



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 10:12 AM GMT

PDB ID : 3L9H
Title : X-ray structure of mitotic kinesin-5 (KSP, KIF11, Eg5)in complex with the hexahydro-2H-pyrano[3,2-c]quinoline EMD 534085
Authors : Knoechel, T.
Deposited on : 2010-01-05
Resolution : 2.00 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
<http://wwpdb.org/validation/2016/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 : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

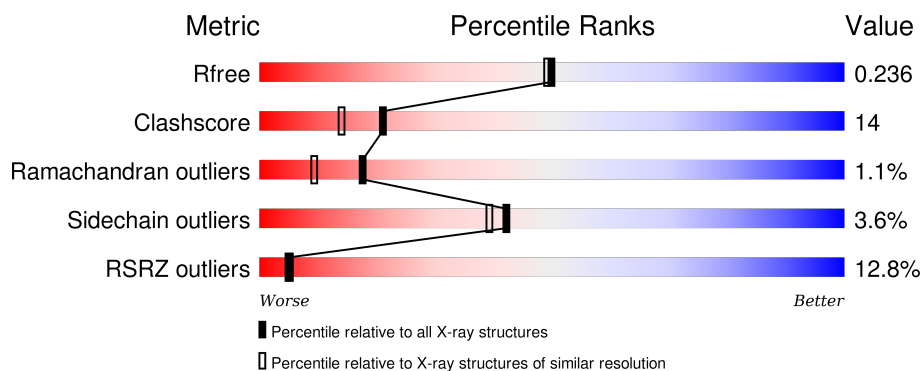
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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}	91344	6249 (2.00-2.00)
Clashscore	102246	7340 (2.00-2.00)
Ramachandran outliers	100387	7248 (2.00-2.00)
Sidechain outliers	100360	7247 (2.00-2.00)
RSRZ outliers	91569	6262 (2.00-2.00)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	368	<div> <div>13%</div> <div> <div></div> <div>67%</div> <div>21%</div> <div>• 10%</div> </div> </div>
1	B	368	<div> <div>10%</div> <div> <div></div> <div>66%</div> <div>22%</div> <div>• 10%</div> </div> </div>

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 5603 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 Kinesin-like protein KIF11.

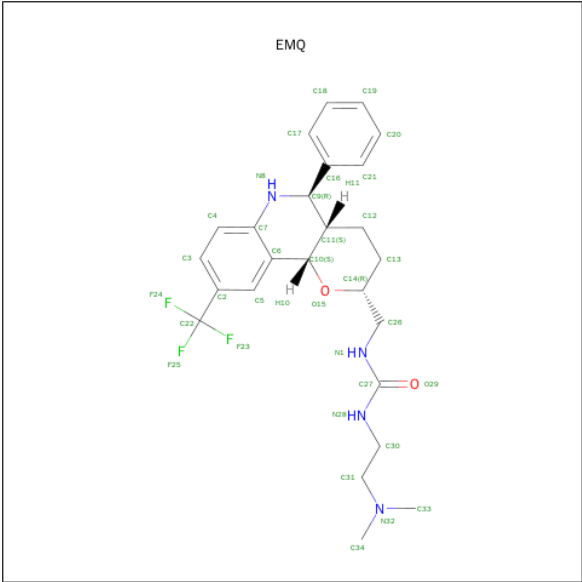
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	331	Total	C	N	O	S	0	0	0
			2599	1628	453	508	10			
1	B	331	Total	C	N	O	S	0	0	0
			2599	1628	453	508	10			

- Molecule 2 is ADENOSINE-5'-DIPHOSPHATE (three-letter code: ADP) (formula: $C_{10}H_{15}N_5O_{10}P_2$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
2	B	1	Total	C	N	O	P	0	0
			27	10	5	10	2		

