



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 07:10 PM UTC

PDB ID : 3ANQ / pdb_00003anq
Title : human DYRK1A/inhibitor complex
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Deposited on : 2010-09-06
Resolution : 2.60 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)	:	2.0
EDS	:	3.0
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

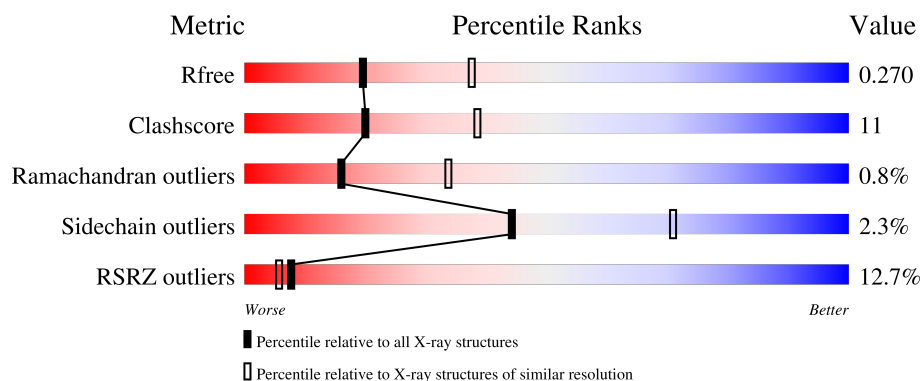
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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	4008 (2.60-2.60)
Clashscore	190562	4347 (2.60-2.60)
Ramachandran outliers	187476	4277 (2.60-2.60)
Sidechain outliers	187428	4277 (2.60-2.60)
RSRZ outliers	180081	4008 (2.60-2.60)

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	368	3% 74% 18% 7%
1	B	368	14% 70% 20% 7%
1	C	368	15% 69% 22% 7%
1	D	368	15% 69% 21% 9%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 11204 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.

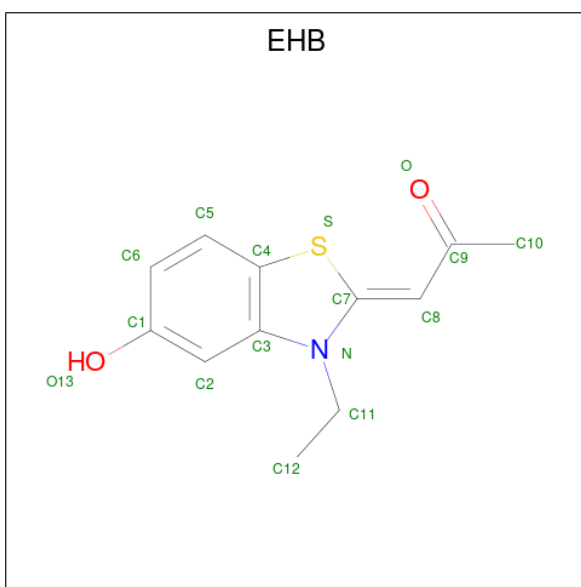
- Molecule 1 is a protein called Dual specificity tyrosine-phosphorylation-regulated kinase 1A.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	343	Total	C	N	O	P	S	0	0	0
			2801	1804	479	500	1	17			
1	B	344	Total	C	N	O	P	S	0	0	0
			2802	1805	477	502	1	17			
1	C	341	Total	C	N	O	P	S	0	0	0
			2781	1792	473	498	1	17			
1	D	335	Total	C	N	O	P	S	0	0	0
			2736	1765	466	487	1	17			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	123	GLY	-	expression tag	UNP Q13627
A	124	ALA	-	expression tag	UNP Q13627
A	125	SER	-	expression tag	UNP Q13627
B	123	GLY	-	expression tag	UNP Q13627
B	124	ALA	-	expression tag	UNP Q13627
B	125	SER	-	expression tag	UNP Q13627
C	123	GLY	-	expression tag	UNP Q13627
C	124	ALA	-	expression tag	UNP Q13627
C	125	SER	-	expression tag	UNP Q13627
D	123	GLY	-	expression tag	UNP Q13627
D	124	ALA	-	expression tag	UNP Q13627
D	125	SER	-	expression tag	UNP Q13627

- Molecule 2 is (1Z)-1-(3-ethyl-5-hydroxy-1,3-benzothiazol-2(3H)-ylidene)propan-2-one (CCD ID: EHB) (formula: C₁₂H₁₃NO₂S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	S	0	0
			16	12	1	2	1		
2	B	1	Total	C	N	O	S	0	0
			16	12	1	2	1		
2	C	1	Total	C	N	O	S	0	0
			16	12	1	2	1		
2	D	1	Total	C	N	O	S	0	0
			16	12	1	2	1		

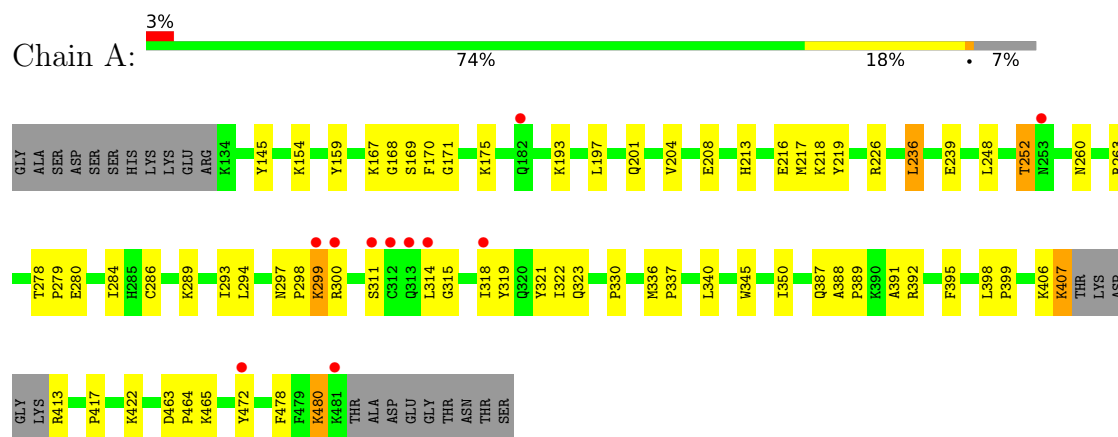
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	11	Total	O	0	0
			11	11		
3	B	3	Total	O	0	0
			3	3		
3	C	4	Total	O	0	0
			4	4		
3	D	2	Total	O	0	0
			2	2		

