O	1:B:207:MET:HG3	2.16	0.46
1:A:204:THR:HA	1:A:207:MET:CE	2.46	0.46
1:A:292:LEU:HD13	1:A:296:MET:HE2	1.97	0.46
1:A:226:TYR:O	1:A:227:ALA:C	2.59	0.46
1:B:396:ILE:HG23	1:B:438:ILE:HG12	1.97	0.46
1:B:285:ASN:HD22	1:B:287:ALA:HB3	1.82	0.45
1:A:87:ALA:O	1:A:91:ARG:HB2	2.17	0.45
1:A:380:ARG:CG	1:A:380:ARG:NH2	2.77	0.45
1:B:84:ARG:HH22	1:B:309:LYS:NZ	2.13	0.45
1:B:288:MET:HG3	1:B:289:ILE:HD12	1.98	0.45
1:A:379:SER:O	1:A:383:ARG:HG3	2.16	0.45
1:A:52:PHE:HZ	1:A:86:THR:HG23	1.81	0.45
1:A:321:VAL:HA	1:A:323:TRP:CZ3	2.51	0.45
1:B:180:ARG:HB2	1:B:180:ARG:NH1	2.32	0.45
1:B:424:VAL:HG23	1:B:431:ILE:HD13	1.98	0.45
1:A:165:VAL:O	1:A:165:VAL:CG1	2.65	0.45
1:B:65:LYS:H	1:B:65:LYS:HG2	1.56	0.45
1:A:339:ILE:H	1:A:339:ILE:HG13	1.44	0.45
1:B:85:VAL:O	1:B:89:VAL:HG23	2.17	0.45
1:B:193:LYS:HZ2	1:B:482:VAL:HG21	1.78	0.45
1:B:2:ILE:HD11	1:B:17:ILE:CG2	2.47	0.44
1:B:169:HIS:N	1:B:170:PRO:CD	2.80	0.44
1:B:384:GLU:O	1:B:388:LEU:HG	2.17	0.44
1:B:429:LEU:HD23	1:B:505:ARG:HH21	1.83	0.44
1:B:444:LYS:HA	1:B:514:TYR:CE2	2.53	0.44
1:B:266:MET:HB2	1:B:367:TYR:CD1	2.53	0.44
1:B:154:VAL:HG13	1:B:199:PHE:CE2	2.53	0.44
1:A:224:GLN:HE22	1:A:256:ASN:HD21	1.66	0.44
1:A:301:ARG:NH1	1:A:322:ASN:ND2	2.65	0.44
1:A:409:LYS:HD2	1:A:409:LYS:N	2.33	0.44
1:B:270:GLN:HE22	1:B:342:GLY:H	1.66	0.44
1:B:155:GLY:O	1:B:156:ASN:C	2.61	0.43
1:B:482:VAL:O	1:B:486:VAL:HG13	2.17	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:516:ARG:O	1:B:520:ILE:HD12	2.17	0.43
1:A:6:LEU:HD22	1:A:90:ALA:HB2	1.99	0.43
1:A:243:ASN:HD22	1:A:243:ASN:N	2.13	0.43
1:B:295:LEU:HD12	1:B:323:TRP:HB2	2.00	0.43
1:B:448:ILE:HD13	1:B:474:SER:HB3	2.00	0.43
1:A:18:VAL:HG22	1:A:290:ALA:HB1	2.00	0.43
1:B:128:VAL:HG12	1:B:133:THR:HG23	2.00	0.43
1:B:161:PHE:O	1:B:162:ALA:C	2.62	0.43
1:B:511:LYS:HG2	1:B:517:TRP:CG	2.53	0.43
1:A:104:VAL:HG22	1:A:296:MET:CE	2.48	0.43
1:A:111:ILE:HB	1:A:125:THR:HG21	1.99	0.43
1:B:383:ARG:O	1:B:387:TYR:HD2	2.01	0.43
1:A:381:THR:HG21	1:A:409:LYS:O	2.19	0.43
1:A:457:PHE:HA	1:A:464:TYR:O	2.19	0.43
