



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 11:16 AM GMT

PDB ID : 3OCB
Title : Akt1 kinase domain with pyrrolopyrimidine inhibitor
Authors : Morales, T.H.; Vigers, G.P.A.; Brandhuber, B.J.
Deposited on : 2010-08-09
Resolution : 2.70 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

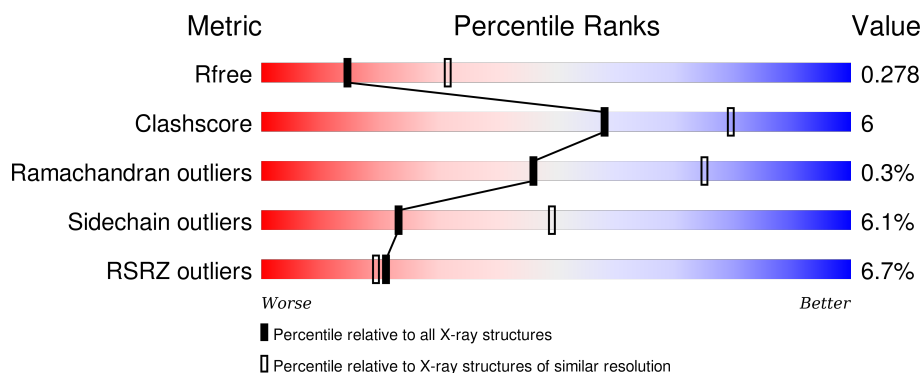
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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	2103 (2.70-2.70)
Clashscore	102246	2422 (2.70-2.70)
Ramachandran outliers	100387	2382 (2.70-2.70)
Sidechain outliers	100360	2382 (2.70-2.70)
RSRZ outliers	91569	2107 (2.70-2.70)

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	341	<div> <div>7%</div> <div> <div></div> <div>80%</div> <div>11%</div> <div>7%</div> </div> </div>
1	B	341	<div> <div>6%</div> <div> <div></div> <div>77%</div> <div>15%</div> <div>6%</div> </div> </div>
2	C	10	<div> <div></div> <div>100%</div> </div>
2	D	10	<div> <div></div> <div>80%</div> <div>20%</div> </div>

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 5519 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 v-akt murine thymoma viral oncogene homolog 1 (AKT1).

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	316	Total	C	N	O	P	S	0	0	0
			2589	1662	436	475	1	15			
1	B	320	Total	C	N	O	P	S	0	0	0
			2619	1682	440	481	1	15			

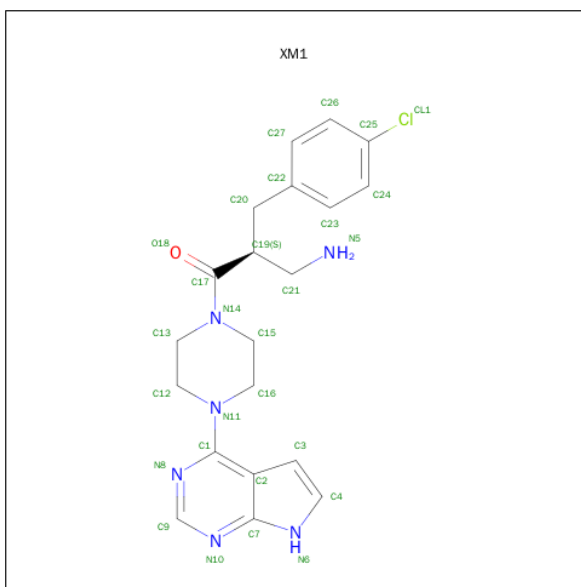
There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	140	GLY	-	EXPRESSION TAG	UNP B2RAM5
A	141	ALA	-	EXPRESSION TAG	UNP B2RAM5
A	142	MET	-	EXPRESSION TAG	UNP B2RAM5
A	143	ALA	-	EXPRESSION TAG	UNP B2RAM5
A	473	ASP	SER	ENGINEERED MUTATION	UNP B2RAM5
B	140	GLY	-	EXPRESSION TAG	UNP B2RAM5
B	141	ALA	-	EXPRESSION TAG	UNP B2RAM5
B	142	MET	-	EXPRESSION TAG	UNP B2RAM5
B	143	ALA	-	EXPRESSION TAG	UNP B2RAM5
B	473	ASP	SER	ENGINEERED MUTATION	UNP B2RAM5

- Molecule 2 is a protein called GSK 3 beta peptide.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	C	10	Total	C	N	O	0	0	0
			78	47	16	15			
2	D	10	Total	C	N	O	0	0	0
			78	47	16	15			