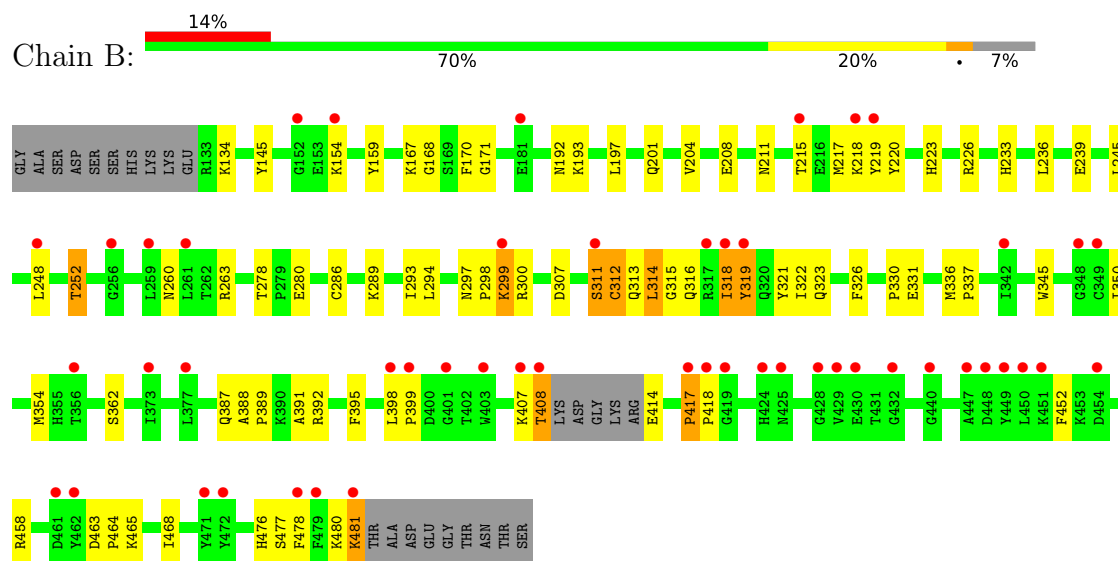
3 Residue-property plots [i](#)

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 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: Dual specificity tyrosine-phosphorylation-regulated kinase 1A

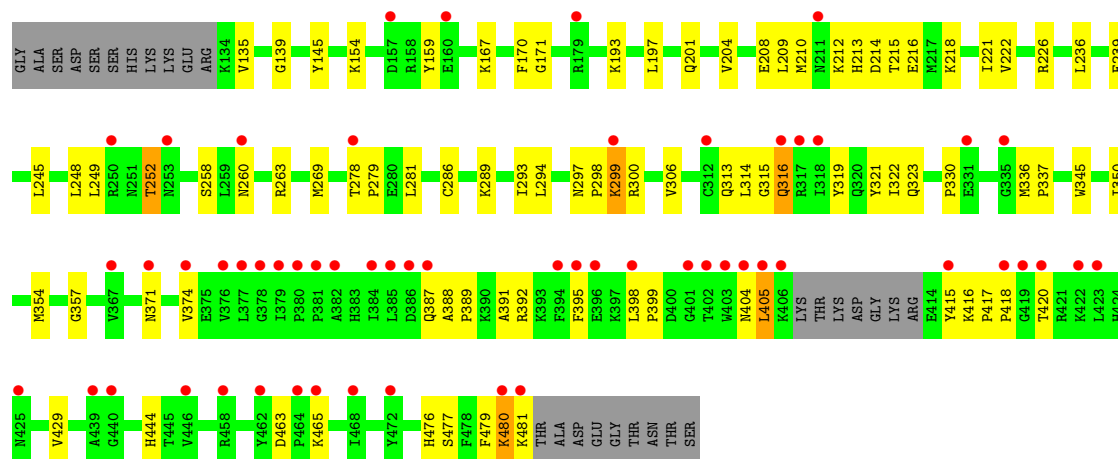


- Molecule 1: Dual specificity tyrosine-phosphorylation-regulated kinase 1A

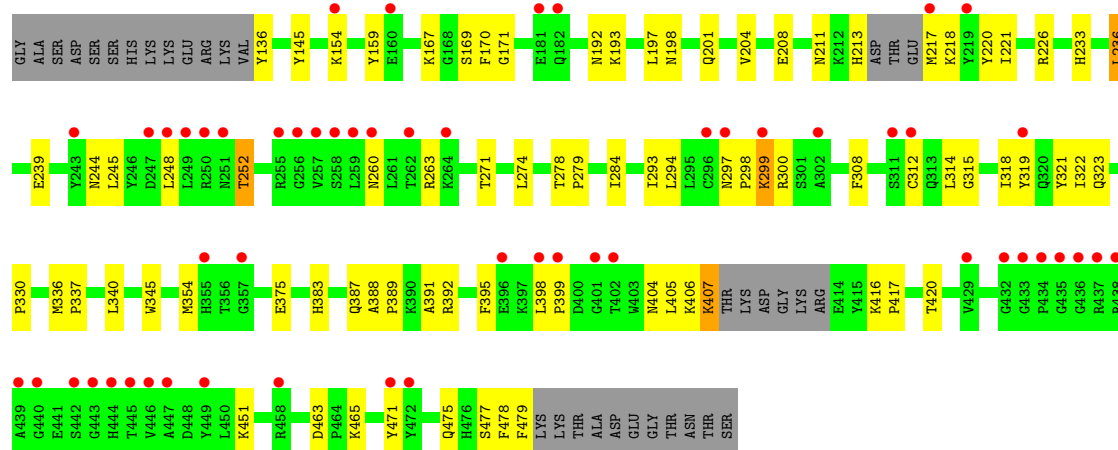


- Molecule 1: Dual specificity tyrosine-phosphorylation-regulated kinase 1A





- Molecule 1: Dual specificity tyrosine-phosphorylation-regulated kinase 1A



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	87.43Å 87.75Å 228.02Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	41.94 – 2.60 41.94 – 2.60	Depositor EDS
% Data completeness (in resolution range)	97.2 (41.94-2.60) 97.2 (41.94-2.60)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.07	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.27 (at 2.61Å)	Xtriage
Refinement program	CNS 1.2	Depositor
R, R_{free}	0.236 , 0.270 0.236 , 0.270	Depositor DCC
R_{free} test set	2656 reflections (4.98%)	wwPDB-VP
Wilson B-factor (Å ²)	53.2	Xtriage
Anisotropy	0.539	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 56.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.014 for k,h,-l	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	11204	wwPDB-VP
Average B, all atoms (Å ²)	62.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.09% 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: PTR, EHB

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	0.70	2/2849 (0.1%)	1.00	9/3840 (0.2%)
1	B	0.57	0/2850	0.98	10/3843 (0.3%)
1	C	0.56	0/2829	0.94	5/3815 (0.1%)
1	D	0.58	0/2783	0.95	5/3751 (0.1%)
All	All	0.61	2/11311 (0.0%)	0.97	29/15249 (0.2%)

