



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 20, 2025 – 11:13 AM EDT

PDB ID : 4QP2
Title : Crystal Structure of ERKs in complex with 5-chlorobenzo[d]oxazol-2-amine
Authors : Yin, J.; Wang, W.
Deposited on : 2014-06-22
Resolution : 2.23 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 : 4.02b-467
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 1.21
EDS : 3.0
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4 : 9.0.004 (Gargrove)
Density-Fitness : 1.0.11
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.41.4

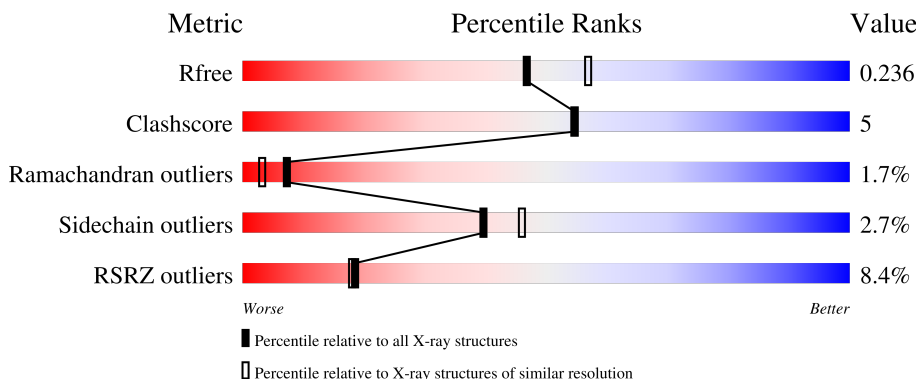
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.23 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}	164625	3139 (2.26-2.22)
Clashscore	180529	3381 (2.26-2.22)
Ramachandran outliers	177936	3334 (2.26-2.22)
Sidechain outliers	177891	3335 (2.26-2.22)
RSRZ outliers	164620	3138 (2.26-2.22)

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	369	
1	B	369	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 5778 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.

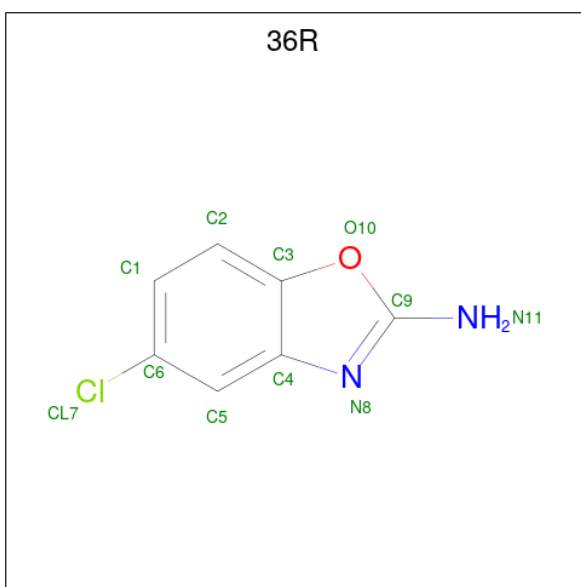
- Molecule 1 is a protein called Mitogen-activated protein kinase 1.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	337	Total	C	N	O	P	S	0	0	0
			2750	1765	470	500	1	14			
1	B	330	Total	C	N	O	P	S	0	0	0
			2692	1723	459	495	1	14			

There are 18 discrepancies between the modelled and reference sequences:

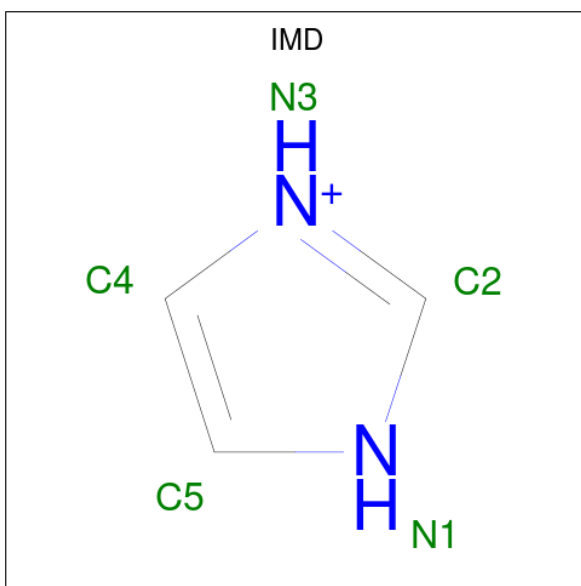
Chain	Residue	Modelled	Actual	Comment	Reference
A	-8	MET	-	expression tag	UNP P28482
A	-7	GLY	-	expression tag	UNP P28482
A	-6	SER	-	expression tag	UNP P28482
A	-5	HIS	-	expression tag	UNP P28482
A	-4	HIS	-	expression tag	UNP P28482
A	-3	HIS	-	expression tag	UNP P28482
A	-2	HIS	-	expression tag	UNP P28482
A	-1	HIS	-	expression tag	UNP P28482
A	0	HIS	-	expression tag	UNP P28482
B	-8	MET	-	expression tag	UNP P28482
B	-7	GLY	-	expression tag	UNP P28482
B	-6	SER	-	expression tag	UNP P28482
B	-5	HIS	-	expression tag	UNP P28482
B	-4	HIS	-	expression tag	UNP P28482
B	-3	HIS	-	expression tag	UNP P28482
B	-2	HIS	-	expression tag	UNP P28482
B	-1	HIS	-	expression tag	UNP P28482
B	0	HIS	-	expression tag	UNP P28482

- Molecule 2 is 5-chloro-1,3-benzoxazol-2-amine (three-letter code: 36R) (formula: C₇H₅ClN₂O).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	Cl	N	O	0	0
			11	7	1	2	1		

- Molecule 3 is IMIDAZOLE (three-letter code: IMD) (formula: $C_3H_5N_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	N	0	0
			5	3	2		

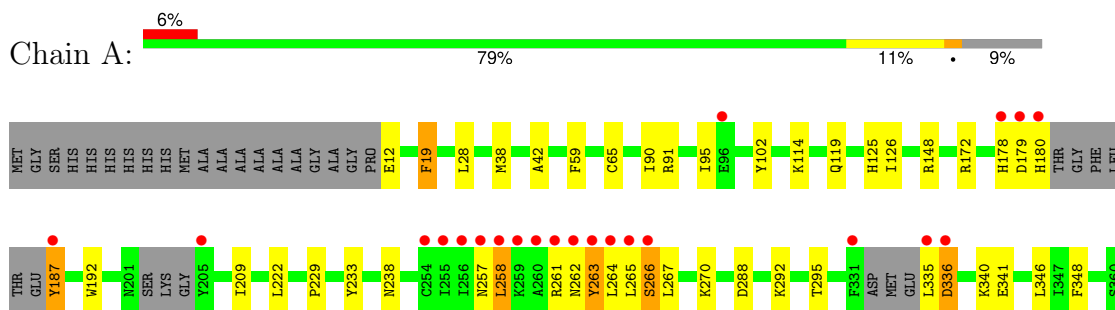
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	178	Total 178	O 178	0	0
4	B	142	Total 142	O 142	0	0