- Molecule 3 is (2S)-2-(4-CHLOROBENZYL)-3-OXO-3-[4-(7H-PYRROLO[2,3-D]PYRIMIDIN-4-YL)PIPERAZIN-1-YL]PROPAN-1-AMINE (three-letter code: XM1) (formula: C₂₀H₂₃ClN₆O).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total 28	C 20	Cl 1	N 6	O 1	0	0
3	B	1	Total 28	C 20	Cl 1	N 6	O 1	0	0

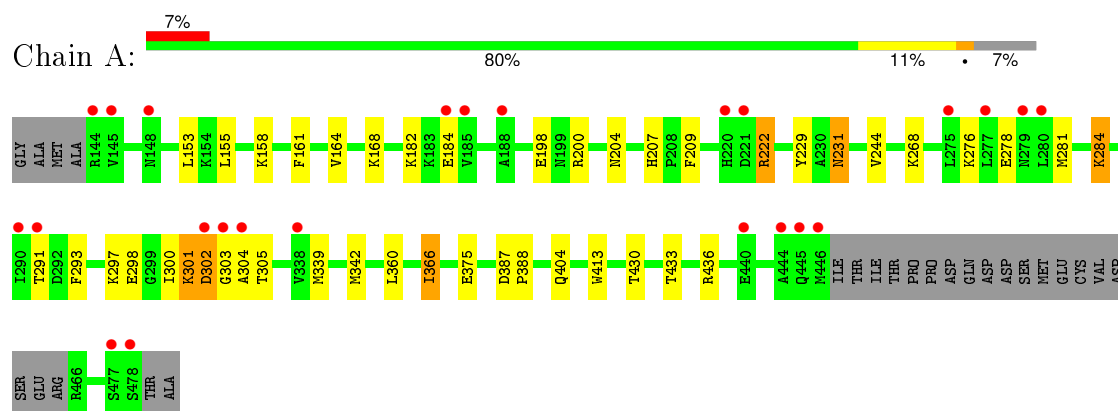
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	57	Total	O	0	0
			57	57		
4	B	38	Total	O	0	0
			38	38		
4	C	1	Total	O	0	0
			1	1		
4	D	3	Total	O	0	0
			3	3		

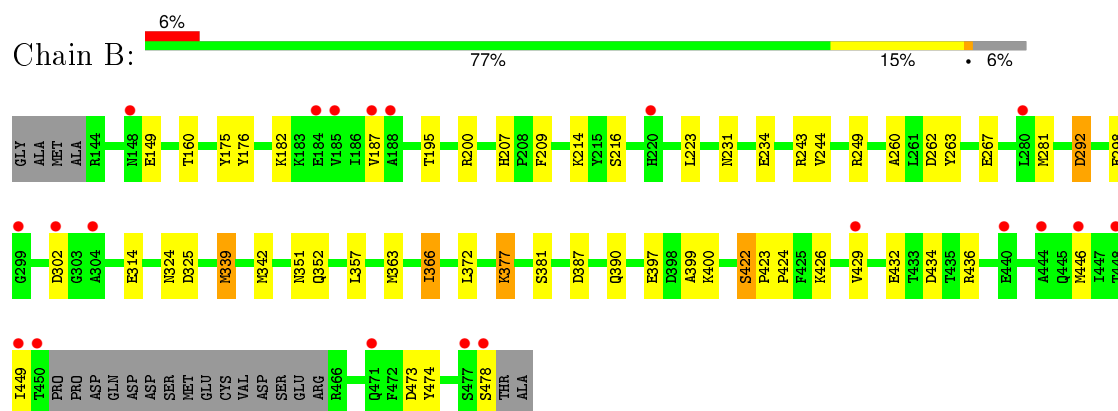
3 Residue-property plots [i](#)

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: v-akt murine thymoma viral oncogene homolog 1 (AKT1)



- Molecule 1: v-akt murine thymoma viral oncogene homolog 1 (AKT1)



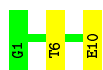
- Molecule 2: GSK 3 beta peptide

Chain C: 100%

There are no outlier residues recorded for this chain.