1:A:175:ILE:HD12	1:A:224:GLN:NE2	2.34	0.42
1:A:266:MET:HE2	1:A:266:MET:O	2.19	0.42
1:A:70:LEU:HD11	1:A:297:HIS:CD2	2.53	0.42
1:A:200:SER:O	1:A:204:THR:HG23	2.19	0.42
1:A:457:PHE:HE1	1:A:465:ILE:HG23	1.82	0.42
1:B:186:VAL:HG11	1:B:214:GLU:HG2	2.01	0.42
1:B:425:ILE:HG23	1:B:426:GLU:N	2.34	0.42
1:B:239:LEU:CD2	1:B:266:MET:HE1	2.49	0.42
1:B:133:THR:CG2	1:B:231:LEU:HD21	2.49	0.42
1:B:259:LEU:HG	1:B:263:LEU:HD12	2.01	0.42
1:B:167:LEU:HD22	1:B:174:TYR:HB3	2.02	0.42
1:A:102:ILE:HD12	1:A:296:MET:HE3	2.01	0.42
1:A:146:PHE:O	1:A:195:MET:HE3	2.19	0.42
1:A:380:ARG:HG3	1:A:380:ARG:NH2	2.34	0.42
1:B:449:HIS:CD2	1:B:451:ASP:N	2.75	0.42
1:A:392:LYS:NZ	1:A:399:PRO:O	2.53	0.42
1:A:526:ASP:HB3	1:A:530:ARG:HH21	1.85	0.41
1:B:3:CYS:HB3	1:B:294:LEU:CD2	2.49	0.41
1:A:215:ARG:HH12	1:A:217:GLU:HB2	1.84	0.41
1:A:415:TYR:CD2	1:A:415:TYR:C	2.98	0.41
1:A:443:HIS:CD2	1:A:510:TYR:OH	2.73	0.41
1:B:30:ILE:HG23	1:B:55:LEU:HD21	2.01	0.41
1:B:129:SER:HA	1:B:253:VAL:HG23	2.01	0.41
1:B:204:THR:C	1:B:206:ALA:H	2.29	0.41
1:B:419:LYS:H	1:B:419:LYS:HG2	1.75	0.41
1:A:253:VAL:O	1:A:253:VAL:HG12	2.19	0.41
1:A:465:ILE:H	1:A:465:ILE:HG13	1.52	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:383:ARG:O	1:B:387:TYR:CD2	2.73	0.41
1:A:521:LEU:HD23	1:A:524:MET:HE2	2.03	0.41
1:B:451:ASP:HB2	1:B:470:LEU:HD12	2.02	0.41
1:B:216:LEU:C	1:B:218:ASP:N	2.78	0.41
1:A:5:GLY:O	1:A:15:VAL:HA	2.21	0.41
1:B:285:ASN:H	1:B:288:MET:HE2	1.85	0.41
1:B:449:HIS:CD2	1:B:449:HIS:C	2.99	0.41
1:A:449:HIS:HD2	1:A:451:ASP:N	2.13	0.41
1:A:26:PHE:CZ	1:A:28:LYS:HB2	2.56	0.40
1:B:6:LEU:HG	1:B:15:VAL:HG12	2.02	0.40
1:B:360:LYS:O	1:B:410:ARG:HA	2.22	0.40
1:A:60:PHE:HE1	1:A:68:ILE:HD12	1.86	0.40
1:A:238:ALA:O	1:A:239:LEU:C	2.63	0.40
1:B:138:TYR:OH	1:B:141:LYS:HA	2.22	0.40
1:A:377:ARG:HG2	1:A:377:ARG:H	1.65	0.40
1:A:372:LEU:HD22	1:A:376:ILE:CD1	2.47	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	515/535 (96%)	454 (88%)	51 (10%)	10 (2%)	6	23
1	B	501/535 (94%)	425 (85%)	63 (13%)	13 (3%)	4	17
All	All	1016/1070 (95%)	879 (86%)	114 (11%)	23 (2%)	5	19

