



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 11:15 PM UTC

PDB ID : 3KYS / pdb_00003kys
Title : Crystal structure of human YAP and TEAD complex
Authors : Li, Z.; Zhao, B.; Wang, P.; Chen, F.; Dong, Z.; Yang, H.; Guan, K.L.; Xu, Y.
Deposited on : 2009-12-07
Resolution : 2.80 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

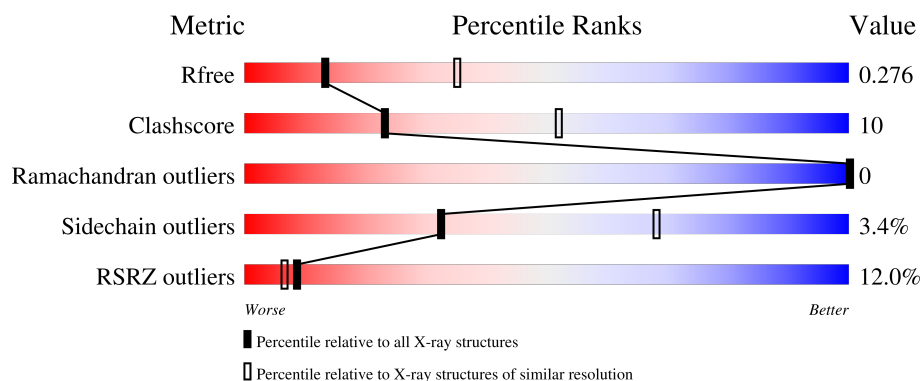
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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	3866 (2.80-2.80)
Clashscore	190562	4276 (2.80-2.80)
Ramachandran outliers	187476	4196 (2.80-2.80)
Sidechain outliers	187428	4198 (2.80-2.80)
RSRZ outliers	180081	3869 (2.80-2.80)

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	219	20% 72% 21% 5%
1	C	219	7% 71% 24% • •
2	B	125	2% 30% 10% 60%
2	D	125	% 27% 12% 61%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4286 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 Transcriptional enhancer factor TEF-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	208	Total	C	N	O	S	0	0	0
			1712	1098	288	314	12			
1	C	211	Total	C	N	O	S	0	0	0
			1736	1113	294	317	12			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	193	MET	-	expression tag	UNP P28347
C	193	MET	-	expression tag	UNP P28347

- Molecule 2 is a protein called 65 kDa Yes-associated protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	50	Total	C	N	O	S	0	0	0
			395	250	71	72	2			
2	D	49	Total	C	N	O	S	0	0	0
			391	248	70	71	2			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	47	SER	-	expression tag	UNP P46937
B	48	HIS	-	expression tag	UNP P46937
B	49	MET	-	expression tag	UNP P46937
D	47	SER	-	expression tag	UNP P46937
D	48	HIS	-	expression tag	UNP P46937
D	49	MET	-	expression tag	UNP P46937

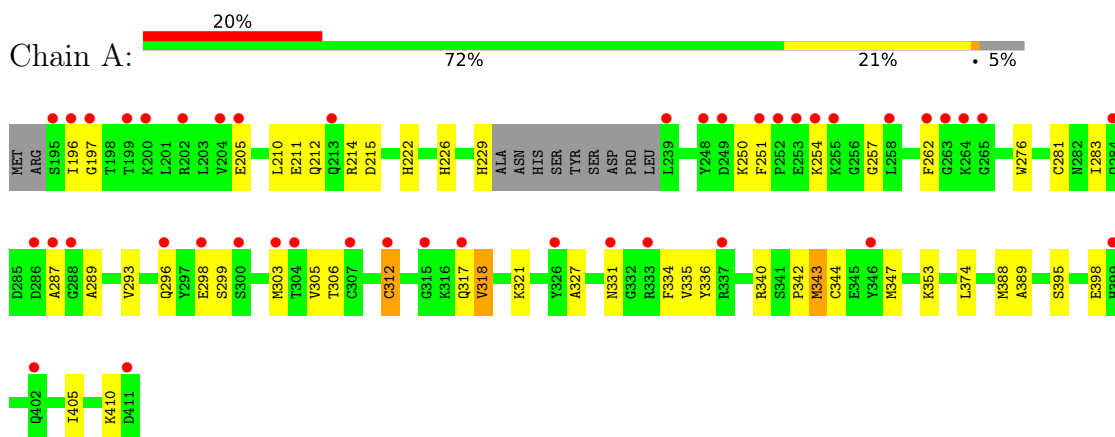
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	8	Total 8	O 8	0	0
3	B	8	Total 8	O 8	0	0
3	C	27	Total 27	O 27	0	0
3	D	9	Total 9	O 9	0	0