- Molecule 3 is 1-[2-(DIMETHYLAMINO)ETHYL]-3-{[(2R,4AS,5R,10BS)-5-PHENYL-9-(TRIFLUOROMETHYL)-3,4,4A,5,6,10B-HEXAHYDRO-2H-PYRANO[3,2-C]QUINOLIN-2-YL]METHYL}UREA (three-letter code: EMQ) (formula: $C_{25}H_{31}F_3N_4O_2$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	F	N	O	0	0
			34	25	3	4	2		
3	B	1	Total	C	F	N	O	0	0
			34	25	3	4	2		

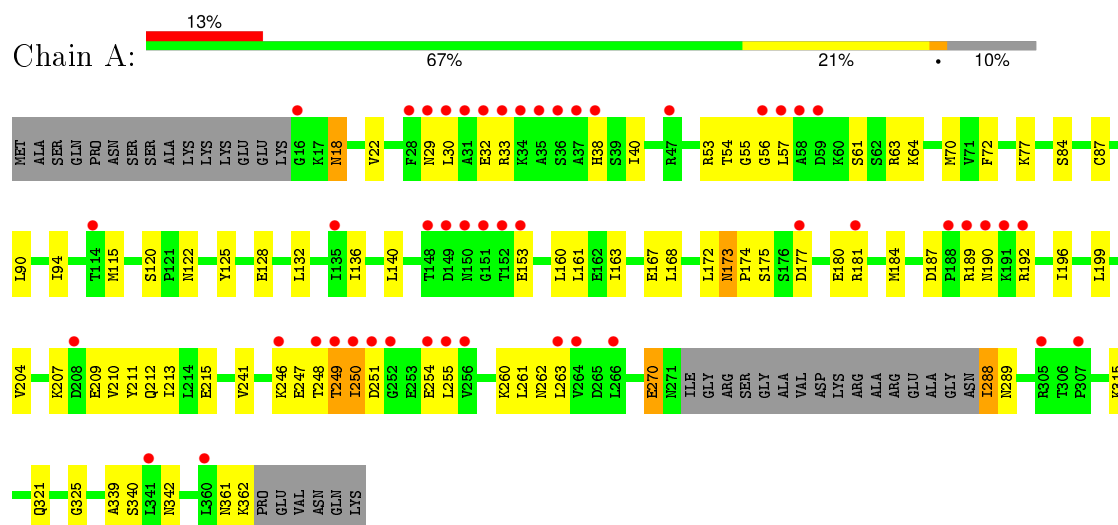
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	144	Total	O	0	0
			144	144		
4	B	139	Total	O	0	0
			139	139		

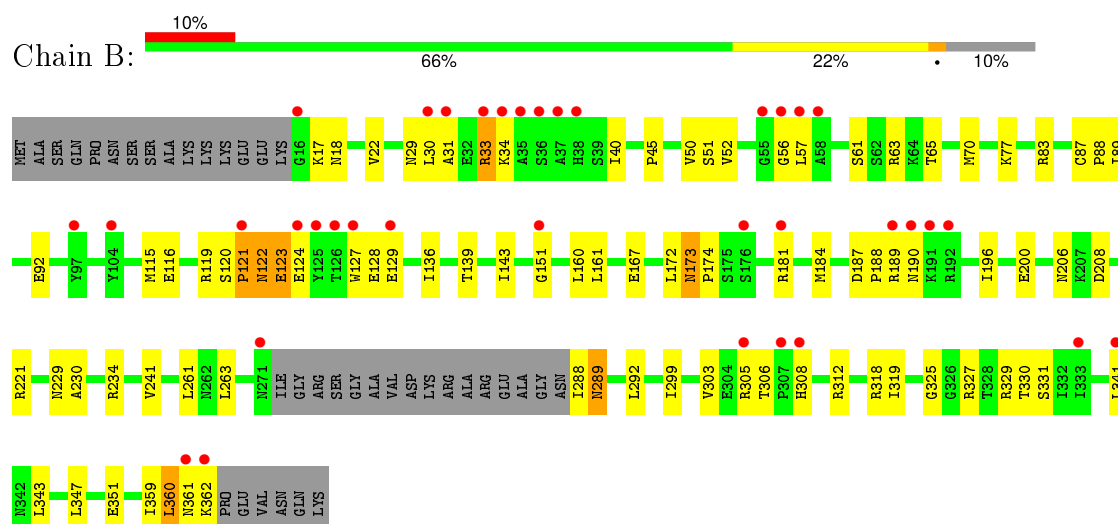
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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: Kinesin-like protein KIF11