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	D	0	1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	417	PRO	CA-C	6.19	1.55	1.51
1	A	217	MET	SD-CE	5.04	1.92	1.79

All (29) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	217	MET	N-CA-C	-7.81	103.21	112.89
1	B	417	PRO	CA-C-N	7.63	129.37	119.84
1	B	417	PRO	C-N-CA	7.63	129.37	119.84
1	B	318	ILE	N-CA-C	-6.57	106.43	111.62
1	C	278	THR	CA-C-N	6.28	127.69	119.84
1	C	278	THR	C-N-CA	6.28	127.69	119.84
1	B	278	THR	CA-C-N	6.19	127.58	119.84

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	278	THR	C-N-CA	6.19	127.58	119.84
1	A	239	GLU	N-CA-C	-6.14	101.84	110.50
1	A	478	PHE	N-CA-C	-5.91	104.92	111.71
1	C	239	GLU	N-CA-C	-5.84	102.41	110.35
1	B	239	GLU	N-CA-C	-5.83	102.28	110.50
1	B	134	LYS	N-CA-C	5.67	118.57	110.24
1	D	278	THR	CA-C-N	5.59	126.82	119.84
1	D	278	THR	C-N-CA	5.59	126.82	119.84
1	A	311	SER	N-CA-C	5.58	118.04	110.35
1	D	252	THR	N-CA-C	-5.51	105.18	113.89
1	B	252	THR	N-CA-C	-5.47	105.25	113.89
1	D	239	GLU	N-CA-C	-5.40	102.88	110.50
1	A	252	THR	N-CA-C	-5.32	105.48	113.89
1	B	314	LEU	N-CA-C	5.26	117.92	110.50
1	A	278	THR	CA-C-N	5.25	126.40	119.84
1	A	278	THR	C-N-CA	5.25	126.40	119.84
1	C	252	THR	N-CA-C	-5.23	105.62	113.89
1	D	318	ILE	N-CA-C	-5.19	107.35	113.42
1	B	220	TYR	N-CA-C	-5.13	105.70	112.94
1	A	175	LYS	N-CA-C	-5.12	101.36	109.76
1	C	429	VAL	N-CA-C	5.08	115.70	110.36
1	A	422	LYS	N-CA-C	5.03	117.60	110.10

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	D	136	TYR	Sidechain

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	2801	0	2800	61	0
1	B	2802	0	2797	71	0
1	C	2781	0	2774	65	0
1	D	2736	0	2732	63	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	16	0	13	2	0
2	B	16	0	12	4	0
2	C	16	0	13	2	0
2	D	16	0	12	3	0
3	A	11	0	0	0	0
3	B	3	0	0	0	0
3	C	4	0	0	0	0
3	D	2	0	0	0	0
All	All	11204	0	11153	254	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 11.