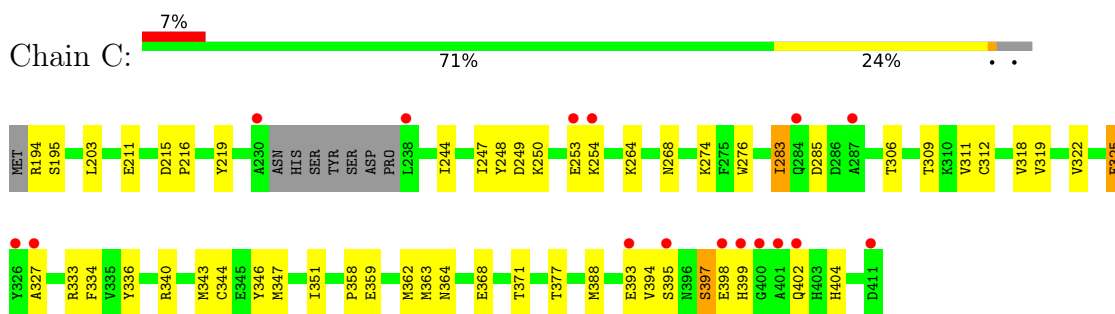
3 Residue-property plots [i](#)

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.

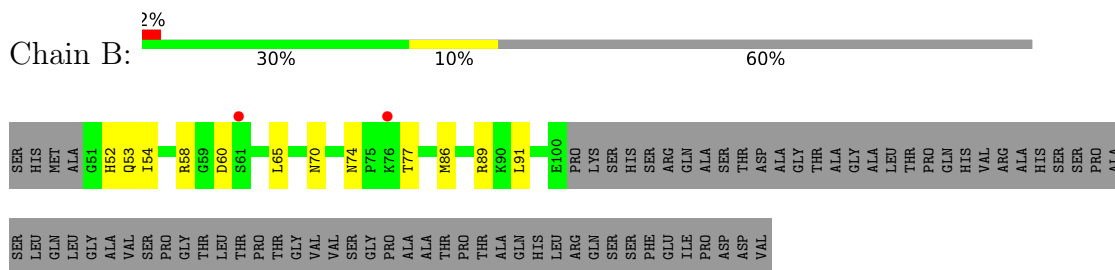
- Molecule 1: Transcriptional enhancer factor TEF-1



- Molecule 1: Transcriptional enhancer factor TEF-1

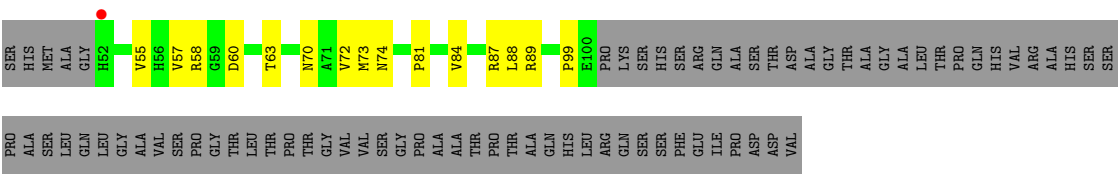


- Molecule 2: 65 kDa Yes-associated protein



- Molecule 2: 65 kDa Yes-associated protein





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	44.64Å 110.50Å 165.69Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.16 – 2.80 40.16 – 2.80	Depositor EDS
% Data completeness (in resolution range)	97.8 (40.16-2.80) 97.8 (40.16-2.80)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.50 (at 2.81Å)	Xtriage
Refinement program	PHENIX 1.18.2_3874	Depositor
R, R_{free}	0.228 , 0.266 0.239 , 0.276	Depositor DCC
R_{free} test set	1052 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	63.2	Xtriage
Anisotropy	0.623	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 67.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	4286	wwPDB-VP
Average B, all atoms (Å ²)	71.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 12.37% 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: P1L

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	0.75	0/1725	0.92	1/2321 (0.0%)
1	C	0.56	0/1749	0.82	1/2353 (0.0%)
2	B	0.62	0/405	1.00	1/550 (0.2%)
2	D	0.61	1/401 (0.2%)	0.85	1/545 (0.2%)
All	All	0.65	1/4280 (0.0%)	0.88	4/5769 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	81	PRO	C-N	-7.71	1.22	1.33