- Molecule 2: GSK 3 beta peptide

Chain D: 80% 20%



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	86.27Å 56.01Å 91.65Å 90.00° 104.27° 90.00°	Depositor
Resolution (Å)	29.72 – 2.70 29.72 – 2.70	Depositor EDS
% Data completeness (in resolution range)	(Not available) (29.72-2.70) 98.3 (29.72-2.70)	Depositor EDS
R_{merge}	0.19	Depositor
R_{sym}	0.15	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.94 (at 2.68Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.214 , 0.282 0.212 , 0.278	Depositor DCC
R_{free} test set	1124 reflections (5.09%)	DCC
Wilson B-factor (Å ²)	40.7	Xtriage
Anisotropy	0.079	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 34.8	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	2 of 23227 reflections (0.009%)	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	5519	wwPDB-VP
Average B, all atoms (Å ²)	54.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 47.38 % of the origin peak, indicating pseudo translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 1.0003e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: TPO, XM1

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	0.46	0/2639	0.58	0/3547
1	B	0.44	0/2669	0.59	0/3589
2	C	0.68	0/79	0.51	0/105
2	D	0.46	0/79	0.52	0/105
All	All	0.46	0/5466	0.58	0/7346

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 [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	2589	0	2550	29	0
1	B	2619	0	2586	31	0
2	C	78	0	77	0	0
2	D	78	0	77	0	0
3	A	28	0	23	4	0
3	B	28	0	23	6	0
4	A	57	0	0	1	0
4	B	38	0	0	1	0
4	C	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	D	3	0	0	0	0
All	All	5519	0	5336	63	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 6.

All (63) 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:222:ARG:HG3	1:A:222:ARG:HH11	1.06	1.08
1:A:222:ARG:HG3	1:A:222:ARG:NH1	1.85	0.84
3:A:1:XM1:H16	3:A:1:XM1:H3	1.59	0.83
3:B:2:XM1:H3	3:B:2:XM1:H16	1.65	0.77
1:A:413:TRP:H	1:B:352:GLN:NE2	1.82	0.77
1:A:413:TRP:H	1:B:352:GLN:HE22	1.35	0.74
1:A:229:TYR:CE2	1:A:231:ASN:HB3	2.24	0.73
1:A:231:ASN:HD21	1:A:284:LYS:HA	1.54	0.72
1:B:200:ARG:NH2	1:B:298:GLU:OE2	2.25	0.69
3:A:1:XM1:C3	3:A:1:XM1:H16	2.19	0.69
3:B:2:XM1:H16	3:B:2:XM1:C3	2.27	0.63
1:B:292:ASP:OD1	3:B:2:XM1:N5	2.34	0.60
1:B:429:VAL:HB	1:B:434:ASP:HB3	1.84	0.59
1:A:222:ARG:CG	1:A:222:ARG:HH11	1.97	0.57
1:A:231:ASN:HD21	1:A:284:LYS:CA	2.16	0.57
1:B:216:SER:HB2	1:B:474:TYR:HB3	1.85	0.57
1:B:281:MET:HE1	3:B:2:XM1:H12	1.87	0.56
1:B:234:GLU:HG2	1:B:281:MET:HE2	1.87	0.56
1:B:207:HIS:HD2	1:B:209:PHE:H	1.52	0.56
1:A:204:ASN:O	1:A:268:LYS:HD2	2.07	0.55
1:A:300:ILE:N	1:A:300:ILE:HD12	2.25	0.52
1:A:207:HIS:HD2	1:A:209:PHE:H	1.57	0.52
1:A:297:LYS:HG3	1:A:300:ILE:HD11	1.91	0.52
1:A:198:GLU:HG3	1:A:293:PHE:HB2	1.90	0.52
1:A:200:ARG:NH2	1:A:298:GLU:OE2	2.44	0.50
1:B:175:TYR:CD1	1:B:432:GLU:HG2	2.47	0.50
1:A:303:GLY:O	1:A:305:THR:HG23	2.12	0.50
1:B:249:ARG:HG3	1:B:424:PRO:HG2	1.93	0.49
1:A:276:LYS:HE3	1:A:278:GLU:HB2	1.94	0.48
1:A:281:MET:CE	1:A:291:THR:HG21	2.44	0.48
1:B:263:TYR:O	1:B:267:GLU:O	2.33	0.47
1:A:404:GLN:HE22	1:B:351:ASN:HD21	1.64	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:397:GLU:HB3	1:B:400:LYS:HB3	1.97	0.46
1:A:339:MET:HA	1:A:342:MET:HE2	1.98	0.46
1:A:366:ILE:HG13	4:A:49:HOH:O	2.16	0.46
1:B:339:MET:HA	1:B:342:MET:HE2	1.98	0.46
1:B:366:ILE:HG13	4:B:25:HOH:O	2.14	0.45
1:B:207:HIS:CD2	1:B:209:PHE:H	2.32	0.45
1:B:231:ASN:ND2	1:B:429:VAL:HG21	2.31	0.45
1:B:176:TYR:OH	1:B:214:LYS:HD3	2.17	0.44
1:A:300:ILE:HG23	1:A:304:ALA:HB3	1.98	0.44
1:B:387:ASP:HB3	1:B:390:GLN:HE21	1.82	0.44
3:A:1:XM1:C3	3:A:1:XM1:C16	2.93	0.44
1:B:324:ASN:O	1:B:325:ASP:HB2	2.18	0.44
1:A:155:LEU:HD21	1:A:158:LYS:HG3	2.00	0.44
1:A:297:LYS:HG3	1:A:300:ILE:CD1	2.48	0.43
1:B:262:ASP:HB2	1:B:399:ALA:CB	2.48	0.43
1:B:249:ARG:HG3	1:B:424:PRO:CG	2.48	0.43
1:B:422:SER:HA	1:B:423:PRO:HD2	1.82	0.43
1:A:301:LYS:O	1:A:302:ASP:HB2	2.18	0.42
1:A:413:TRP:N	1:B:352:GLN:HE22	2.11	0.42
1:B:377:LYS:O	1:B:381:SER:HB2	2.20	0.41
3:B:2:XM1:H19	3:B:2:XM1:H15	1.79	0.41
1:B:234:GLU:HG2	1:B:281:MET:CE	2.50	0.41
1:B:234:GLU:CG	1:B:281:MET:HE2	2.50	0.41
1:A:153:LEU:HD11	1:A:168:LYS:HB2	2.02	0.41
1:A:164:VAL:HG21	3:A:1:XM1:H15A	2.03	0.41
1:A:268:LYS:HA	1:A:268:LYS:HD3	1.90	0.41
3:B:2:XM1:C16	3:B:2:XM1:C3	2.97	0.41
1:B:260:ALA:O	1:B:263:TYR:HB3	2.21	0.41
1:B:195:THR:HG21	1:B:223:LEU:HD13	2.03	0.40
1:B:314:GLU:HA	1:B:357:LEU:HD21	2.04	0.40
1:A:387:ASP:HA	1:A:388:PRO:HD2	1.96	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	311/341 (91%)	291 (94%)	19 (6%)	1 (0%)	46	75
1	B	315/341 (92%)	297 (94%)	17 (5%)	1 (0%)	46	75
2	C	8/10 (80%)	8 (100%)	0	0	100	100
2	D	8/10 (80%)	8 (100%)	0	0	100	100
All	All	642/702 (92%)	604 (94%)	36 (6%)	2 (0%)	46	75