All (254) 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:297:ASN:HD22	1:A:298:PRO:HD2	1.14	1.11
1:D:297:ASN:HD22	1:D:298:PRO:HD2	1.18	1.08
1:C:297:ASN:HD22	1:C:298:PRO:HD2	1.19	1.07
1:B:297:ASN:HD22	1:B:298:PRO:HD2	1.19	1.04
1:A:299:LYS:HA	1:A:299:LYS:HZ3	1.31	0.96
1:B:299:LYS:HA	1:B:299:LYS:HZ3	1.30	0.94
1:B:215:THR:HG22	1:B:217:MET:H	1.29	0.94
1:C:299:LYS:HA	1:C:299:LYS:HZ3	1.30	0.93
1:A:297:ASN:HD22	1:A:298:PRO:CD	1.82	0.92
1:C:297:ASN:HD22	1:C:298:PRO:CD	1.86	0.89
1:B:297:ASN:HD22	1:B:298:PRO:CD	1.85	0.89
1:A:299:LYS:HA	1:A:299:LYS:NZ	1.86	0.88
1:D:297:ASN:HD22	1:D:298:PRO:CD	1.87	0.87
1:B:299:LYS:HA	1:B:299:LYS:NZ	1.90	0.87
1:C:299:LYS:HA	1:C:299:LYS:NZ	1.90	0.84
1:D:299:LYS:NZ	1:D:299:LYS:HA	1.92	0.83
1:D:406:LYS:C	1:D:407:LYS:HD3	2.03	0.83
1:D:299:LYS:HA	1:D:299:LYS:HZ3	1.39	0.82
1:B:407:LYS:HG2	1:B:408:THR:H	1.43	0.82
1:A:407:LYS:NZ	1:A:407:LYS:HB3	1.94	0.81
1:A:407:LYS:HB3	1:A:407:LYS:HZ2	1.45	0.79
1:B:481:LYS:N	1:B:481:LYS:HE2	1.99	0.78
1:A:297:ASN:ND2	1:A:298:PRO:HD2	1.96	0.78
1:B:297:ASN:ND2	1:B:298:PRO:HD2	2.00	0.75
1:A:213:HIS:O	1:A:218:LYS:HD3	1.88	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:481:LYS:H	1:B:481:LYS:CE	2.02	0.73
1:D:297:ASN:ND2	1:D:298:PRO:HD2	2.00	0.72
1:B:314:LEU:O	1:C:315:GLY:HA3	1.89	0.72
1:A:406:LYS:O	1:A:407:LYS:HB3	1.90	0.71
1:A:201:GLN:HE22	1:B:318:ILE:CG2	2.04	0.70
1:C:477:SER:HA	1:C:480:LYS:HB2	1.73	0.70
1:C:297:ASN:ND2	1:C:298:PRO:HD2	2.00	0.69
1:D:375:GLU:OE2	1:D:416:LYS:HG3	1.92	0.68
1:B:481:LYS:HE2	1:B:481:LYS:H	1.58	0.68
1:D:387:GLN:O	1:D:389:PRO:HD3	1.94	0.68
1:B:388:ALA:HB3	1:B:391:ALA:HB2	1.76	0.68
1:C:479:PHE:O	1:C:481:LYS:N	2.27	0.68
1:D:407:LYS:HD3	1:D:407:LYS:N	2.07	0.68
1:B:337:PRO:HG3	1:C:279:PRO:HG3	1.76	0.67
1:A:279:PRO:HG3	1:D:337:PRO:HG3	1.75	0.67
1:C:388:ALA:HB3	1:C:391:ALA:HB2	1.78	0.65
1:C:417:PRO:HB2	1:C:420:THR:HG21	1.79	0.64
1:C:371:ASN:HB3	1:C:415:TYR:CD2	2.32	0.64
1:C:387:GLN:O	1:C:389:PRO:HD3	1.98	0.64
1:A:284:ILE:HG12	1:A:340:LEU:HD12	1.80	0.64
2:C:1:EHB:H8	2:C:1:EHB:C12	2.28	0.64
1:A:297:ASN:ND2	1:A:298:PRO:CD	2.59	0.62
1:A:322:ILE:O	1:A:323:GLN:HB2	1.98	0.62
2:D:1:EHB:H8	2:D:1:EHB:C12	2.30	0.61
2:B:1:EHB:H8	2:B:1:EHB:C12	2.31	0.61
1:D:217:MET:HE1	1:D:274:LEU:HD23	1.83	0.61
1:B:387:GLN:O	1:B:389:PRO:HD3	2.00	0.61
1:A:388:ALA:HB3	1:A:391:ALA:HB2	1.82	0.61
1:B:215:THR:HG22	1:B:217:MET:N	2.11	0.61
1:B:480:LYS:HA	1:B:481:LYS:NZ	2.15	0.61
1:A:480:LYS:HB3	1:A:480:LYS:HZ2	1.66	0.60
1:D:388:ALA:HB3	1:D:391:ALA:HB2	1.83	0.60
1:A:169:SER:HB3	1:B:145:TYR:OH	2.02	0.59
1:B:398:LEU:HB3	1:B:399:PRO:HD2	1.83	0.59
1:C:398:LEU:HB3	1:C:399:PRO:HD2	1.84	0.59
1:B:407:LYS:HG2	1:B:408:THR:N	2.13	0.59
1:B:314:LEU:HG	1:B:315:GLY:N	2.17	0.59
1:B:481:LYS:H	1:B:481:LYS:CD	2.16	0.59
1:C:374:VAL:HG11	1:C:405:LEU:HD21	1.84	0.59
1:D:398:LEU:HB3	1:D:399:PRO:HD2	1.84	0.58
1:B:311:SER:O	1:B:312:CYS:HB3	2.04	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:299:LYS:NZ	1:A:299:LYS:CA	2.66	0.57
1:D:213:HIS:C	1:D:218:LYS:HZ2	2.14	0.56
1:B:211:ASN:OD1	1:B:223:HIS:HD2	1.88	0.56
1:D:217:MET:HE2	1:D:271:THR:HG23	1.88	0.56
1:C:281:LEU:O	1:C:313:GLN:NE2	2.33	0.56
1:A:300:ARG:HG3	1:A:300:ARG:HH11	1.71	0.56
1:C:398:LEU:HG	1:C:404:ASN:HD22	1.71	0.56
1:A:145:TYR:CE1	1:A:193:LYS:HD3	2.41	0.56
1:C:297:ASN:ND2	1:C:298:PRO:CD	2.63	0.55
1:D:300:ARG:HG3	1:D:300:ARG:HH11	1.72	0.55
1:B:307:ASP:HB2	2:B:1:EHB:H10B	1.89	0.55
1:C:204:VAL:O	1:C:208:GLU:HG3	2.07	0.55
1:C:222:VAL:HB	1:C:306:VAL:HG12	1.89	0.55
1:C:300:ARG:HG3	1:C:300:ARG:HH11	1.71	0.55
1:C:322:ILE:O	1:C:323:GLN:HB2	2.06	0.54
1:D:213:HIS:C	1:D:218:LYS:NZ	2.65	0.54
1:A:398:LEU:HB3	1:A:399:PRO:HD2	1.88	0.54
1:D:336:MET:HB3	1:D:337:PRO:CD	2.38	0.54
1:C:417:PRO:HB2	1:C:420:THR:CG2	2.37	0.54
1:D:204:VAL:O	1:D:208:GLU:HG3	2.07	0.54
1:C:404:ASN:O	1:C:405:LEU:O	2.25	0.54
1:D:145:TYR:CE1	1:D:193:LYS:HD3	2.42	0.54
1:B:260:ASN:HA	1:B:263:ARG:NH1	2.24	0.53
1:B:297:ASN:ND2	1:B:298:PRO:CD	2.62	0.53
1:A:387:GLN:O	1:A:389:PRO:HD3	2.08	0.53
1:A:314:LEU:O	1:D:315:GLY:HA2	2.09	0.53
1:B:452:PHE:HB2	1:B:478:PHE:CE1	2.44	0.53
1:A:318:ILE:HG13	1:A:319:TYR:CE1	2.44	0.53
1:C:336:MET:HB3	1:C:337:PRO:CD	2.38	0.53
1:A:204:VAL:O	1:A:208:GLU:HG3	2.09	0.52
1:C:371:ASN:HB3	1:C:415:TYR:HD2	1.71	0.52
1:B:245:LEU:HD13	1:B:354:MET:HE2	1.91	0.52
1:B:263:ARG:HG3	1:B:478:PHE:CE2	2.44	0.52
1:B:260:ASN:HA	1:B:263:ARG:HH12	1.73	0.52
1:C:245:LEU:HD13	1:C:354:MET:HE2	1.91	0.52
1:B:300:ARG:HG3	1:B:300:ARG:HH11	1.75	0.52
1:C:145:TYR:CE1	1:C:193:LYS:HD3	2.44	0.52
1:A:472:TYR:OH	1:D:383:HIS:HB2	2.10	0.52
1:B:299:LYS:NZ	1:B:299:LYS:CA	2.70	0.52
1:D:297:ASN:ND2	1:D:298:PRO:CD	2.64	0.52
1:D:260:ASN:HA	1:D:263:ARG:HH12	1.73	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:451:LYS:HD3	1:D:477:SER:OG	2.10	0.52
1:D:260:ASN:HA	1:D:263:ARG:NH1	2.24	0.51
1:A:406:LYS:O	1:A:407:LYS:CB	2.55	0.51
1:C:209:LEU:O	1:C:212:LYS:HB3	2.10	0.51
1:D:398:LEU:HD11	1:D:404:ASN:ND2	2.25	0.51
1:A:336:MET:HB3	1:A:337:PRO:CD	2.40	0.51
1:C:145:TYR:OH	1:D:169:SER:HB3	2.10	0.50
1:B:477:SER:HA	1:B:480:LYS:HG3	1.94	0.50
1:D:471:TYR:CZ	1:D:475:GLN:NE2	2.80	0.50
1:B:336:MET:HB3	1:B:337:PRO:CD	2.41	0.50
1:D:217:MET:HE2	1:D:271:THR:CG2	2.42	0.50
1:A:407:LYS:O	1:A:407:LYS:HG2	2.11	0.50
1:B:145:TYR:CE1	1:B:193:LYS:HD3	2.47	0.50
1:B:204:VAL:O	1:B:208:GLU:HG3	2.11	0.50
1:D:314:LEU:HD12	1:D:315:GLY:H	1.76	0.50
1:A:318:ILE:HG13	1:A:319:TYR:CD1	2.47	0.49
1:D:213:HIS:C	1:D:218:LYS:HD3	2.36	0.49
2:C:1:EHB:H8	2:C:1:EHB:H12B	1.94	0.49
1:A:284:ILE:CG1	1:A:340:LEU:HD12	2.41	0.49
1:C:260:ASN:HA	1:C:263:ARG:NH1	2.27	0.49
1:C:213:HIS:O	1:C:218:LYS:HD3	2.13	0.49
1:C:197:LEU:O	1:C:201:GLN:HG3	2.13	0.48
1:C:260:ASN:HA	1:C:263:ARG:HH12	1.78	0.48