• Molecule 1: Kinesin-like protein KIF11



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	160.95Å 79.72Å 69.51Å 90.00° 96.88° 90.00°	Depositor
Resolution (Å)	30.00 – 2.00 35.69 – 2.00	Depositor EDS
% Data completeness (in resolution range)	88.0 (30.00-2.00) 88.0 (35.69-2.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.59 (at 2.00Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.234 , 0.258 0.232 , 0.236	Depositor DCC
R_{free} test set	2637 reflections (5.36%)	DCC
Wilson B-factor (Å ²)	32.6	Xtriage
Anisotropy	0.047	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 52.2	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Outliers	0 of 51847 reflections	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	5603	wwPDB-VP
Average B, all atoms (Å ²)	39.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 9.48% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: EMQ, ADP

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	0.32	0/2637	0.61	0/3564
1	B	0.31	0/2637	0.60	0/3564
All	All	0.31	0/5274	0.60	0/7128

There are no bond length outliers.

There are no bond angle outliers.

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	2599	0	2628	77	0
1	B	2599	0	2628	82	0
2	A	27	0	12	0	0
2	B	27	0	12	0	0
3	A	34	0	31	0	0
3	B	34	0	31	1	0
4	A	144	0	0	11	0
4	B	139	0	0	2	0
All	All	5603	0	5342	152	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 14.