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	302	ASP
1	B	292	ASP

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	276/297 (93%)	262 (95%)	14 (5%)	29	59
1	B	280/297 (94%)	261 (93%)	19 (7%)	20	43
2	C	8/8 (100%)	8 (100%)	0	100	100
2	D	8/8 (100%)	6 (75%)	2 (25%)	1	2
All	All	572/610 (94%)	537 (94%)	35 (6%)	23	49

All (35) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	161	PHE
1	A	182	LYS
1	A	184	GLU
1	A	222	ARG
1	A	231	ASN
1	A	244	VAL

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Mol	Chain	Res	Type
1	A	284	LYS
1	A	301	LYS
1	A	360	LEU
1	A	366	ILE
1	A	375	GLU
1	A	430	THR
1	A	433	THR
1	A	436	ARG
1	B	149	GLU
1	B	160	THR
1	B	182	LYS
1	B	187	VAL
1	B	243	ARG
1	B	244	VAL
1	B	302	ASP
1	B	339	MET
1	B	363	MET
1	B	366	ILE
1	B	372	LEU
1	B	377	LYS
1	B	422	SER
1	B	426	LYS
1	B	436	ARG
1	B	446	MET
1	B	449	ILE
1	B	473	ASP
1	B	478	SER
2	D	6	THR
2	D	10	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	207	HIS
1	A	231	ASN
1	A	324	ASN
1	A	404	GLN
1	B	148	ASN
1	B	207	HIS
1	B	352	GLN
1	B	390	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

2 non-standard protein/DNA/RNA residues 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	$\# Z > 2$
1	TPO	A	308	1	8,10,11	0.64	0	7,14,16	1.52	1 (14%)
1	TPO	B	308	1	8,10,11	0.65	0	7,14,16	1.69	2 (28%)

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
1	TPO	A	308	1	-	0/8/11/13	0/0/0/0
1	TPO	B	308	1	-	0/8/11/13	0/0/0/0

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	308	TPO	O3P-P-O1P	2.02	117.08	110.58
1	B	308	TPO	C-CA-N	2.21	114.45	109.83
1	B	308	TPO	O3P-P-O1P	2.30	117.99	110.58