2:B:1:EHB:S	2:B:1:EHB:O	2.71	0.48
1:B:331:GLU:OE2	1:B:464:PRO:HB3	2.13	0.48
1:D:293:ILE:C	1:D:294:LEU:HD12	2.39	0.48
1:A:260:ASN:HA	1:A:263:ARG:NH1	2.29	0.48
1:D:314:LEU:HD12	1:D:315:GLY:N	2.29	0.48
1:D:417:PRO:HB2	1:D:420:THR:HG21	1.96	0.48
1:D:197:LEU:O	1:D:201:GLN:HG3	2.14	0.47
1:A:154:LYS:HA	1:A:159:TYR:O	2.14	0.47
1:A:407:LYS:NZ	1:A:407:LYS:CB	2.71	0.47
1:A:293:ILE:C	1:A:294:LEU:HD12	2.40	0.47
2:A:1:EHB:S	2:A:1:EHB:O	2.72	0.47
1:C:371:ASN:HB3	1:C:415:TYR:CE2	2.50	0.47
1:B:197:LEU:O	1:B:201:GLN:HG3	2.15	0.47
1:C:398:LEU:CD1	1:C:404:ASN:ND2	2.78	0.47
1:D:322:ILE:O	1:D:323:GLN:HB2	2.13	0.47
1:A:260:ASN:HA	1:A:263:ARG:HH12	1.80	0.47
1:A:472:TYR:CZ	1:D:383:HIS:HB2	2.50	0.46
1:B:480:LYS:HA	1:B:481:LYS:HZ1	1.78	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:330:PRO:HD3	1:C:345:TRP:CE2	2.50	0.46
1:A:463:ASP:OD1	1:A:465:LYS:HB2	2.15	0.46
1:B:417:PRO:HA	1:B:418:PRO:HD3	1.66	0.46
1:D:145:TYR:CD1	1:D:193:LYS:HD3	2.51	0.46
2:A:1:EHB:C12	2:A:1:EHB:H8	2.45	0.46
1:A:315:GLY:HA2	1:D:314:LEU:O	2.16	0.46
1:B:477:SER:HA	1:B:480:LYS:CG	2.46	0.46
1:C:299:LYS:NZ	1:C:299:LYS:CA	2.70	0.46
1:B:248:LEU:O	1:B:252:THR:HG23	2.16	0.46
1:C:371:ASN:CB	1:C:415:TYR:CE2	2.97	0.46
1:D:330:PRO:HD3	1:D:345:TRP:CE2	2.51	0.46
1:B:476:HIS:O	1:B:480:LYS:HG3	2.16	0.46
1:B:463:ASP:OD1	1:B:465:LYS:HB2	2.15	0.46
1:C:463:ASP:OD1	1:C:465:LYS:HB2	2.15	0.46
1:B:311:SER:O	1:B:312:CYS:CB	2.63	0.46
1:C:135:VAL:HG13	1:C:139:GLY:N	2.31	0.46
1:C:154:LYS:HA	1:C:159:TYR:O	2.16	0.45
1:A:413:ARG:O	1:A:413:ARG:HG2	2.16	0.45
1:A:248:LEU:O	1:A:252:THR:HG23	2.15	0.45
1:D:392:ARG:HA	1:D:395:PHE:O	2.17	0.45
1:D:463:ASP:OD1	1:D:465:LYS:HB2	2.15	0.45
1:A:216:GLU:OE2	1:A:216:GLU:N	2.50	0.45
1:B:477:SER:HA	1:B:480:LYS:HD3	1.98	0.45
1:C:216:GLU:O	1:C:216:GLU:HG2	2.17	0.45
1:A:197:LEU:HD23	1:B:319:TYR:CD1	2.51	0.45
1:C:289:LYS:HA	1:C:350:ILE:HD11	1.98	0.45
1:A:145:TYR:CD1	1:A:193:LYS:HD3	2.51	0.45
1:A:280:GLU:OE1	1:A:280:GLU:N	2.40	0.45
1:B:217:MET:C	1:B:219:TYR:H	2.25	0.44
1:D:248:LEU:O	1:D:252:THR:HG23	2.17	0.44
1:B:314:LEU:CG	1:B:315:GLY:N	2.80	0.44
1:D:220:TYR:C	1:D:221:ILE:HD13	2.42	0.44
1:B:452:PHE:HB2	1:B:478:PHE:HE1	1.83	0.44
1:C:248:LEU:O	1:C:252:THR:HG23	2.17	0.44
1:B:477:SER:HA	1:B:480:LYS:CD	2.47	0.44
1:C:258:SER:HB2	1:C:444:HIS:CE1	2.52	0.44
1:B:326:PHE:CD1	1:B:362:SER:HA	2.53	0.44
1:C:415:TYR:N	1:C:415:TYR:HD1	2.16	0.44
1:D:154:LYS:HA	1:D:159:TYR:O	2.16	0.44
1:C:415:TYR:N	1:C:415:TYR:CD1	2.86	0.43
1:A:197:LEU:HD23	1:B:319:TYR:HD1	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:168:GLY:HA3	1:B:170:PHE:CE2	2.53	0.43
1:C:417:PRO:O	1:C:418:PRO:C	2.59	0.43
1:D:336:MET:HB3	1:D:337:PRO:HD2	1.99	0.43
1:C:170:PHE:CD1	1:C:171:GLY:N	2.86	0.43
1:C:480:LYS:O	1:C:481:LYS:C	2.61	0.43
1:A:197:LEU:O	1:A:201:GLN:HG3	2.17	0.43
1:A:216:GLU:HG3	1:A:219:TYR:HE2	1.83	0.43
1:D:417:PRO:HB2	1:D:420:THR:CG2	2.48	0.43
1:B:215:THR:O	1:B:218:LYS:HG2	2.18	0.43
1:D:244:ASN:HA	1:D:294:LEU:HA	2.00	0.43
1:C:210:MET:C	1:C:212:LYS:H	2.26	0.43
1:D:284:ILE:HG12	1:D:340:LEU:HD12	2.00	0.43
1:B:280:GLU:OE1	1:B:280:GLU:N	2.43	0.43
1:B:154:LYS:HA	1:B:159:TYR:O	2.19	0.43
1:B:322:ILE:O	1:B:323:GLN:HB2	2.17	0.43
1:D:398:LEU:HD11	1:D:404:ASN:HD22	1.83	0.43
1:A:337:PRO:HG3	1:D:279:PRO:HG3	2.00	0.43
1:B:297:ASN:HD22	1:B:298:PRO:N	2.16	0.43
1:D:221:ILE:HG23	1:D:308:PHE:CE2	2.54	0.42
1:A:392:ARG:HA	1:A:395:PHE:O	2.19	0.42
1:B:330:PRO:HD3	1:B:345:TRP:CE2	2.53	0.42
1:C:392:ARG:HA	1:C:395:PHE:O	2.20	0.42
1:D:170:PHE:CD1	1:D:171:GLY:N	2.87	0.42
1:B:170:PHE:CD1	1:B:171:GLY:N	2.88	0.42
1:B:458:ARG:O	1:B:468:ILE:HG22	2.19	0.42
1:C:214:ASP:O	1:C:215:THR:C	2.60	0.42
2:D:1:EHB:H8	2:D:1:EHB:H12A	2.01	0.42
1:C:145:TYR:CD1	1:C:193:LYS:HD3	2.54	0.42
2:B:1:EHB:H8	2:B:1:EHB:H12B	1.99	0.42
1:D:477:SER:O	1:D:479:PHE:N	2.52	0.42
1:A:472:TYR:OH	1:D:383:HIS:CD2	2.73	0.42
1:A:297:ASN:HD22	1:A:298:PRO:N	2.17	0.42
1:C:371:ASN:CB	1:C:415:TYR:HE2	2.33	0.42
1:C:315:GLY:O	1:C:316:GLN:C	2.63	0.41
1:A:168:GLY:HA3	1:A:170:PHE:CE2	2.55	0.41
1:A:299:LYS:HA	1:A:299:LYS:HZ2	1.81	0.41
1:B:145:TYR:CD1	1:B:193:LYS:HD3	2.53	0.41
1:D:192:ASN:HB2	1:D:233:HIS:CE1	2.55	0.41
1:A:170:PHE:CD1	1:A:171:GLY:N	2.89	0.41
1:C:269:MET:HE2	1:C:293:ILE:HD11	2.02	0.41
1:D:245:LEU:HD13	1:D:354:MET:HE2	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:330:PRO:HD3	1:D:345:TRP:CD2	2.55	0.41
1:C:221:ILE:O	1:C:222:VAL:C	2.63	0.41
1:C:415:TYR:C	1:C:416:LYS:HG3	2.45	0.41
2:D:1:EHB:H8	2:D:1:EHB:H12B	2.01	0.41
1:A:236:LEU:N	1:A:236:LEU:HD23	2.36	0.41
1:A:330:PRO:HD3	1:A:345:TRP:CE2	2.56	0.41
1:C:293:ILE:C	1:C:294:LEU:HD12	2.46	0.41
1:D:312:CYS:HB3	1:D:319:TYR:HE2	1.86	0.41
1:A:201:GLN:HE22	1:B:318:ILE:HG22	1.82	0.41
1:A:336:MET:HB3	1:A:337:PRO:HD2	2.02	0.41
1:B:289:LYS:HA	1:B:350:ILE:HD11	2.02	0.41
1:B:293:ILE:C	1:B:294:LEU:HD12	2.45	0.41
1:B:392:ARG:HA	1:B:395:PHE:O	2.20	0.41
1:A:289:LYS:HA	1:A:350:ILE:HD11	2.03	0.41
1:B:192:ASN:HB2	1:B:233:HIS:CE1	2.56	0.41
1:B:480:LYS:HB3	1:B:480:LYS:HE2	1.89	0.40
1:C:336:MET:HB3	1:C:337:PRO:HD2	2.02	0.40
1:A:463:ASP:HA	1:A:464:PRO:HD2	1.99	0.40
1:C:319:TYR:HE1	1:D:198:ASN:HD21	1.69	0.40
1:C:330:PRO:HD3	1:C:345:TRP:CD2	2.56	0.40
1:D:236:LEU:HD23	1:D:236:LEU:N	2.36	0.40
1:B:336:MET:HB3	1:B:337:PRO:HD2	2.04	0.40
1:C:249:LEU:HD22	1:C:357:GLY:HA2	2.03	0.40
1:D:244:ASN:OD1	1:D:244:ASN:C	2.64	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	338/368 (92%)	318 (94%)	20 (6%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	339/368 (92%)	315 (93%)	20 (6%)	4 (1%)	10	23
1	C	336/368 (91%)	302 (90%)	29 (9%)	5 (2%)	8	18
1	D	328/368 (89%)	303 (92%)	23 (7%)	2 (1%)	21	42
All	All	1341/1472 (91%)	1238 (92%)	92 (7%)	11 (1%)	16	34