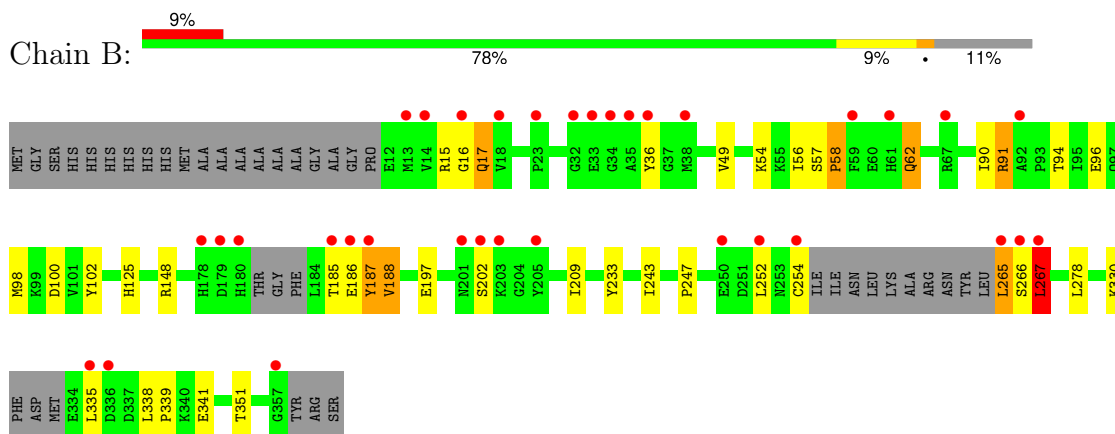
3 Residue-property plots

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: Mitogen-activated protein kinase 1



• Molecule 1: Mitogen-activated protein kinase 1



4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	82.72Å 82.72Å 277.55Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	41.36 – 2.23 41.36 – 2.23	Depositor EDS
% Data completeness (in resolution range)	99.7 (41.36-2.23) 99.8 (41.36-2.23)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.23 (at 2.22Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.2_1309)	Depositor
R, R_{free}	0.183 , 0.234 0.185 , 0.236	Depositor DCC
R_{free} test set	2396 reflections (4.98%)	wwPDB-VP
Wilson B-factor (Å ²)	40.4	Xtriage
Anisotropy	0.239	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 50.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	5778	wwPDB-VP
Average B, all atoms (Å ²)	56.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.16% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: 36R, NEP, IMD

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	0/2798	0.57	0/3787
1	B	0.38	0/2737	0.56	1/3704 (0.0%)
All	All	0.38	0/5535	0.57	1/7491 (0.0%)

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

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

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	B	267	LEU	N-CA-C	5.59	126.10	111.00

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	336	ASP	Peptide

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	2750	0	2726	26	0
1	B	2692	0	2681	25	0
2	A	11	0	5	0	0
3	A	5	0	5	1	0
4	A	178	0	0	1	0
4	B	142	0	0	1	0
All	All	5778	0	5417	51	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 5.