All (23) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	170	PRO
1	A	337	HIS

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Mol	Chain	Res	Type
1	A	339	ILE
1	B	166	ASN
1	A	80	GLY
1	A	314	TYR
1	A	529	ARG
1	B	27	ASN
1	B	80	GLY
1	B	427	ASP
1	B	25	LEU
1	B	212	ALA
1	B	217	GLU
1	B	499	PHE
1	A	177	GLU
1	A	516	ARG
1	B	208	ARG
1	A	425	ILE
1	B	500	ASP
1	B	515	ASP
1	A	8	GLY
1	B	169	HIS
1	B	376	ILE

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	443/457 (97%)	362 (82%)	81 (18%)	2	7
1	B	431/457 (94%)	369 (86%)	62 (14%)	3	12
All	All	874/914 (96%)	731 (84%)	143 (16%)	2	9

All (143) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	ILE
1	A	13	THR

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Mol	Chain	Res	Type
1	A	15	VAL
1	A	19	THR
1	A	20	SER
1	A	29	THR
1	A	52	PHE
1	A	61	GLU
1	A	63	VAL
1	A	70	LEU
1	A	71	ILE
1	A	79	LEU
1	A	84	ARG
1	A	91	ARG
1	A	93	LEU
1	A	97	LEU
1	A	111	ILE
1	A	125	THR
1	A	128	VAL
1	A	136	ILE
1	A	154	VAL
1	A	186	VAL
1	A	187	ASP
1	A	197	ILE
1	A	202	LEU
1	A	214	GLU
1	A	216	LEU
1	A	234	ILE
1	A	243	ASN
1	A	258	ARG
1	A	266	MET
1	A	270	GLN
1	A	272	VAL
1	A	273	ASP
1	A	282	CYS
1	A	289	ILE
1	A	291	TRP
1	A	292	LEU
1	A	295	LEU
1	A	301	ARG
1	A	304	SER
1	A	305	LEU
1	A	314	TYR
1	A	319	VAL

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Mol	Chain	Res	Type
1	A	332	ARG
1	A	339	ILE
1	A	341	LYS
1	A	344	GLU
1	A	346	ASP
1	A	357	VAL
1	A	358	ILE
1	A	369	ASP
1	A	370	GLU
1	A	372	LEU
1	A	374	GLU
1	A	377	ARG
1	A	380	ARG
1	A	381	THR
1	A	386	ARG
1	A	410	ARG
1	A	417	ASN
1	A	420	LEU
1	A	426	GLU
1	A	429	LEU
1	A	431	ILE
1	A	448	ILE
1	A	465	ILE
1	A	466	ILE
1	A	468	PHE
1	A	474	SER
1	A	492	LEU
1	A	493	SER
1	A	494	THR
1	A	508	GLU
1	A	515	ASP
1	A	516	ARG
1	A	517	TRP
1	A	521	LEU
1	A	523	LEU
1	A	527	VAL
1	A	529	ARG
1	B	2	ILE
1	B	11	GLU
1	B	13	THR
1	B	15	VAL
1	B	30	ILE

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Mol	Chain	Res	Type
1	B	31	MET
1	B	57	LYS
1	B	63	VAL
1	B	65	LYS
1	B	70	LEU
1	B	71	ILE
1	B	91	ARG
1	B	111	ILE
1	B	116	LEU
1	B	125	THR
1	B	126	LEU
1	B	136	ILE
1	B	154	VAL
1	B	175	ILE
1	B	180	ARG
1	B	191	THR
1	B	197	ILE
1	B	204	THR
1	B	211	ASP
1	B	216	LEU
1	B	234	ILE
1	B	237	ARG
1	B	258	ARG
1	B	268	GLU
1	B	272	VAL
1	B	279	LYS
1	B	289	ILE
1	B	292	LEU
1	B	294	LEU
1	B	295	LEU
1	B	310	ILE
1	B	319	VAL
1	B	322	ASN
1	B	324	ILE
1	B	325	LYS
1	B	357	VAL
1	B	358	ILE
1	B	362	ARG
1	B	370	GLU
1	B	372	LEU
1	B	377	ARG
1	B	380	ARG