All (152) 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:167:GLU:HG2	1:A:181:ARG:HH21	1.05	1.09
1:B:167:GLU:HG2	1:B:181:ARG:HH21	1.18	1.04
1:A:153:GLU:HB3	1:A:246:LYS:HB3	1.55	0.89
1:A:248:THR:HG22	1:A:254:GLU:HG2	1.57	0.84
1:A:249:THR:HG22	1:A:250:ILE:HD13	1.62	0.82
1:A:167:GLU:HG2	1:A:181:ARG:NH2	1.91	0.79
1:A:270:GLU:OE1	4:A:369:HOH:O	2.04	0.76
1:B:56:GLY:HA3	1:B:61:SER:HA	1.68	0.74
1:B:51:SER:HB3	1:B:63:ARG:HE	1.53	0.74
1:B:17:LYS:HG2	1:B:18:ASN:N	2.04	0.73
1:A:128:GLU:HG2	1:A:207:LYS:NZ	2.04	0.72
1:A:260:LYS:NZ	1:A:262:ASN:HD21	1.88	0.71
1:B:167:GLU:CG	1:B:181:ARG:HH21	1.99	0.71
1:B:18:ASN:ND2	1:B:360:LEU:HD22	2.06	0.70
1:A:173:ASN:ND2	1:A:175:SER:H	1.90	0.69
1:B:87:CYS:HB2	1:B:88:PRO:HD3	1.75	0.69
1:B:22:VAL:HG12	1:B:70:MET:HB2	1.74	0.69
1:A:18:ASN:HD22	1:A:18:ASN:N	1.89	0.68
1:A:187:ASP:HB3	4:A:454:HOH:O	1.94	0.67
1:B:83:ARG:HA	1:B:87:CYS:SG	2.35	0.66
1:B:173:ASN:CG	1:B:200:GLU:HG3	2.17	0.65
1:B:299:ILE:HG23	1:B:359:ILE:HD11	1.78	0.65
1:B:30:LEU:HD22	1:B:33:ARG:HD2	1.79	0.65
1:A:29:ASN:OD1	1:A:32:GLU:HG3	1.97	0.65
1:B:22:VAL:CG1	1:B:70:MET:HB2	2.27	0.64
1:A:72:PHE:HZ	1:A:84:SER:HG	1.47	0.63
1:B:167:GLU:HG2	1:B:181:ARG:NH2	2.03	0.62
1:B:57:LEU:O	1:B:61:SER:HB3	1.99	0.62
1:A:339:ALA:HB3	1:A:342:ASN:ND2	2.14	0.62
1:B:92:GLU:HG3	1:B:329:ARG:NH1	2.15	0.62
1:A:247:GLU:O	1:A:254:GLU:HA	1.99	0.61
1:A:161:LEU:HD22	1:A:196:ILE:HD13	1.82	0.61
1:A:56:GLY:C	1:A:57:LEU:HD22	2.22	0.60
1:B:327:ARG:HH12	1:B:362:LYS:HE2	1.66	0.60
1:B:241:VAL:HG13	1:B:261:LEU:HB3	1.84	0.60
1:A:128:GLU:HG2	1:A:207:LYS:HZ2	1.66	0.59
1:A:77:LYS:HE3	4:A:394:HOH:O	2.01	0.59
1:A:249:THR:HG22	1:A:250:ILE:CD1	2.32	0.58
1:B:230:ALA:HB3	1:B:234:ARG:HD3	1.84	0.58
1:A:175:SER:HB3	1:B:34:LYS:NZ	2.19	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:306:THR:HG22	1:B:308:HIS:H	1.69	0.58
1:B:29:ASN:HD21	1:B:31:ALA:HB3	1.68	0.57
1:A:189:ARG:C	4:A:454:HOH:O	2.42	0.57
1:A:260:LYS:HZ1	1:A:262:ASN:HD21	1.50	0.57
1:A:270:GLU:HB3	4:A:369:HOH:O	2.05	0.57
1:A:190:ASN:N	4:A:454:HOH:O	2.37	0.56
1:B:136:ILE:HG12	1:B:263:LEU:HD13	1.87	0.56
1:B:17:LYS:HG2	1:B:18:ASN:H	1.70	0.56
1:A:40:ILE:HD13	1:A:340:SER:HA	1.87	0.56
1:A:288:ILE:N	1:A:288:ILE:HD12	2.21	0.55
1:B:206:ASN:OD1	1:B:208:ASP:HB2	2.06	0.55