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	77	THR	CB-CA-C	-5.47	104.49	111.22
1	A	197	GLY	CA-C-O	-5.30	118.33	122.52
2	D	88	LEU	N-CA-C	-5.14	106.60	112.92
1	C	333	ARG	CB-CG-CD	5.02	122.86	111.30

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	1712	0	1688	35	0
1	C	1736	0	1717	40	0
2	B	395	0	394	11	0
2	D	391	0	391	9	0
3	A	8	0	0	0	0
3	B	8	0	0	0	0
3	C	27	0	0	1	0
3	D	9	0	0	1	0
All	All	4286	0	4190	87	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 10.

All (87) 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:210:LEU:HD11	1:A:289:ALA:HB1	1.63	0.81
1:C:203:LEU:HD22	1:C:388:MET:HE1	1.62	0.79
1:C:402:GLN:HB3	2:D:99:PRO:HD2	1.65	0.78
1:C:253:GLU:HA	1:C:253:GLU:OE1	1.86	0.74
1:C:358:PRO:HG2	1:C:362:MET:HE1	1.69	0.73
1:C:250:LYS:NZ	1:C:368:GLU:O	2.21	0.71
2:B:58:ARG:NH1	2:B:60:ASP:OD1	2.23	0.71
1:A:398:GLU:CD	1:A:398:GLU:H	2.00	0.69
1:A:312:CYS:HA	1:A:317:GLN:HA	1.74	0.69
1:A:226:HIS:HB2	1:A:229:HIS:CE1	2.32	0.64
1:C:343:MET:HE3	1:C:347:MET:HB3	1.78	0.64
1:C:283:ILE:HG22	1:C:285:ASP:OD1	1.98	0.64
1:A:196:ILE:HD12	1:A:405:ILE:HG21	1.81	0.62
2:B:70:ASN:HB2	2:B:74:ASN:OD1	2.00	0.61
1:A:299:SER:HB3	1:A:336:TYR:HE1	1.66	0.61
1:C:311:VAL:HG22	1:C:319:VAL:HB	1.84	0.60
1:A:205:GLU:HB3	1:A:296:GLN:HB3	1.84	0.59
1:A:353:LYS:NZ	2:B:65:LEU:HD23	2.18	0.58
1:C:254:LYS:N	1:C:254:LYS:HD2	2.20	0.56
2:D:60:ASP:HB2	2:D:63:THR:OG1	2.05	0.56
1:C:274:LYS:HE3	1:C:393:GLU:HB2	1.88	0.56
2:D:70:ASN:HB2	2:D:74:ASN:OD1	2.05	0.56
1:C:327:ALA:HB1	1:C:334:PHE:HB3	1.88	0.55
1:C:194:ARG:NH1	1:C:195:SER:O	2.39	0.55
1:A:327:ALA:HB1	1:A:334:PHE:HB3	1.87	0.55
1:C:343:MET:HE1	1:C:351:ILE:HD12	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:363:MET:HE2	1:C:394:VAL:HG21	1.87	0.55
1:A:212:GLN:HE22	1:A:283:ILE:HA	1.73	0.54
2:D:84:VAL:O	2:D:89:ARG:NH1	2.40	0.53
1:A:321:LYS:HD2	2:B:53:GLN:CD	2.34	0.53
2:B:53:GLN:O	2:B:53:GLN:HG2	2.08	0.52
1:C:306:THR:HB	1:C:377:THR:HG23	1.92	0.52
1:A:342:PRO:HG2	2:B:53:GLN:HE22	1.73	0.52
1:C:249:ASP:OD1	1:C:250:LYS:HG3	2.09	0.52
1:A:211:GLU:CD	1:A:340:ARG:HH12	2.17	0.52
1:A:344:P1L:H223	1:A:344:P1L:H171	1.92	0.52
1:C:268:ASN:ND2	3:C:506:HOH:O	2.42	0.52
1:C:343:MET:HG2	1:C:344:P1L:H102	1.93	0.51
1:C:318:VAL:HG11	1:C:346:TYR:CE2	2.46	0.51
2:D:70:ASN:HA	2:D:73:MET:HB2	1.93	0.50
1:C:276:TRP:HB3	1:C:395:SER:HB2	1.92	0.50
1:C:309:THR:HG21	1:C:344:P1L:H112	1.95	0.49
2:B:86:MET:HA	2:B:89:ARG:HD2	1.93	0.49