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Mol	Chain	Res	Type
1	B	381	THR
1	B	386	ARG
1	B	391	VAL
1	B	404	VAL
1	B	419	LYS
1	B	420	LEU
1	B	424	VAL
1	B	426	GLU
1	B	466	ILE
1	B	468	PHE
1	B	492	LEU
1	B	501	GLU
1	B	517	TRP
1	B	523	LEU
1	B	524	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (31) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	27	ASN
1	A	75	GLN
1	A	132	ASN
1	A	160	GLN
1	A	224	GLN
1	A	241	HIS
1	A	243	ASN
1	A	271	ASN
1	A	285	ASN
1	A	297	HIS
1	A	299	ASN
1	A	322	ASN
1	A	375	ASN
1	A	417	ASN
1	A	443	HIS
1	A	449	HIS
1	B	134	GLN
1	B	224	GLN
1	B	270	GLN
1	B	271	ASN
1	B	285	ASN
1	B	297	HIS
1	B	299	ASN

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Mol	Chain	Res	Type
1	B	313	ASN
1	B	322	ASN
1	B	375	ASN
1	B	408	ASN
1	B	417	ASN
1	B	443	HIS
1	B	445	ASN
1	B	449	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

2 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	ANP	B	1533	-	33,33,33	2.21	10 (30%)	45,52,52	2.07	12 (26%)
2	ANP	A	1531	-	33,33,33	2.10	9 (27%)	45,52,52	2.07	11 (24%)

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	ANP	B	1533	-	-	4/18/38/38	0/3/3/3
2	ANP	A	1531	-	-	1/18/38/38	0/3/3/3

All (19) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1533	ANP	PG-N3B	5.30	1.77	1.63
2	A	1531	ANP	PG-N3B	5.19	1.76	1.63
2	B	1533	ANP	PB-N3B	5.11	1.76	1.63
2	A	1531	ANP	PB-N3B	5.04	1.76	1.63
2	B	1533	ANP	C5-C4	4.97	1.48	1.39
2	A	1531	ANP	C5-C4	4.69	1.47	1.39
2	B	1533	ANP	PB-O1B	3.92	1.52	1.46
2	A	1531	ANP	PB-O1B	3.64	1.51	1.46
2	B	1533	ANP	PA-O3A	3.33	1.63	1.59
2	B	1533	ANP	PG-O1G	3.26	1.51	1.46
2	A	1531	ANP	PG-O1G	3.16	1.51	1.46
2	B	1533	ANP	C5-C6	2.88	1.49	1.41
2	A	1531	ANP	C8-N7	2.69	1.36	1.31
2	A	1531	ANP	C5-C6	2.63	1.48	1.41
2	A	1531	ANP	C5-N7	-2.53	1.34	1.39
2	B	1533	ANP	C8-N7	2.50	1.36	1.31
2	A	1531	ANP	PA-O3A	2.46	1.62	1.59
2	B	1533	ANP	PB-O3A	2.27	1.61	1.59
2	B	1533	ANP	C5-N7	-2.26	1.35	1.39

All (23) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1531	ANP	C5-C4-N3	-6.37	117.95	126.72
2	B	1533	ANP	C5-C4-N3	-6.19	118.20	126.72
2	B	1533	ANP	N3-C4-N9	4.96	135.60	127.17
2	A	1531	ANP	N3-C4-N9	4.77	135.28	127.17
2	A	1531	ANP	C2-N3-C4	4.09	121.83	111.83
2	A	1531	ANP	O2B-PB-O1B	4.09	118.63	109.87
2	B	1533	ANP	C2-N3-C4	3.80	121.11	111.83
2	B	1533	ANP	O2G-PG-O3G	3.74	117.65	107.59
2	A	1531	ANP	O2G-PG-O3G	3.66	117.44	107.59
2	B	1533	ANP	C4-C5-N7	-3.54	106.53	110.58
2	A	1531	ANP	N3-C2-N1	-3.38	123.46	128.58

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1533	ANP	N3-C2-N1	-3.29	123.60	128.58
2	B	1533	ANP	O2B-PB-O1B	3.29	116.93	109.87
2	A	1531	ANP	C4-C5-N7	-3.13	107.00	110.58
2	B	1533	ANP	O4'-C1'-N9	3.02	113.89	108.09
2	A	1531	ANP	O1G-PG-N3B	-2.84	107.58	111.77
2	A	1531	ANP	O4'-C1'-N9	2.84	113.54	108.09
2	B	1533	ANP	O1G-PG-N3B	-2.77	107.69	111.77
2	B	1533	ANP	C5-N7-C8	2.57	107.49	103.45
2	B	1533	ANP	C4-N9-C8	2.50	108.37	105.74
2	A	1531	ANP	O3G-PG-O1G	-2.24	107.82	113.45
2	A	1531	ANP	C5-N7-C8	2.16	106.84	103.45
2	B	1533	ANP	C6-C5-N7	2.14	136.21	132.09

There are no chirality outliers.