All (11) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	312	CYS
1	C	405	LEU
1	C	480	LYS
1	B	311	SER
1	B	316	GLN
1	C	316	GLN
1	D	478	PHE
1	C	476	HIS
1	D	405	LEU
1	C	314	LEU
1	B	313	GLN

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	301/324 (93%)	294 (98%)	7 (2%)	44	71
1	B	301/324 (93%)	292 (97%)	9 (3%)	36	64
1	C	299/324 (92%)	294 (98%)	5 (2%)	53	78
1	D	294/324 (91%)	288 (98%)	6 (2%)	48	74
All	All	1195/1296 (92%)	1168 (98%)	27 (2%)	44	71

All (27) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	167	LYS
1	A	226	ARG
1	A	236	LEU
1	A	286	CYS
1	A	299	LYS
1	A	407	LYS
1	A	480	LYS
1	B	167	LYS
1	B	226	ARG
1	B	236	LEU
1	B	286	CYS
1	B	299	LYS
1	B	319	TYR
1	B	408	THR
1	B	414	GLU
1	B	481	LYS
1	C	167	LYS
1	C	226	ARG
1	C	236	LEU
1	C	286	CYS
1	C	299	LYS
1	D	167	LYS
1	D	211	ASN
1	D	226	ARG
1	D	236	LEU
1	D	299	LYS
1	D	407	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (41) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	198	ASN
1	A	201	GLN
1	A	211	ASN
1	A	223	HIS
1	A	232	ASN
1	A	267	GLN
1	A	297	ASN
1	A	320	GLN
1	A	387	GLN
1	A	404	ASN
1	A	425	ASN
1	B	182	GLN

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Mol	Chain	Res	Type
1	B	198	ASN
1	B	201	GLN
1	B	213	HIS
1	B	223	HIS
1	B	297	ASN
1	B	425	ASN
1	B	475	GLN
1	C	198	ASN
1	C	201	GLN
1	C	211	ASN
1	C	223	HIS
1	C	232	ASN
1	C	297	ASN
1	C	320	GLN
1	C	404	ASN
1	C	425	ASN
1	D	144	ASN
1	D	182	GLN
1	D	198	ASN
1	D	211	ASN
1	D	213	HIS
1	D	232	ASN
1	D	267	GLN
1	D	297	ASN
1	D	383	HIS
1	D	387	GLN
1	D	404	ASN
1	D	425	ASN
1	D	475	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