1:A:187:ASP:CB	4:A:454:HOH:O	2.53	0.55
1:B:305:ARG:HG3	1:B:305:ARG:HH11	1.71	0.55
1:B:122:ASN:O	1:B:124:GLU:N	2.39	0.55
1:B:128:GLU:HB2	1:B:129:GLU:OE2	2.08	0.54
1:A:128:GLU:HG2	1:A:207:LYS:HZ1	1.72	0.54
1:B:29:ASN:O	1:B:33:ARG:HG2	2.08	0.54
1:A:18:ASN:ND2	1:A:18:ASN:N	2.55	0.53
1:A:251:ASP:HA	4:A:449:HOH:O	2.08	0.53
1:B:122:ASN:C	1:B:124:GLU:H	2.11	0.53
1:A:136:ILE:HG12	1:A:263:LEU:HD13	1.91	0.53
1:A:38:HIS:CD2	1:A:53:ARG:HH21	2.26	0.53
1:B:50:VAL:O	1:B:65:THR:HA	2.09	0.53
1:B:299:ILE:O	1:B:303:VAL:HG13	2.09	0.52
1:A:54:THR:HG21	1:A:64:LYS:NZ	2.24	0.52
1:A:90:LEU:O	1:A:94:ILE:HG12	2.09	0.52
1:B:136:ILE:HG12	1:B:263:LEU:CD1	2.38	0.52
1:A:339:ALA:HB3	1:A:342:ASN:HD22	1.74	0.52
1:B:30:LEU:C	1:B:30:LEU:HD13	2.31	0.52
1:B:161:LEU:HD22	1:B:196:ILE:HD13	1.92	0.52
1:B:18:ASN:HD22	1:B:18:ASN:N	2.08	0.52
1:B:327:ARG:HH11	1:B:327:ARG:HG2	1.75	0.52
1:B:139:THR:O	1:B:143:ILE:HG13	2.09	0.51
1:B:30:LEU:HD13	1:B:30:LEU:O	2.10	0.51
1:B:241:VAL:CG1	1:B:261:LEU:HB3	2.40	0.51
1:A:362:LYS:HG3	4:A:460:HOH:O	2.10	0.51
1:A:53:ARG:HB2	1:A:63:ARG:HH22	1.75	0.50
1:A:172:LEU:O	1:A:174:PRO:HD3	2.12	0.50
1:B:161:LEU:HD21	1:B:319:ILE:HD13	1.94	0.50
1:A:192:ARG:HH11	1:A:192:ARG:HG2	1.77	0.50
1:A:175:SER:HB3	1:B:34:LYS:HZ3	1.76	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:53:ARG:HB2	1:A:63:ARG:NH2	2.27	0.49
1:B:120:SER:O	1:B:122:ASN:N	2.45	0.49
1:B:362:LYS:NZ	1:B:362:LYS:CB	2.75	0.49
1:A:22:VAL:HG12	1:A:70:MET:HB2	1.95	0.49
1:B:51:SER:OG	1:B:65:THR:HG22	2.12	0.49
1:A:57:LEU:O	1:A:61:SER:HB3	2.13	0.49
1:B:305:ARG:HG3	1:B:305:ARG:NH1	2.27	0.49
1:A:212:GLN:HG2	1:B:121:PRO:O	2.12	0.49
1:B:33:ARG:HB2	1:B:33:ARG:HH11	1.77	0.48
1:B:115:MET:CE	1:B:263:LEU:HB3	2.43	0.48
1:A:184:MET:SD	1:A:315:LYS:HD2	2.53	0.48
1:A:22:VAL:CG1	1:A:70:MET:HB2	2.44	0.47
1:B:327:ARG:NH1	1:B:327:ARG:HG2	2.29	0.47
1:B:119:ARG:HB2	3:B:602:EMQ:H30	1.96	0.47
1:A:204:VAL:HG22	1:A:213:ILE:CD1	2.45	0.47
1:A:54:THR:HG21	1:A:64:LYS:HG3	1.96	0.46
1:A:136:ILE:HG12	1:A:263:LEU:CD1	2.45	0.46
1:B:52:VAL:O	1:B:63:ARG:HA	2.16	0.46
1:B:173:ASN:OD1	1:B:200:GLU:HG3	2.16	0.46
1:A:207:LYS:C	1:A:209:GLU:H	2.19	0.46
1:B:160:LEU:HB3	1:B:172:LEU:HG	1.97	0.46
1:B:89:ILE:O	1:B:92:GLU:HB2	2.16	0.46
1:A:175:SER:O	1:B:31:ALA:HB2	2.16	0.45