All (5) torsion outliers are listed below:

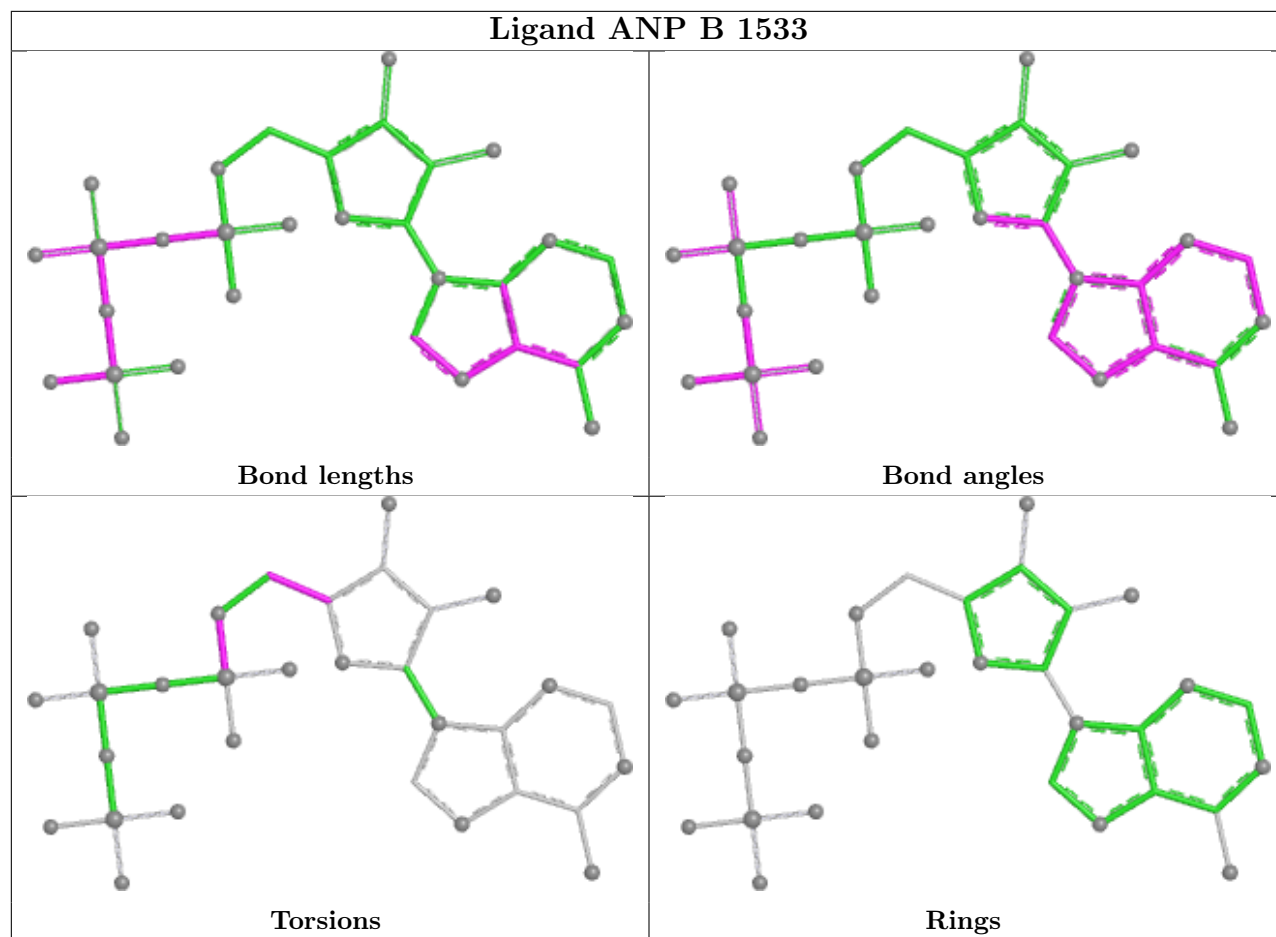
Mol	Chain	Res	Type	Atoms
2	A	1531	ANP	PG-N3B-PB-O3A
2	B	1533	ANP	C5'-O5'-PA-O1A
2	B	1533	ANP	C3'-C4'-C5'-O5'
2	B	1533	ANP	O4'-C4'-C5'-O5'
2	B	1533	ANP	C5'-O5'-PA-O3A