4 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	PTR	B	321	1	15,16,17	1.71	5 (33%)	17,22,24	0.71	0
1	PTR	A	321	1	15,16,17	1.38	3 (20%)	17,22,24	0.76	0
1	PTR	C	321	1	15,16,17	1.12	1 (6%)	17,22,24	0.72	0
1	PTR	D	321	1	15,16,17	1.25	1 (6%)	17,22,24	0.87	1 (5%)

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	PTR	B	321	1	-	0/10/11/13	0/1/1/1
1	PTR	A	321	1	-	0/10/11/13	0/1/1/1
1	PTR	C	321	1	-	0/10/11/13	0/1/1/1
1	PTR	D	321	1	-	0/10/11/13	0/1/1/1

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	321	PTR	CE2-CD2	3.35	1.44	1.38
1	A	321	PTR	CE2-CD2	2.53	1.42	1.38
1	A	321	PTR	CE2-CZ	2.52	1.43	1.38
1	B	321	PTR	CD2-CG	2.41	1.43	1.38
1	B	321	PTR	CE1-CD1	2.22	1.42	1.38
1	A	321	PTR	CE1-CZ	2.12	1.42	1.38
1	D	321	PTR	CE2-CZ	2.08	1.42	1.38
1	C	321	PTR	CE2-CZ	2.07	1.42	1.38
1	B	321	PTR	CE2-CZ	2.07	1.42	1.38
1	B	321	PTR	P-OH	2.02	1.63	1.59

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	321	PTR	O2P-P-O1P	2.03	118.74	110.83

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](#)

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	EHB	C	1	-	17,17,17	4.14	3 (17%)	23,24,24	2.73	5 (21%)
2	EHB	B	1	-	17,17,17	4.15	4 (23%)	23,24,24	2.63	6 (26%)
2	EHB	D	1	-	17,17,17	4.49	3 (17%)	23,24,24	2.86	6 (26%)
2	EHB	A	1	-	17,17,17	4.14	3 (17%)	23,24,24	2.99	8 (34%)

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	EHB	C	1	-	-	2/6/6/6	0/2/2/2
2	EHB	B	1	-	-	2/6/6/6	0/2/2/2
2	EHB	D	1	-	-	2/6/6/6	0/2/2/2
2	EHB	A	1	-	-	2/6/6/6	0/2/2/2

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	1	EHB	C4-S	-14.47	1.45	1.74

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	1	EHB	C4-S	-14.10	1.46	1.74
2	B	1	EHB	C4-S	-13.18	1.48	1.74
2	A	1	EHB	C4-S	-12.61	1.49	1.74
2	D	1	EHB	C7-S	-9.14	1.56	1.74
2	A	1	EHB	C7-S	-8.82	1.57	1.74
2	B	1	EHB	C7-S	-8.04	1.59	1.74
2	C	1	EHB	C7-S	-7.34	1.60	1.74
2	A	1	EHB	C3-N	-6.44	1.27	1.39
2	B	1	EHB	C3-N	-6.09	1.28	1.39
2	D	1	EHB	C3-N	-5.43	1.29	1.39
2	C	1	EHB	C3-N	-4.68	1.31	1.39
2	B	1	EHB	C8-C9	-2.24	1.37	1.43

All (25) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1	EHB	C11-N-C7	9.97	133.27	122.61
2	B	1	EHB	C11-N-C7	8.45	131.64	122.61
2	C	1	EHB	C11-N-C7	8.40	131.59	122.61
2	D	1	EHB	C11-N-C7	8.24	131.42	122.61
2	D	1	EHB	C4-S-C7	6.97	96.80	91.26
2	D	1	EHB	C3-N-C7	-6.68	109.18	114.64
2	C	1	EHB	C3-N-C7	-6.46	109.36	114.64
2	A	1	EHB	C3-N-C7	-6.31	109.48	114.64
2	B	1	EHB	C3-N-C7	-6.25	109.53	114.64
2	C	1	EHB	C4-S-C7	6.07	96.09	91.26
2	B	1	EHB	C4-S-C7	4.51	94.85	91.26
2	A	1	EHB	C4-S-C7	4.50	94.84	91.26
2	A	1	EHB	C11-N-C3	-3.45	117.25	124.49
2	A	1	EHB	C8-C7-S	-3.15	121.88	125.39
2	B	1	EHB	C11-N-C3	-2.70	118.82	124.49
2	C	1	EHB	C11-N-C3	-2.59	119.05	124.49
2	D	1	EHB	C11-N-C3	-2.42	119.40	124.49
2	A	1	EHB	C8-C7-N	2.38	126.75	124.25
2	D	1	EHB	C3-C2-C1	2.34	121.43	117.95
2	C	1	EHB	C12-C11-N	2.32	119.72	111.57
2	A	1	EHB	C12-C11-N	2.27	119.57	111.57
2	B	1	EHB	C8-C7-S	-2.23	122.91	125.39
2	D	1	EHB	C12-C11-N	2.20	119.30	111.57
2	B	1	EHB	C12-C11-N	2.08	118.87	111.57
2	A	1	EHB	C5-C4-C3	-2.07	118.69	120.97

There are no chirality outliers.

All (8) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1	EHB	C12-C11-N-C3
2	A	1	EHB	C12-C11-N-C7
2	B	1	EHB	C12-C11-N-C3
2	B	1	EHB	C12-C11-N-C7
2	C	1	EHB	C12-C11-N-C3
2	C	1	EHB	C12-C11-N-C7
2	D	1	EHB	C12-C11-N-C3
2	D	1	EHB	C12-C11-N-C7

There are no ring outliers.