1:B:362:LYS:NZ	1:B:362:LYS:HB3	2.31	0.45
1:A:325:GLY:H	1:A:361:ASN:HD21	1.63	0.45
1:A:160:LEU:HB3	1:A:172:LEU:HG	1.98	0.45
1:B:115:MET:HE3	1:B:263:LEU:HB3	1.99	0.45
1:B:187:ASP:HA	1:B:188:PRO:HD3	1.86	0.45
1:B:92:GLU:HG3	1:B:329:ARG:HH11	1.80	0.45
1:A:215:GLU:OE1	1:B:121:PRO:O	2.35	0.44
1:A:63:ARG:HD2	4:A:401:HOH:O	2.17	0.44
1:B:127:TRP:CZ2	1:B:128:GLU:HG2	2.53	0.44
1:A:192:ARG:NH1	1:A:192:ARG:HG2	2.33	0.44
1:A:174:PRO:O	1:B:30:LEU:HD12	2.18	0.43
1:B:184:MET:HE1	1:B:318:ARG:CZ	2.48	0.43
1:B:289:ASN:HD22	1:B:292:LEU:H	1.64	0.43
1:B:77:LYS:HE2	4:B:430:HOH:O	2.18	0.43
1:B:181:ARG:HG3	1:B:181:ARG:HH11	1.82	0.43
1:A:260:LYS:HZ2	1:A:262:ASN:HD21	1.64	0.43
1:A:325:GLY:H	1:A:361:ASN:ND2	2.16	0.43
1:B:128:GLU:HG3	4:B:448:HOH:O	2.17	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:249:THR:HG22	1:A:250:ILE:N	2.34	0.43
1:A:163:ILE:HG12	1:A:168:LEU:HD23	2.01	0.43
1:A:54:THR:HG21	1:A:64:LYS:HZ3	1.84	0.42
1:A:120:SER:HA	1:A:132:LEU:HD12	2.00	0.42
1:A:136:ILE:O	1:A:140:LEU:HD23	2.19	0.42
1:A:30:LEU:HG	1:A:33:ARG:HH22	1.82	0.42
1:B:229:ASN:N	1:B:229:ASN:HD22	2.17	0.42
1:A:173:ASN:HD21	1:A:175:SER:HB2	1.83	0.42
1:A:196:ILE:HG22	1:A:199:LEU:HB2	2.02	0.42
1:B:325:GLY:H	1:B:361:ASN:HD21	1.67	0.42
1:B:40:ILE:HD12	1:B:343:LEU:HD13	2.00	0.42
1:A:33:ARG:HB2	1:A:33:ARG:NH1	2.34	0.42
1:A:321:GLN:NE2	4:A:405:HOH:O	2.51	0.42
1:A:211:TYR:HD2	1:B:122:ASN:ND2	2.18	0.41
1:B:77:LYS:HE2	1:B:77:LYS:HB3	1.75	0.41
1:B:120:SER:HA	1:B:121:PRO:HD3	1.90	0.41
1:B:92:GLU:CG	1:B:329:ARG:NH1	2.82	0.41
1:B:18:ASN:HD21	1:B:360:LEU:HD22	1.83	0.41
1:A:136:ILE:O	1:A:140:LEU:CD2	2.69	0.41
1:B:229:ASN:N	1:B:229:ASN:ND2	2.67	0.41
1:B:347:LEU:O	1:B:351:GLU:HG2	2.21	0.41
1:A:207:LYS:HA	1:A:210:VAL:HG23	2.03	0.41
1:A:30:LEU:HG	1:A:33:ARG:NH2	2.36	0.41
1:B:330:THR:CG2	1:B:331:SER:N	2.84	0.41
1:B:172:LEU:O	1:B:174:PRO:HD3	2.22	0.40
1:A:241:VAL:CG1	1:A:261:LEU:HB3	2.51	0.40
1:B:116:GLU:CD	1:B:221:ARG:HH12	2.24	0.40
1:A:288:ILE:CD1	1:A:288:ILE:N	2.81	0.40
1:B:312:ARG:HA	1:B:318:ARG:CG	2.52	0.40
1:A:55:GLY:O	1:A:61:SER:HB2	2.21	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	327/368 (89%)	320 (98%)	6 (2%)	1 (0%)	46	41
1	B	327/368 (89%)	313 (96%)	8 (2%)	6 (2%)	11	4
All	All	654/736 (89%)	633 (97%)	14 (2%)	7 (1%)	17	9

