Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 10:30 AM UTC

PDB ID	:	1KXP / pdb_00001kxp
Title	:	CRYSTAL STRUCTURE OF HUMAN VITAMIN D-BINDING PROTEIN IN COMPLEX WITH SKELETAL ACTIN
Authors	:	Otterbein, L.R.; Dominguez, R.
Deposited on	:	2002-02-01
Resolution	:	2.10 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references ⓘ) were used in the production of this report:

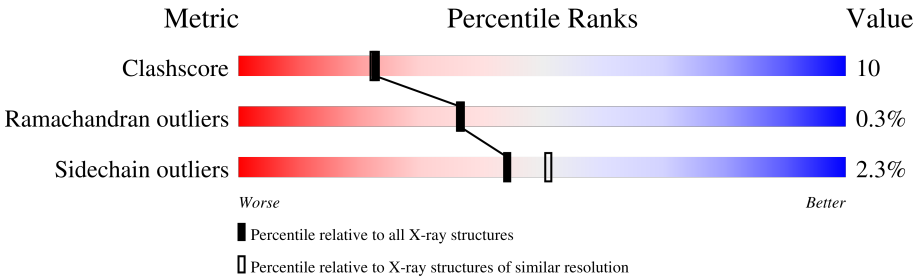
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.10 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))
Clashscore	190562	7164 (2.10-2.10)
Ramachandran outliers	187476	7099 (2.10-2.10)
Sidechain outliers	187428	7100 (2.10-2.10)

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%

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	375	74% 17% · 7%
2	D	458	75% 19% · ·

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 6587 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 ACTIN,ALPHA SKELETAL MUSCLE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	349	2736	1735	456	527	18	0	0	0

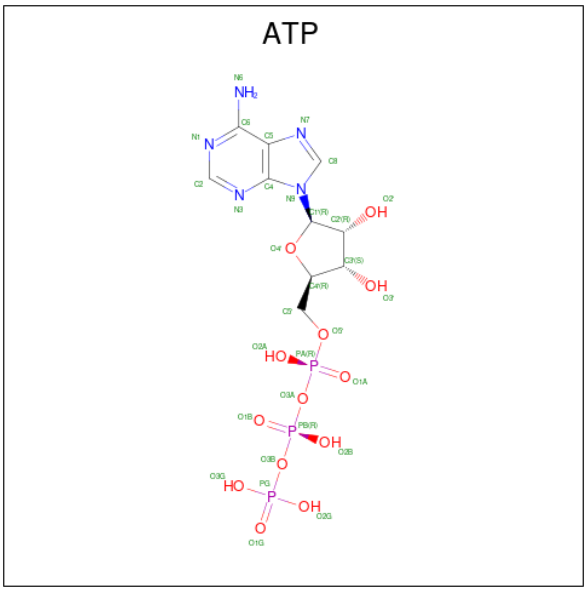
- Molecule 2 is a protein called HUMAN VITAMIN D-BINDING PROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	D	438	3431	2155	558	687	31	0	0	0

- Molecule 3 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Mg		
3	A	1	1	1	0	0

- Molecule 4 is ADENOSINE-5'-TRIPHOSPHATE (CCD ID: ATP) (formula: $C_{10}H_{16}N_5O_{13}P_3$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	P	0	0
			31	10	5	13	3		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	168	Total	O	0	0
			168	168		
5	D	220	Total	O	0	0
			220	220		

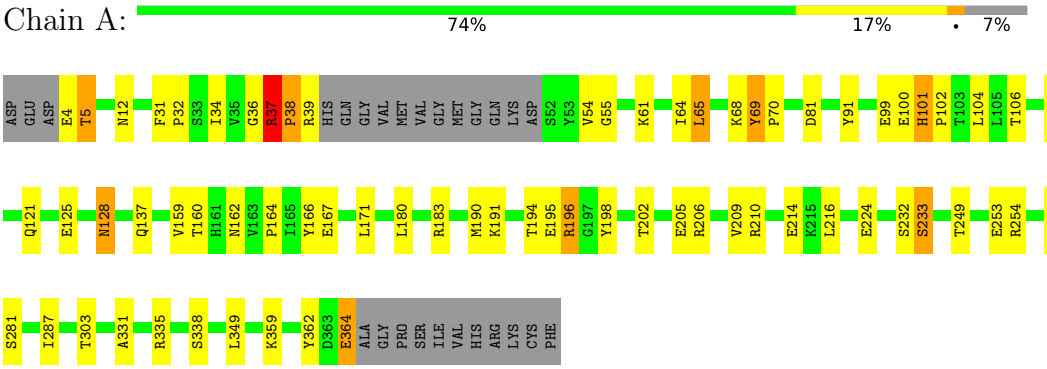
3 Residue-property plots (i)

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. 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. 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.