4 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	1	EHB	2	0
2	B	1	EHB	4	0
2	D	1	EHB	3	0
2	A	1	EHB	2	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	342/368 (92%)	-0.10	11 (3%) 50 44	18, 40, 72, 91	2 (0%)
1	B	343/368 (93%)	0.92	50 (14%) 6 4	33, 67, 101, 121	2 (0%)
1	C	340/368 (92%)	0.84	57 (16%) 4 3	29, 66, 109, 133	2 (0%)
1	D	334/368 (90%)	0.84	54 (16%) 4 3	28, 62, 104, 119	2 (0%)
All	All	1359/1472 (92%)	0.62	172 (12%) 8 6	18, 60, 103, 133	8 (0%)

All (172) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	443	GLY	7.7
1	D	256	GLY	5.7
1	C	419	GLY	5.5
1	C	402	THR	4.5
1	D	432	GLY	4.3
1	D	449	TYR	4.3
1	C	403	TRP	4.2
1	C	401	GLY	4.2
1	C	381	PRO	4.1
1	A	318	ILE	3.9
1	C	382	ALA	3.9
1	C	160	GLU	3.9
1	C	385	LEU	3.8
1	D	446	VAL	3.8
1	D	444	HIS	3.8
1	C	299	LYS	3.7
1	D	312	CYS	3.7
1	B	425	ASN	3.7
1	C	380	PRO	3.7
1	B	319	TYR	3.6
1	D	438	ARG	3.6

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Mol	Chain	Res	Type	RSRZ
1	D	439	ALA	3.5
1	B	429	VAL	3.5
1	C	405	LEU	3.5
1	D	434	PRO	3.4
1	A	472	TYR	3.3
1	C	253	ASN	3.3
1	C	420	THR	3.3
1	C	211	ASN	3.2
1	C	312	CYS	3.2
1	D	402	THR	3.2
1	B	478	PHE	3.2
1	C	371	ASN	3.2
1	B	430	GLU	3.2
1	C	440	GLY	3.2
1	D	471	TYR	3.1
1	D	257	VAL	3.1
1	B	152	GLY	3.1
1	D	296	CYS	3.1
1	B	218	LYS	3.1
1	C	250	ARG	3.1
1	C	480	LYS	3.0
1	C	379	ILE	3.0
1	C	394	PHE	3.0
1	C	425	ASN	3.0
1	B	154	LYS	2.9
1	C	472	TYR	2.9
1	B	448	ASP	2.9
1	B	408	THR	2.9
1	D	250	ARG	2.9
1	D	219	TYR	2.9
1	B	373	ILE	2.9
1	B	424	HIS	2.9
1	D	311	SER	2.9
1	D	442	SER	2.9
1	B	450	LEU	2.9
1	D	355	HIS	2.9
1	C	458	ARG	2.8
1	D	437	ARG	2.8
1	C	377	LEU	2.8
1	C	316	GLN	2.8
1	B	403	TRP	2.8
1	B	318	ILE	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	299	LYS	2.8
1	D	248	LEU	2.7
1	D	357	GLY	2.7
1	B	417	PRO	2.7
1	D	447	ALA	2.7
1	D	433	GLY	2.7
1	D	440	GLY	2.7
1	B	481	LYS	2.7
1	B	215	THR	2.7
1	C	395	PHE	2.7
1	D	264	LYS	2.7
1	B	407	LYS	2.6
1	B	428	GLY	2.6
1	C	422	LYS	2.6
1	D	182	GLN	2.6
1	D	435	GLY	2.6
1	D	436	GLY	2.6
1	D	260	ASN	2.6
1	D	302	ALA	2.6
1	D	429	VAL	2.6
1	C	398	LEU	2.6
1	C	378	GLY	2.6
1	C	157	ASP	2.5
1	D	319	TYR	2.5
1	A	312	CYS	2.5
1	C	278	THR	2.5
1	C	318	ILE	2.5
1	B	472	TYR	2.5
1	D	243	TYR	2.5
1	C	367	VAL	2.5
1	C	404	ASN	2.5
1	D	255	ARG	2.5
1	B	419	GLY	2.5
1	D	251	ASN	2.4
1	B	259	LEU	2.4
1	B	418	PRO	2.4
1	B	471	TYR	2.4
1	C	415	TYR	2.4
1	C	418	PRO	2.4
1	B	342	ILE	2.4
1	B	398	LEU	2.4
1	C	406	LYS	2.4

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Mol	Chain	Res	Type	RSRZ
1	D	299	LYS	2.4
1	B	462	TYR	2.3
1	C	384	ILE	2.3
1	B	356	THR	2.3
1	B	181	GLU	2.3
1	B	451	LYS	2.3
1	B	401	GLY	2.3
1	B	432	GLY	2.3
1	B	317	ARG	2.3
1	C	317	ARG	2.3
1	D	458	ARG	2.3
1	D	181	GLU	2.3
1	D	401	GLY	2.3
1	C	446	VAL	2.3
1	B	447	ALA	2.3
1	C	462	TYR	2.3
1	B	399	PRO	2.3
1	B	461	ASP	2.3
1	B	261	LEU	2.3
1	D	259	LEU	2.3
1	A	481	LYS	2.3
1	B	299	LYS	2.3
1	C	331	GLU	2.2
1	B	454	ASP	2.2
1	A	314	LEU	2.2
1	B	248	LEU	2.2
1	C	423	LEU	2.2
1	B	349	CYS	2.2
1	A	311	SER	2.2
1	C	335	GLY	2.2
1	D	247	ASP	2.2
1	D	398	LEU	2.2
1	C	374	VAL	2.2
1	C	376	VAL	2.2
1	C	179	ARG	2.2
1	C	387	GLN	2.2
1	D	154	LYS	2.1
1	B	311	SER	2.1
1	A	313	GLN	2.1
1	B	449	TYR	2.1
1	D	249	LEU	2.1
1	B	440	GLY	2.1

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Mol	Chain	Res	Type	RSRZ
1	D	258	SER	2.1
1	D	160	GLU	2.1
1	D	262	THR	2.1
1	A	182	GLN	2.1
1	D	297	ASN	2.1
1	C	396	GLU	2.1
1	C	439	ALA	2.1
1	D	396	GLU	2.1
1	A	253	ASN	2.1
1	C	260	ASN	2.1
1	B	256	GLY	2.1
1	C	468	ILE	2.1
1	C	386	ASP	2.0
1	C	465	LYS	2.0
1	D	445	THR	2.0
1	C	464	PRO	2.0
1	D	217	MET	2.0
1	B	377	LEU	2.0
1	A	300	ARG	2.0
1	B	479	PHE	2.0
1	C	481	LYS	2.0
1	D	399	PRO	2.0
1	B	348	GLY	2.0
1	B	219	TYR	2.0
1	D	472	TYR	2.0

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

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($\text{\AA}^2$)	Q<0.9
1	PTR	B	321	16/17	0.96	0.08	48,59,63,64	0
1	PTR	C	321	16/17	0.96	0.07	45,56,66,66	0
1	PTR	D	321	16/17	0.96	0.07	35,40,44,46	0
1	PTR	A	321	16/17	0.98	0.06	31,41,44,46	0

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($\text{\AA}^2$)	Q<0.9
2	EHB	D	1	16/16	0.92	0.10	48,58,63,69	0
2	EHB	C	1	16/16	0.94	0.09	38,45,53,53	0
2	EHB	A	1	16/16	0.94	0.09	33,37,41,41	0
2	EHB	B	1	16/16	0.96	0.08	35,44,61,61	0

6.5 Other polymers [i](#)

There are no such residues in this entry.