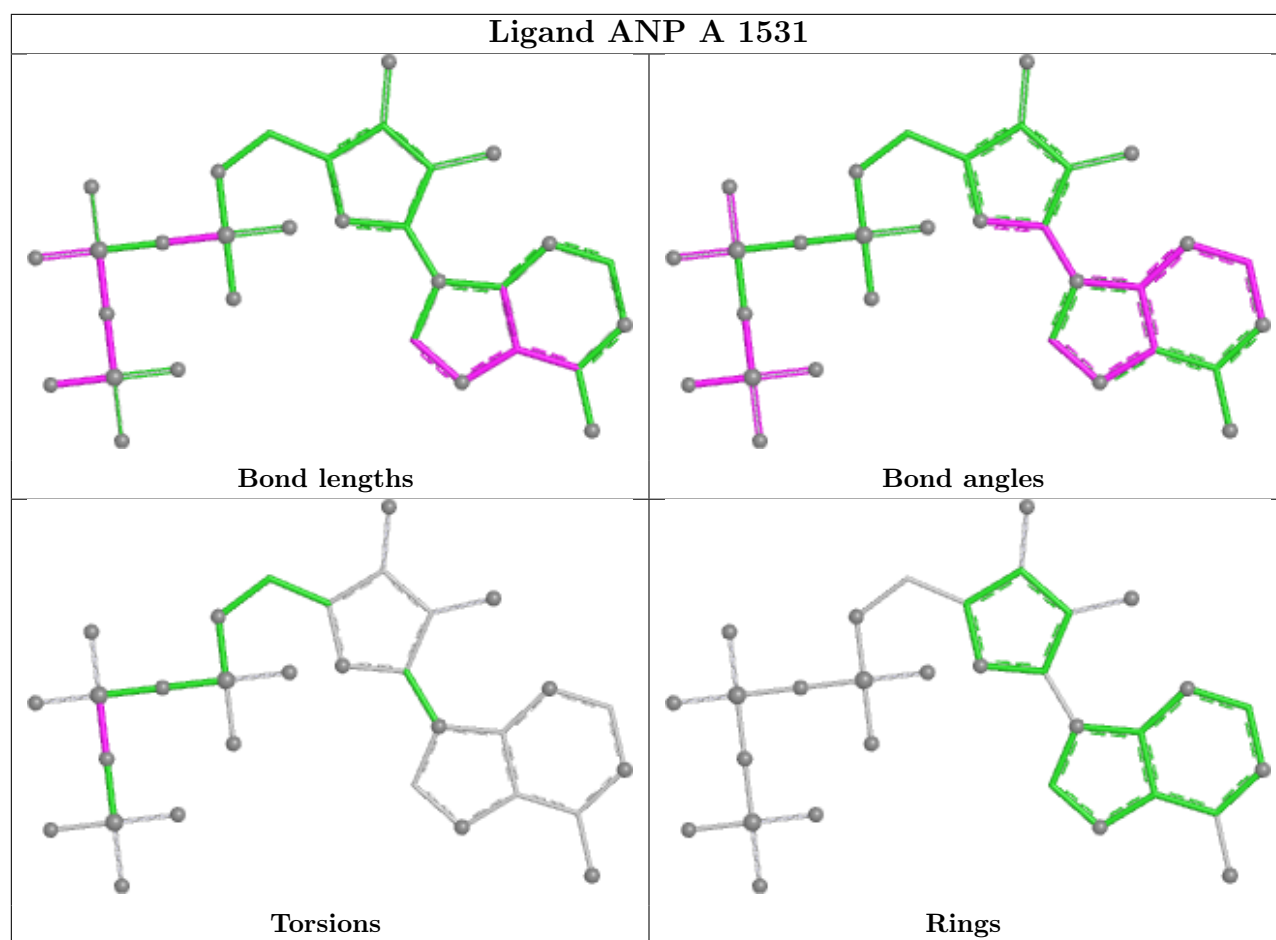
There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	1533	ANP	1	0
2	A	1531	ANP	2	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	519/535 (97%)	-0.46	1 (0%) 91 83	34, 56, 85, 107	0
1	B	507/535 (94%)	-0.39	0 100 100	35, 60, 93, 112	0
All	All	1026/1070 (95%)	-0.43	1 (0%) 92 86	34, 58, 90, 112	0