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	121	PRO
1	A	249	THR
1	B	123	GLU
1	B	189	ARG
1	B	190	ASN
1	B	45	PRO
1	B	151	GLY

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	293/322 (91%)	280 (96%)	13 (4%)	35	30
1	B	293/322 (91%)	285 (97%)	8 (3%)	52	52
All	All	586/644 (91%)	565 (96%)	21 (4%)	42	39

All (21) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	18	ASN
1	A	87	CYS
1	A	115	MET
1	A	122	ASN
1	A	125	TYR
1	A	173	ASN

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Mol	Chain	Res	Type
1	A	177	ASP
1	A	180	GLU
1	A	250	ILE
1	A	255	LEU
1	A	270	GLU
1	A	288	ILE
1	A	289	ASN
1	B	33	ARG
1	B	122	ASN
1	B	123	GLU
1	B	173	ASN
1	B	288	ILE
1	B	289	ASN
1	B	341	LEU
1	B	360	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (23) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	18	ASN
1	A	122	ASN
1	A	173	ASN
1	A	190	ASN
1	A	229	ASN
1	A	262	ASN
1	A	289	ASN
1	A	321	GLN
1	A	342	ASN
1	A	358	ASN
1	A	361	ASN
1	B	18	ASN
1	B	122	ASN
1	B	142	GLN
1	B	173	ASN
1	B	183	GLN
1	B	212	GLN
1	B	229	ASN
1	B	262	ASN
1	B	289	ASN
1	B	321	GLN
1	B	358	ASN
1	B	361	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 carbohydrates in this entry.

5.6 Ligand geometry ⓘ

4 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	ADP	A	501	-	22,29,29	1.02	1 (4%)	27,45,45	1.86	3 (11%)
3	EMQ	A	601	-	37,37,37	1.46	7 (18%)	51,53,53	1.01	3 (5%)
2	ADP	B	502	-	22,29,29	1.06	2 (9%)	27,45,45	1.85	3 (11%)
3	EMQ	B	602	-	37,37,37	1.38	5 (13%)	51,53,53	1.36	8 (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
2	ADP	A	501	-	-	0/12/32/32	0/3/3/3
3	EMQ	A	601	-	-	0/21/46/46	0/4/4/4
2	ADP	B	502	-	-	0/12/32/32	0/3/3/3
3	EMQ	B	602	-	-	0/21/46/46	0/4/4/4

All (15) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	502	ADP	C6-N6	-2.01	1.28	1.34
3	A	601	EMQ	F24-C22	2.01	1.40	1.32
3	B	602	EMQ	F24-C22	2.03	1.40	1.32
3	A	601	EMQ	F25-C22	2.07	1.40	1.32
3	A	601	EMQ	C13-C14	2.08	1.56	1.51
3	A	601	EMQ	F23-C22	2.15	1.40	1.32
3	A	601	EMQ	C21-C16	2.16	1.42	1.39
3	B	602	EMQ	C9-N8	2.39	1.48	1.46
3	B	602	EMQ	C13-C14	2.46	1.57	1.51
3	B	602	EMQ	C3-C2	2.48	1.43	1.39
3	B	602	EMQ	C21-C16	2.52	1.43	1.39
2	A	501	ADP	C2-N1	2.96	1.39	1.33
2	B	502	ADP	C2-N1	3.19	1.40	1.33
3	A	601	EMQ	C26-C14	3.58	1.56	1.51
3	A	601	EMQ	C9-N8	3.98	1.49	1.46

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	502	ADP	N3-C2-N1	-7.61	123.07	128.89
2	A	501	ADP	N3-C2-N1	-7.47	123.18	128.89
3	B	602	EMQ	C2-C5-C6	-3.38	118.92	122.60
3	B	602	EMQ	O29-C27-N28	-2.80	117.56	122.75
3	B	602	EMQ	C17-C16-C9	-2.38	116.99	120.78
3	A	601	EMQ	C2-C5-C6	-2.38	120.01	122.60
3	B	602	EMQ	C34-N32-C33	-2.32	103.51	109.72
3	A	601	EMQ	C16-C9-C11	-2.11	109.92	113.14
3	B	602	EMQ	F23-C22-C2	-2.08	108.49	112.95
3	B	602	EMQ	C12-C11-C10	-2.01	107.67	110.34
3	A	601	EMQ	C9-C11-C10	2.27	110.15	108.52
3	B	602	EMQ	C5-C6-C7	2.43	121.41	118.70
2	B	502	ADP	C2-N1-C6	2.63	123.46	118.77
2	B	502	ADP	C4'-O4'-C1'	2.63	112.61	109.72
2	A	501	ADP	C2-N1-C6	2.69	123.57	118.77
2	A	501	ADP	C4'-O4'-C1'	2.92	112.93	109.72
3	B	602	EMQ	N28-C27-N1	3.66	120.91	115.63