All (51) 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:91:ARG:NH1	1:A:348:PHE:O	2.22	0.72
1:A:340:LYS:NZ	1:A:341:GLU:OE2	2.25	0.69
1:B:90:ILE:HG13	1:B:102:TYR:HB2	1.76	0.68
1:B:247:PRO:HB2	1:B:252:LEU:HD23	1.78	0.65
1:B:243:ILE:HD12	1:B:278:LEU:HD11	1.77	0.64
1:A:90:ILE:HB	1:A:102:TYR:HB2	1.82	0.60
1:B:91:ARG:HD2	1:B:98:MET:SD	2.43	0.59
1:A:148:ARG:HG2	1:A:209:ILE:HD11	1.88	0.55
1:B:185:THR:HG22	1:B:186:GLU:H	1.73	0.52
1:B:94:THR:HG22	1:B:96:GLU:H	1.75	0.52
1:A:261:ARG:N	1:A:262:ASN:O	2.43	0.51
1:A:264:LEU:HG	1:A:267:LEU:CB	2.41	0.51
1:A:238:ASN:OD1	1:A:270:LYS:NZ	2.43	0.51
1:A:172:ARG:HH22	1:A:187:TYR:HE2	1.58	0.50
1:B:16:GLY:O	1:B:17:GLN:NE2	2.44	0.50
1:A:288:ASP:O	1:A:292:LYS:HG2	2.11	0.50
1:B:57:SER:OG	1:B:100:ASP:OD1	2.30	0.50
1:A:179:ASP:HA	1:A:180:HIS:C	2.32	0.49
1:B:330:LYS:NZ	4:B:628:HOH:O	2.43	0.49
1:A:264:LEU:HA	1:A:266:SER:N	2.29	0.48
1:B:265:LEU:HB3	1:B:266:SER:OG	2.14	0.48
1:B:62:GLN:OE1	1:B:338:LEU:O	2.32	0.48
1:A:263:TYR:CE1	1:A:264:LEU:HD13	2.49	0.48
1:A:19:PHE:O	1:A:102:TYR:CZ	2.67	0.47
1:A:178:HIS:HA	1:A:179:ASP:C	2.35	0.47
1:B:187:TYR:CB	1:B:188:VAL:HB	2.45	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:91:ARG:HD3	1:B:351:THR:OG1	2.16	0.46
1:A:12:GLU:N	4:A:670:HOH:O	2.48	0.46
1:B:197:GLU:HB2	1:B:202:SER:HB2	1.98	0.45
1:B:148:ARG:HG2	1:B:209:ILE:HD11	1.99	0.45
1:A:95:ILE:HG12	1:A:348:PHE:CD1	2.52	0.44
1:B:265:LEU:CB	1:B:266:SER:HA	2.47	0.44
1:B:265:LEU:HD23	1:B:266:SER:HA	2.00	0.44
1:B:266:SER:C	1:B:267:LEU:HG	2.39	0.43
1:A:178:HIS:HA	1:A:179:ASP:O	2.19	0.42
1:B:56:ILE:HG22	1:B:58:PRO:HD3	2.00	0.42
1:A:264:LEU:H	1:A:266:SER:CB	2.33	0.42
1:B:185:THR:C	1:B:187:TYR:H	2.23	0.42
1:A:59:PHE:HA	1:A:65:CYS:SG	2.59	0.41
1:B:335:LEU:HD23	1:B:338:LEU:HG	2.02	0.41
1:B:265:LEU:HB3	1:B:266:SER:HA	2.03	0.41
1:A:28:LEU:HD23	1:A:42:ALA:HB2	2.03	0.41
1:A:114:LYS:HZ2	3:A:402:IMD:H5	1.85	0.41
1:B:339:PRO:HB2	1:B:341:GLU:OE1	2.21	0.41
1:A:263:TYR:CZ	1:A:264:LEU:HD22	2.56	0.40
1:B:54:LYS:HD2	1:B:56:ILE:HD11	2.02	0.40
1:B:187:TYR:CG	1:B:188:VAL:HB	2.56	0.40
1:A:192:TRP:CD1	1:A:229:PRO:HA	2.56	0.40
1:A:346:LEU:HD23	1:A:346:LEU:HA	1.84	0.40
1:A:126:ILE:HD13	1:A:222:LEU:HD23	2.03	0.40
1:A:19:PHE:HE1	1:A:38:MET:HG3	1.85	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	328/369 (89%)	298 (91%)	25 (8%)	5 (2%)	8 4

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	321/369 (87%)	297 (92%)	18 (6%)	6 (2%)	6	2
All	All	649/738 (88%)	595 (92%)	43 (7%)	11 (2%)	7	3

All (11) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	265	LEU
1	A	266	SER
1	B	267	LEU
1	A	263	TYR
1	B	15	ARG
1	B	36	TYR
1	A	257	ASN
1	A	258	LEU
1	B	17	GLN
1	B	187	TYR
1	B	58	PRO

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	299/325 (92%)	291 (97%)	8 (3%)	40	46
1	B	297/325 (91%)	289 (97%)	8 (3%)	40	46
All	All	596/650 (92%)	580 (97%)	16 (3%)	40	46

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

Mol	Chain	Res	Type
1	A	19	PHE
1	A	119	GLN
1	A	187	TYR
1	A	233	TYR
1	A	258	LEU

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Mol	Chain	Res	Type
1	A	295	THR
1	A	335	LEU
1	A	336	ASP
1	B	49	VAL
1	B	62	GLN
1	B	91	ARG
1	B	188	VAL
1	B	233	TYR
1	B	254	CYS
1	B	265	LEU
1	B	267	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	17	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	NEP	B	125	1	11,14,15	1.99	4 (36%)	4,20,22	1.33	1 (25%)
1	NEP	A	125	1	11,14,15	4.88	5 (45%)	4,20,22	3.78	3 (75%)

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	NEP	B	125	1	-	0/5/12/14	0/1/1/1
1	NEP	A	125	1	-	0/5/12/14	0/1/1/1