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	327	ILE	2.7

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.

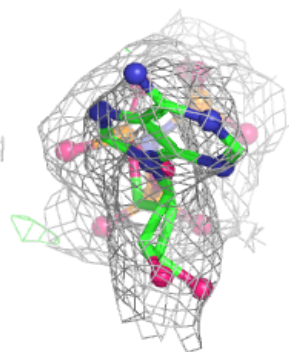
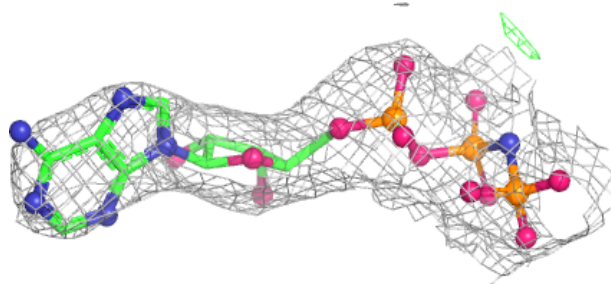
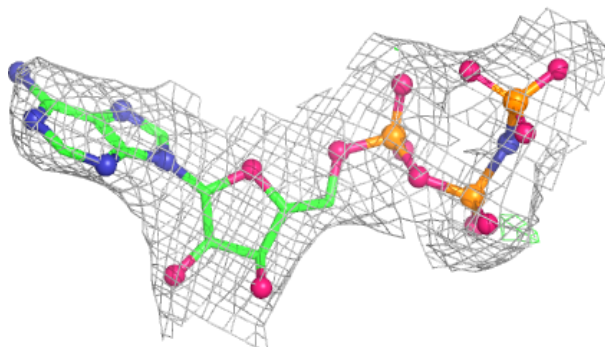
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	ANP	B	1533	31/31	0.92	0.08	66,70,87,87	0
2	ANP	A	1531	31/31	0.95	0.06	43,45,74,74	0

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.

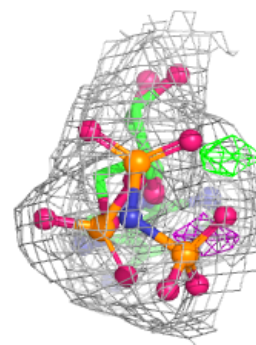
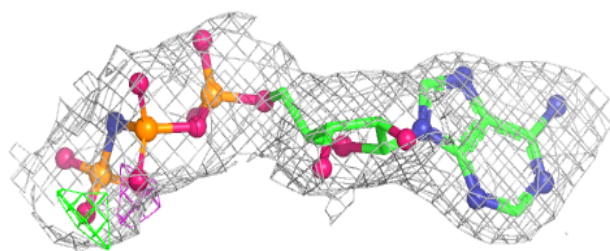
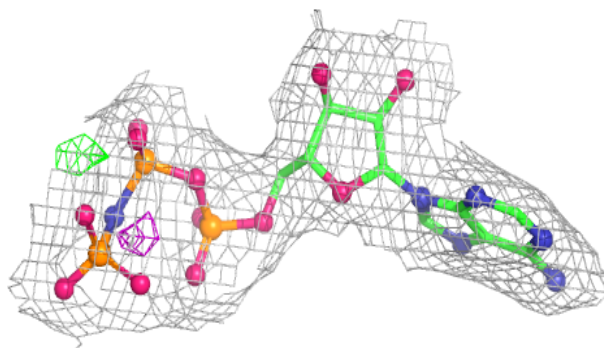
Electron density around ANP B 1533:

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



Electron density around ANP A 1531:

$2mF_o-DF_c$ (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.