Note EDS was not executed.

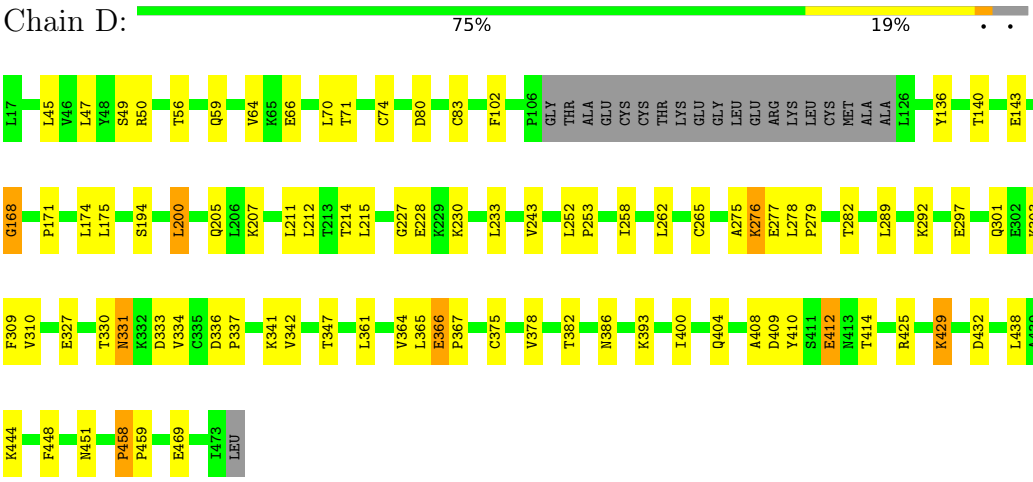
• Molecule 1: ACTIN,ALPHA SKELETAL MUSCLE

Chain A:



• Molecule 2: HUMAN VITAMIN D-BINDING PROTEIN

Chain D:



4 Data and refinement statistics (i)

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	80.76Å 87.36Å 162.69Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.00 – 2.10	Depositor
% Data completeness (in resolution range)	99.8 (40.00-2.10)	Depositor
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS	Depositor
R, R_{free}	0.217 , 0.236	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	6587	wwPDB-VP
Average B, all atoms (Å^2)	37.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

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

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	0.38	0/2794	0.90	9/3788 (0.2%)
2	D	0.37	0/3497	0.87	13/4730 (0.3%)
All	All	0.37	0/6291	0.88	22/8518 (0.3%)

There are no bond length outliers.

All (22) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	D	303	LYS	N-CA-C	7.92	119.99	111.36
2	D	227	GLY	N-CA-C	-7.92	103.42	112.29
2	D	414	THR	N-CA-C	-6.77	101.60	110.53
1	A	37	ARG	CA-C-N	6.73	128.26	119.84
1	A	37	ARG	C-N-CA	6.73	128.26	119.84
2	D	265	CYS	N-CA-C	6.69	121.53	113.23
1	A	91	TYR	N-CA-C	6.39	119.55	111.69
2	D	228	GLU	N-CA-C	6.20	118.55	111.11
1	A	331	ALA	CA-C-N	6.05	124.07	119.66
1	A	331	ALA	C-N-CA	6.05	124.07	119.66
1	A	102	PRO	N-CA-C	-5.99	101.80	111.14
2	D	458	PRO	CA-C-N	5.59	126.82	119.84
2	D	458	PRO	C-N-CA	5.59	126.82	119.84
2	D	194	SER	CA-C-N	5.47	124.93	119.24
2	D	194	SER	C-N-CA	5.47	124.93	119.24
2	D	49	SER	N-CA-C	-5.23	105.66	111.36
1	A	101	HIS	N-CA-C	5.18	118.45	108.45
2	D	277	GLU	N-CA-C	5.16	116.71	111.14
2	D	410	TYR	N-CA-C	5.09	116.64	111.14
1	A	69	TYR	CA-C-N	5.09	124.88	119.28
1	A	69	TYR	C-N-CA	5.09	124.88	119.28
2	D	168	GLY	N-CA-C	5.09	120.27	114.67

There are no chirality outliers.