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	602	EMQ	1	0

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	331/368 (89%)	0.92	49 (14%) 3 3	19, 36, 62, 68	0
1	B	331/368 (89%)	0.65	36 (10%) 7 8	20, 38, 60, 66	0
All	All	662/736 (89%)	0.79	85 (12%) 5 5	19, 37, 61, 68	0

All (85) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	250	ILE	10.4
1	A	36	SER	9.9
1	B	57	LEU	9.0
1	A	37	ALA	7.6
1	A	58	ALA	7.5
1	A	249	THR	7.3
1	A	56	GLY	6.9
1	A	256	VAL	6.6
1	B	16	GLY	6.6
1	B	58	ALA	6.5
1	A	255	LEU	6.2
1	A	38	HIS	6.2
1	B	55	GLY	6.0
1	A	150	ASN	5.9
1	A	248	THR	5.7
1	A	57	LEU	5.7
1	A	35	ALA	5.6
1	A	251	ASP	5.3
1	A	34	LYS	5.3
1	B	34	LYS	5.2
1	B	35	ALA	5.2
1	A	192	ARG	5.1
1	A	30	LEU	5.1
1	A	148	THR	5.0

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Mol	Chain	Res	Type	RSRZ
1	B	30	LEU	4.9
1	A	16	GLY	4.5
1	A	149	ASP	4.3
1	A	151	GLY	4.3
1	B	33	ARG	4.2
1	B	271	ASN	4.0
1	A	153	GLU	3.9
1	B	190	ASN	3.9
1	A	191	LYS	3.8
1	B	362	LYS	3.7
1	A	33	ARG	3.7
1	A	190	ASN	3.6
1	B	307	PRO	3.6
1	B	191	LYS	3.5
1	B	192	ARG	3.5
1	B	305	ARG	3.4
1	B	121	PRO	3.4
1	B	37	ALA	3.4
1	A	59	ASP	3.3
1	B	31	ALA	3.3
1	B	36	SER	3.3
1	A	31	ALA	3.2
1	A	360	LEU	3.2
1	B	129	GLU	3.1
1	A	254	GLU	3.0
1	B	38	HIS	3.0
1	B	56	GLY	3.0
1	A	305	ARG	2.9
1	A	252	GLY	2.9
1	A	152	THR	2.8
1	A	307	PRO	2.7
1	A	246	LYS	2.7
1	A	28	PHE	2.7
1	A	188	PRO	2.7
1	A	29	ASN	2.6
1	B	125	TYR	2.6
1	B	97	TYR	2.6
1	A	208	ASP	2.6
1	B	176	SER	2.5
1	A	181	ARG	2.5
1	A	264	VAL	2.5
1	A	263	LEU	2.5

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Mol	Chain	Res	Type	RSRZ
1	B	189	ARG	2.5
1	B	104	TYR	2.5
1	A	177	ASP	2.5
1	A	135	ILE	2.3
1	A	189	ARG	2.3
1	B	333	ILE	2.3
1	A	341	LEU	2.3
1	B	341	LEU	2.3
1	B	308	HIS	2.3
1	A	266	LEU	2.3
1	B	151	GLY	2.2
1	B	127	TRP	2.2
1	B	126	THR	2.2
1	A	32	GLU	2.1
1	B	124	GLU	2.1
1	B	181	ARG	2.1
1	A	114	THR	2.1
1	A	47	ARG	2.1
1	B	361	ASN	2.0

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 carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å ²)	Q<0.9
3	EMQ	B	602	34/34	0.91	0.17	1.54	28,35,65,67	0
3	EMQ	A	601	34/34	0.92	0.18	1.38	25,32,58,59	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
2	ADP	B	502	27/27	0.97	0.16	0.11	25,37,47,48	0
2	ADP	A	501	27/27	0.98	0.14	-0.49	21,27,30,32	0

6.5 Other polymers [i](#)

There are no such residues in this entry.