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	125	NEP	P-O3P	14.54	1.60	1.47
1	A	125	NEP	P-O1P	-3.91	1.46	1.54
1	A	125	NEP	CD2-CG	3.81	1.41	1.36
1	B	125	NEP	CD2-CG	3.58	1.41	1.36
1	A	125	NEP	P-NE2	-3.18	1.59	1.76
1	B	125	NEP	P-NE2	-3.09	1.60	1.76
1	B	125	NEP	P-O1P	2.62	1.60	1.54
1	B	125	NEP	P-O2P	2.17	1.59	1.54
1	A	125	NEP	P-O2P	2.01	1.59	1.54

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	125	NEP	O2P-P-O3P	-6.70	99.69	113.76
1	A	125	NEP	O1P-P-O2P	2.58	116.72	106.57
1	A	125	NEP	O1P-P-O3P	-2.26	109.01	113.76
1	B	125	NEP	O1P-P-O2P	-2.01	98.68	106.57

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 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	36R	A	401	-	10,12,12	0.89	0	11,17,17	1.43	2 (18%)
3	IMD	A	402	-	3,5,5	0.48	0	4,5,5	0.51	0

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	36R	A	401	-	-	-	0/2/2/2
3	IMD	A	402	-	-	-	0/1/1/1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	401	36R	N11-C9-N8	2.89	126.86	123.19
2	A	401	36R	C5-C4-C3	-2.71	118.39	121.12

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	A	402	IMD	1	0

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

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	336/369 (91%)	0.01	22 (6%) 26 25	24, 43, 102, 154	0
1	B	329/369 (89%)	0.30	34 (10%) 13 13	26, 49, 130, 151	0
All	All	665/738 (90%)	0.15	56 (8%) 18 18	24, 46, 121, 154	0

All (56) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	266	SER	7.1
1	B	187	TYR	6.0
1	B	357	GLY	5.3
1	B	180	HIS	5.2
1	B	335	LEU	4.7
1	B	252	LEU	4.7
1	A	262	ASN	4.6
1	A	335	LEU	4.6
1	B	14	VAL	4.6
1	A	187	TYR	4.6
1	B	265	LEU	4.3
1	B	267	LEU	4.2
1	B	185	THR	4.2
1	A	259	LYS	4.1
1	A	263	TYR	4.1
1	A	256	ILE	4.0
1	A	336	ASP	3.9
1	A	205	TYR	3.9
1	A	264	LEU	3.9
1	A	258	LEU	3.8
1	A	180	HIS	3.7
1	A	261	ARG	3.7
1	A	260	ALA	3.7
1	A	178	HIS	3.6

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Mol	Chain	Res	Type	RSRZ
1	B	35	ALA	3.6
1	B	36	TYR	3.5
1	B	202	SER	3.4
1	A	254	CYS	3.3
1	B	205	TYR	3.3
1	B	13	MET	3.2
1	B	254	CYS	3.0
1	B	34	GLY	3.0
1	B	336	ASP	2.9
1	A	257	ASN	2.9
1	A	331	PHE	2.9
1	B	38	MET	2.9
1	B	203	LYS	2.8
1	B	18	VAL	2.8
1	B	186	GLU	2.7
1	B	67	ARG	2.7
1	B	201	ASN	2.7
1	A	265	LEU	2.6
1	B	61	HIS	2.6
1	B	92	ALA	2.4
1	B	16	GLY	2.4
1	B	250	GLU	2.3
1	A	255	ILE	2.3
1	B	179	ASP	2.3
1	B	178	HIS	2.3
1	B	32	GLY	2.2
1	B	59	PHE	2.1
1	A	179	ASP	2.1
1	B	33	GLU	2.0
1	A	266	SER	2.0
1	A	96	GLU	2.0
1	B	23	PRO	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. 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
1	NEP	A	125	14/15	0.98	0.05	27,33,36,37	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
1	NEP	B	125	14/15	0.98	0.05	23,33,39,42	0

6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	IMD	A	402	5/5	0.77	0.24	78,78,85,86	0
2	36R	A	401	11/11	0.93	0.10	28,58,66,77	0

6.5 Other polymers [i](#)

There are no such residues in this entry.