There are no planarity outliers.

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	2736	0	2704	67	0
2	D	3431	0	3365	67	0
3	A	1	0	0	0	0
4	A	31	0	12	0	0
5	A	168	0	0	2	0
5	D	220	0	0	5	0
All	All	6587	0	6081	129	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 10.

All (129) 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:366:GLU:HG3	2:D:367:PRO:HD3	1.25	1.11
2:D:408:ALA:HB1	2:D:425:ARG:HH12	1.26	0.97
1:A:37:ARG:HH22	1:A:68:LYS:HD2	1.30	0.96
2:D:408:ALA:HB1	2:D:425:ARG:NH1	1.82	0.95
1:A:4:GLU:HG2	1:A:5:THR:H	1.31	0.92
1:A:4:GLU:N	1:A:100:GLU:HB3	1.85	0.92
1:A:37:ARG:NH2	1:A:68:LYS:HD2	1.90	0.86
1:A:37:ARG:HB2	1:A:37:ARG:HH11	1.44	0.83
1:A:64:ILE:HG13	1:A:65:LEU:HD23	1.61	0.80
1:A:216:LEU:O	1:A:254:ARG:HD2	1.81	0.80
1:A:128:ASN:HD22	1:A:128:ASN:N	1.80	0.80
1:A:113:LYS:HD3	1:A:116:ARG:HH12	1.58	0.68
2:D:56:THR:OG1	2:D:59:GLN:HG3	1.94	0.67
1:A:37:ARG:HB2	1:A:37:ARG:NH1	2.10	0.66
1:A:287:ILE:HD11	2:D:451:ASN:HA	1.78	0.66
2:D:333:ASP:HB3	2:D:342:VAL:HG11	1.78	0.65
1:A:190:MET:HG2	1:A:209:VAL:HG21	1.78	0.64