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no carbohydrates 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	$\# Z > 2$
3	XM1	A	1	-	29,31,31	1.24	3 (10%)	31,43,43	1.60	10 (32%)
3	XM1	B	2	-	29,31,31	1.21	1 (3%)	31,43,43	1.52	8 (25%)

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
3	XM1	A	1	-	-	0/18/28/28	0/4/4/4
3	XM1	B	2	-	-	0/18/28/28	0/4/4/4

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1	XM1	C26-C25	2.06	1.42	1.38
3	A	1	XM1	C24-C25	2.13	1.42	1.38
3	B	2	XM1	C19-C17	2.60	1.55	1.51
3	A	1	XM1	C19-C17	2.67	1.55	1.51

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	2	XM1	O18-C17-C19	-2.96	116.19	120.81
3	B	2	XM1	C22-C20-C19	-2.42	109.15	113.70
3	A	1	XM1	C2-C1-N8	-2.37	117.97	123.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1	XM1	C22-C20-C19	-2.34	109.29	113.70
3	A	1	XM1	O18-C17-C19	-2.19	117.39	120.81
3	B	2	XM1	C3-C2-C7	2.00	110.58	105.27
3	A	1	XM1	C19-C17-N14	2.02	120.97	119.06
3	B	2	XM1	N8-C1-N11	2.03	119.80	117.28
3	B	2	XM1	C21-C19-C20	2.06	114.39	110.11
3	A	1	XM1	C3-C2-C7	2.23	111.19	105.27
3	B	2	XM1	C15-C16-N11	2.60	115.79	110.63
3	A	1	XM1	C15-C16-N11	2.65	115.88	110.63
3	A	1	XM1	C21-C19-C20	2.67	115.64	110.11
3	B	2	XM1	C9-N8-C1	2.74	117.25	111.43
3	A	1	XM1	C13-C12-N11	2.99	116.55	110.63
3	A	1	XM1	C9-N8-C1	3.08	117.99	111.43
3	A	1	XM1	N8-C1-N11	3.43	121.54	117.28
3	B	2	XM1	C13-C12-N11	3.57	117.69	110.63

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1	XM1	4	0
3	B	2	XM1	6	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	315/341 (92%)	0.42	24 (7%) 17 15	30, 49, 76, 98	0
1	B	319/341 (93%)	0.38	20 (6%) 23 22	31, 51, 85, 104	0
2	C	10/10 (100%)	0.30	0 100 100	46, 50, 54, 58	0
2	D	10/10 (100%)	0.18	0 100 100	55, 57, 58, 60	0
All	All	654/702 (93%)	0.40	44 (6%) 21 19	30, 50, 83, 104	0

All (44) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	446	MET	6.4
1	B	448	THR	5.4
1	B	444	ALA	4.7
1	B	187	VAL	4.7
1	B	478	SER	4.5
1	A	478	SER	4.3
1	A	220	HIS	4.2
1	B	440	GLU	3.8
1	A	304	ALA	3.6
1	A	184	GLU	3.4
1	A	144	ARG	3.3
1	B	184	GLU	3.3
1	B	220	HIS	3.3
1	B	449	ILE	3.2
1	B	446	MET	3.2
1	A	477	SER	3.1
1	A	444	ALA	3.1
1	B	148	ASN	3.0
1	A	280	LEU	2.8
1	B	302	ASP	2.8
1	A	185	VAL	2.7

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Mol	Chain	Res	Type	RSRZ
1	A	188	ALA	2.7
1	A	279	ASN	2.7
1	A	221	ASP	2.7
1	B	185	VAL	2.6
1	A	440	GLU	2.6
1	A	302	ASP	2.5
1	B	450	THR	2.5
1	A	145	VAL	2.4
1	B	429	VAL	2.4
1	A	148	ASN	2.4
1	A	338	VAL	2.4
1	B	477	SER	2.3
1	A	290	ILE	2.3
1	B	471	GLN	2.2
1	B	299	GLY	2.2
1	A	303	GLY	2.2
1	B	280	LEU	2.1
1	A	275	LEU	2.1
1	B	188	ALA	2.1
1	A	291	THR	2.1
1	B	304	ALA	2.1
1	A	445	GLN	2.0
1	A	277	LEU	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [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
1	TPO	B	308	11/12	0.94	0.14	-	45,46,50,53	0
1	TPO	A	308	11/12	0.98	0.11	-	43,45,48,48	0

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(\AA^2)	Q<0.9
3	XM1	B	2	28/28	0.92	0.25	0.51	52,59,66,68	0
3	XM1	A	1	28/28	0.92	0.23	-0.05	45,49,60,64	0

6.5 Other polymers [i](#)

There are no such residues in this entry.