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:196:ARG:HD3	1:A:253:GLU:OE2	1.97	0.64
1:A:349:LEU:HD11	2:D:200:LEU:HD13	1.79	0.64
2:D:375:CYS:O	2:D:378:VAL:HG22	1.99	0.63
2:D:297:GLU:O	2:D:301:GLN:HG3	1.99	0.62
2:D:140:THR:OG1	2:D:143:GLU:HG3	1.99	0.62
2:D:80:ASP:HB3	2:D:83:CYS:HB2	1.83	0.61
1:A:61:LYS:HB3	1:A:65:LEU:HD21	1.82	0.61
1:A:128:ASN:HA	1:A:359:LYS:HZ1	1.65	0.61
2:D:366:GLU:HG3	2:D:367:PRO:CD	2.16	0.61
1:A:64:ILE:HG13	1:A:65:LEU:CD2	2.29	0.59
2:D:212:LEU:HD21	2:D:275:ALA:HA	1.85	0.58
1:A:164:PRO:HG3	1:A:281:SER:OG	2.03	0.58
1:A:113:LYS:HD3	1:A:116:ARG:NH1	2.20	0.57
1:A:12:ASN:ND2	5:A:469:HOH:O	2.38	0.57
1:A:37:ARG:HH22	1:A:68:LYS:CD	2.12	0.57
1:A:128:ASN:HA	1:A:359:LYS:NZ	2.19	0.56
1:A:37:ARG:HH11	1:A:37:ARG:CB	2.16	0.56
2:D:400:ILE:O	2:D:404:GLN:HG3	2.05	0.56
1:A:128:ASN:N	1:A:128:ASN:ND2	2.48	0.56
2:D:366:GLU:CG	2:D:367:PRO:HD3	2.17	0.56
2:D:136:TYR:HD1	2:D:162:GLU:HG2	1.71	0.55
1:A:335:ARG:HA	1:A:338:SER:OG	2.08	0.54
1:A:4:GLU:HG2	1:A:5:THR:N	2.13	0.53
1:A:70:PRO:HG3	1:A:81:ASP:HB3	1.90	0.53
2:D:361:LEU:O	2:D:365:LEU:HB2	2.08	0.53
1:A:362:TYR:C	1:A:364:GLU:H	2.16	0.53
1:A:69:TYR:N	1:A:69:TYR:CD1	2.77	0.53
1:A:104:LEU:HD23	1:A:104:LEU:C	2.34	0.52
2:D:45:LEU:HA	2:D:64:VAL:HG21	1.92	0.52
2:D:215:LEU:HD13	2:D:309:PHE:HD2	1.73	0.52
2:D:276:LYS:HB3	2:D:276:LYS:NZ	2.25	0.52
1:A:166:TYR:OH	2:D:214:THR:HG21	2.09	0.51
2:D:444:LYS:HG3	5:D:672:HOH:O	2.09	0.51
1:A:38:PRO:O	1:A:39:ARG:HB2	2.10	0.51
1:A:191:LYS:O	1:A:195:GLU:HG3	2.11	0.50
2:D:243:VAL:HG13	2:D:243:VAL:O	2.12	0.50
1:A:162:ASN:ND2	1:A:277:THR:OG1	2.45	0.50
1:A:4:GLU:CG	1:A:5:THR:H	2.08	0.50
2:D:408:ALA:CB	2:D:425:ARG:NH1	2.66	0.50
1:A:362:TYR:C	1:A:364:GLU:N	2.70	0.49
1:A:232:SER:OG	1:A:233:SER:N	2.44	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:382:THR:HG22	2:D:386:ASN:HD21	1.77	0.49
2:D:171:PRO:HD2	2:D:174:LEU:HD12	1.95	0.49
1:A:39:ARG:HG3	1:A:65:LEU:HA	1.94	0.49
1:A:113:LYS:O	1:A:117:GLU:HG2	2.12	0.49
2:D:70:LEU:C	2:D:70:LEU:HD12	2.38	0.48
2:D:258:ILE:O	2:D:262:LEU:HG	2.13	0.48
1:A:4:GLU:N	1:A:100:GLU:O	2.46	0.48
1:A:303:THR:HG22	1:A:303:THR:O	2.13	0.48
1:A:128:ASN:HD22	1:A:128:ASN:H	1.57	0.48
2:D:215:LEU:HD13	2:D:309:PHE:CD2	2.48	0.48
1:A:167:GLU:HG3	2:D:211:LEU:HD21	1.96	0.48
2:D:47:LEU:C	2:D:47:LEU:HD23	2.39	0.48
1:A:210:ARG:O	1:A:214:GLU:HG3	2.14	0.47
2:D:282:THR:HG21	2:D:308:VAL:HB	1.96	0.47
1:A:194:THR:HA	1:A:198:TYR:O	2.14	0.47
1:A:113:LYS:CD	1:A:116:ARG:HH12	2.26	0.47
2:D:448:PHE:CD1	2:D:469:GLU:HG3	2.49	0.47
2:D:207:LYS:HE2	2:D:307:ASP:OD1	2.15	0.46
2:D:230:LYS:HZ2	2:D:366:GLU:HG2	1.80	0.46
1:A:36:GLY:HA3	1:A:65:LEU:HD12	1.98	0.46
2:D:152:PRO:HD2	5:D:655:HOH:O	2.16	0.45
1:A:196:ARG:NH2	1:A:249:THR:O	2.50	0.45
2:D:425:ARG:O	2:D:429:LYS:HE3	2.17	0.45
1:A:106:THR:HB	1:A:137:GLN:HG3	1.96	0.45
1:A:183:ARG:HG3	1:A:206:ARG:HH22	1.81	0.45
1:A:183:ARG:HG3	1:A:206:ARG:NH2	2.31	0.45
1:A:159:VAL:HG22	1:A:160:THR:N	2.31	0.45
2:D:66:GLU:HG3	2:D:102:PHE:HZ	1.81	0.45
2:D:70:LEU:HD12	2:D:71:THR:N	2.32	0.45
2:D:458:PRO:HA	2:D:459:PRO:HD3	1.79	0.45
1:A:37:ARG:HA	1:A:38:PRO:HD3	1.84	0.45
1:A:190:MET:HG3	1:A:209:VAL:HG11	1.99	0.45
2:D:278:LEU:CB	2:D:279:PRO:HD3	2.47	0.45
1:A:34:ILE:HG22	1:A:69:TYR:CD2	2.51	0.44
2:D:252:LEU:N	2:D:253:PRO:HD2	2.32	0.44
1:A:31:PHE:HB2	1:A:32:PRO:HD2	1.99	0.44
2:D:330:THR:O	2:D:334:VAL:HG23	2.18	0.44
2:D:341:LYS:HB3	5:D:537:HOH:O	2.18	0.44
2:D:278:LEU:HB2	2:D:279:PRO:HD3	2.00	0.44
2:D:412:GLU:H	2:D:412:GLU:CD	2.26	0.44
5:A:513:HOH:O	2:D:205:GLN:HG3	2.18	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:409:ASP:OD2	2:D:425:ARG:CZ	2.66	0.43
1:A:54:VAL:HG12	1:A:55:GLY:N	2.32	0.43
2:D:136:TYR:CD1	2:D:162:GLU:HG2	2.53	0.43
2:D:66:GLU:HG3	2:D:102:PHE:CZ	2.54	0.43
2:D:50:ARG:HD2	2:D:175:LEU:HD12	1.99	0.42
1:A:121:GLN:HE21	1:A:125:GLU:HB2	1.84	0.42
2:D:215:LEU:HD11	2:D:310:VAL:HG22	2.01	0.42
2:D:74:CYS:SG	2:D:83:CYS:C	3.03	0.42
2:D:327:GLU:OE1	2:D:393:LYS:HE2	2.20	0.42
1:A:202:THR:OG1	1:A:205:GLU:HG3	2.19	0.42
1:A:303:THR:O	1:A:303:THR:CG2	2.68	0.42
2:D:289:LEU:HA	2:D:292:LYS:HG2	2.02	0.42
1:A:128:ASN:CA	1:A:359:LYS:NZ	2.83	0.41
2:D:438:LEU:O	2:D:442:VAL:HG23	2.20	0.41
2:D:230:LYS:NZ	2:D:366:GLU:HG2	2.35	0.41
2:D:364:VAL:O	2:D:367:PRO:HD2	2.21	0.41
1:A:180:LEU:HD23	1:A:180:LEU:C	2.45	0.41
2:D:440:LYS:HE2	2:D:444:LYS:NZ	2.35	0.41
1:A:167:GLU:O	2:D:207:LYS:HE3	2.20	0.41
2:D:152:PRO:HG3	5:D:557:HOH:O	2.21	0.41
1:A:37:ARG:O	1:A:39:ARG:N	2.54	0.41
2:D:50:ARG:HG3	2:D:168:GLY:O	2.20	0.40
2:D:212:LEU:HA	2:D:306:MET:HE2	2.03	0.40
2:D:331:ASN:HB2	5:D:618:HOH:O	2.21	0.40
2:D:331:ASN:OD1	2:D:331:ASN:N	2.54	0.40
1:A:4:GLU:HB3	1:A:101:HIS:CE1	2.56	0.40
1:A:180:LEU:HD11	1:A:260:THR:HG22	2.03	0.40
2:D:336:ASP:HA	2:D:337:PRO:HD3	1.96	0.40
1:A:64:ILE:C	1:A:65:LEU:HD23	2.46	0.40
2:D:233:LEU:HD12	2:D:347:THR:HG21	2.04	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	345/375 (92%)	335 (97%)	8 (2%)	2 (1%)	21 18
2	D	434/458 (95%)	426 (98%)	8 (2%)	0	100 100
All	All	779/833 (94%)	761 (98%)	16 (2%)	2 (0%)	36 36

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	38	PRO
1	A	233	SER

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	297/318 (93%)	288 (97%)	9 (3%)	36 41
2	D	400/415 (96%)	393 (98%)	7 (2%)	51 60
All	All	697/733 (95%)	681 (98%)	16 (2%)	44 51

All (16) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	5	THR
1	A	37	ARG
1	A	65	LEU
1	A	99	GLU
1	A	128	ASN
1	A	171	LEU
1	A	196	ARG
1	A	224	GLU
1	A	364	GLU
2	D	200	LEU
2	D	276	LYS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	D	331	ASN
2	D	366	GLU
2	D	412	GLU
2	D	429	LYS
2	D	432	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (16) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	87	HIS
1	A	92	ASN
1	A	115	ASN
1	A	121	GLN
1	A	128	ASN
1	A	161	HIS
1	A	162	ASN
1	A	263	GLN
1	A	297	ASN
2	D	26	ASN
2	D	169	GLN
2	D	235	ASN
2	D	241	GLN
2	D	260	ASN
2	D	386	ASN
2	D	472	ASN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

Of 2 ligands modelled in this entry, 1 is monoatomic - leaving 1 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	ATP	A	390	3	32,33,33	1.42	4 (12%)	48,52,52	0.91	1 (2%)

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	ATP	A	390	3	-	3/22/38/38	0/3/3/3

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	390	ATP	C2-N1	3.39	1.40	1.33
4	A	390	ATP	PA-O3A	-3.20	1.56	1.59
4	A	390	ATP	PA-O2A	-2.17	1.45	1.55
4	A	390	ATP	C1'-N9	2.15	1.52	1.46

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	A	390	ATP	O4'-C4'-C5'	-2.67	100.79	109.33

There are no chirality outliers.

All (3) torsion outliers are listed below:

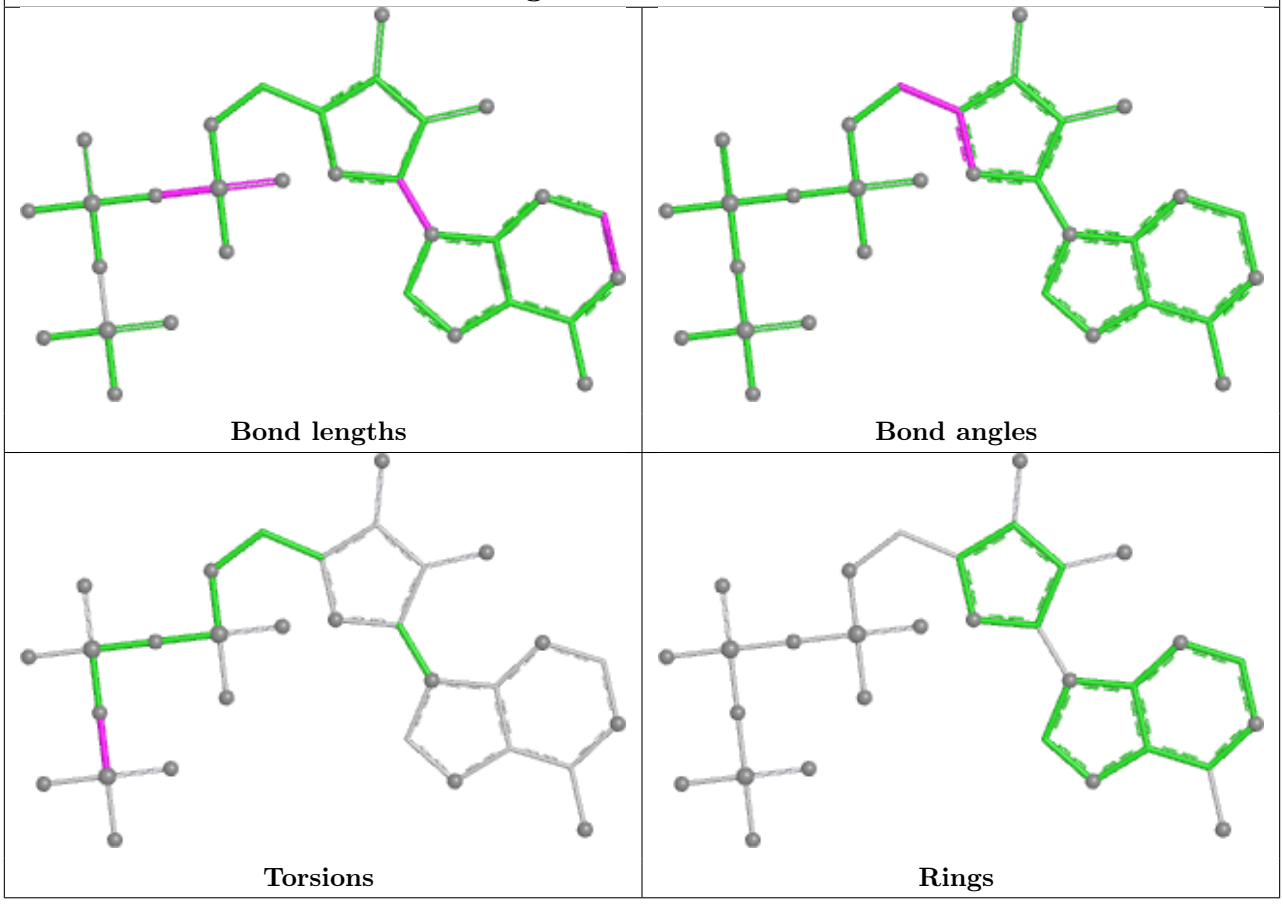
Mol	Chain	Res	Type	Atoms
4	A	390	ATP	PB-O3B-PG-O2G
4	A	390	ATP	PB-O3B-PG-O1G
4	A	390	ATP	PB-O3B-PG-O3G

There are no ring outliers.

No monomer is involved in short contacts.

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 ATP A 390



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

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.