1:A:214:ARG:HA	1:A:287:ALA:HB2	1.93	0.49
1:C:211:GLU:CD	1:C:340:ARG:HH12	2.21	0.49
2:D:58:ARG:NH2	3:D:201:HOH:O	2.45	0.49
1:A:254:LYS:O	1:A:257:GLY:N	2.47	0.48
2:D:55:VAL:HG12	2:D:57:VAL:HG23	1.96	0.48
1:A:196:ILE:CD1	1:A:405:ILE:HD13	2.45	0.47
1:C:359:GLU:H	1:C:362:MET:HE3	1.78	0.47
1:C:344:P1L:H9C1	1:C:344:P1L:H	1.80	0.47
1:C:211:GLU:OE2	1:C:219:TYR:OH	2.27	0.47
1:C:276:TRP:HA	1:C:393:GLU:O	2.14	0.47
1:A:251:PHE:CZ	1:A:389:ALA:HB1	2.51	0.46
2:D:72:VAL:HG12	2:D:73:MET:HE2	1.96	0.46
1:C:249:ASP:OD2	2:D:89:ARG:NH2	2.43	0.46
1:A:222:HIS:CD2	1:A:281:CYS:HB3	2.51	0.46
1:A:298:GLU:HG2	1:A:335:VAL:HG22	1.98	0.45
2:B:86:MET:HE3	2:B:91:LEU:HD11	1.98	0.45
1:A:398:GLU:CD	1:A:398:GLU:N	2.73	0.45
1:A:276:TRP:HB3	1:A:395:SER:HB2	1.98	0.45
1:C:244:ILE:HG12	1:C:248:TYR:CE2	2.52	0.44
1:C:344:P1L:H172	1:C:344:P1L:H141	1.42	0.44
1:A:336:TYR:CD1	1:A:336:TYR:N	2.86	0.44
1:C:254:LYS:HD2	1:C:254:LYS:H	1.82	0.44
1:A:262:PHE:HE2	1:A:410:LYS:HB2	1.83	0.44
2:B:74:ASN:OD1	2:B:74:ASN:N	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:247:ILE:HD13	1:C:247:ILE:HA	1.78	0.43
1:C:397:SER:OG	1:C:398:GLU:N	2.51	0.43
1:C:336:TYR:N	1:C:336:TYR:CD1	2.86	0.43
1:A:293:VAL:HG21	1:A:344:P1L:H111	2.00	0.43
1:A:303:MET:HE3	1:A:303:MET:HB2	1.90	0.43
1:C:343:MET:HE1	1:C:351:ILE:CD1	2.49	0.42
1:C:364:ASN:OD1	1:C:394:VAL:N	2.53	0.42
1:A:318:VAL:HA	2:B:58:ARG:HE	1.85	0.42
1:A:343:MET:HE3	1:A:347:MET:HB3	2.01	0.42
1:C:359:GLU:HB2	1:C:362:MET:HE2	2.02	0.41
1:C:325:GLU:HG3	1:C:336:TYR:HB3	2.01	0.41
1:A:374:LEU:HD23	1:A:388:MET:HE2	2.02	0.41
1:A:344:P1L:H172	1:A:344:P1L:H141	1.67	0.41
1:C:215:ASP:HB2	1:C:216:PRO:HD2	2.03	0.41
1:A:215:ASP:HB2	1:C:399:HIS:HA	2.03	0.40
1:A:344:P1L:H131	1:A:347:MET:HG3	2.03	0.40
1:A:353:LYS:HZ2	2:B:65:LEU:HD23	1.84	0.40
1:C:312:CYS:HB2	1:C:371:THR:OG1	2.21	0.40
1:A:196:ILE:CD1	1:A:405:ILE:HG21	2.47	0.40
1:A:210:LEU:CD1	1:A:289:ALA:HB1	2.43	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	203/219 (93%)	191 (94%)	12 (6%)	0	100	100
1	C	206/219 (94%)	200 (97%)	6 (3%)	0	100	100
2	B	48/125 (38%)	46 (96%)	2 (4%)	0	100	100
2	D	47/125 (38%)	44 (94%)	3 (6%)	0	100	100
All	All	504/688 (73%)	481 (95%)	23 (5%)	0	100	100

There are no Ramachandran outliers to report.

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	188/198 (95%)	181 (96%)	7 (4%)	30	65
1	C	190/198 (96%)	184 (97%)	6 (3%)	34	70
2	B	45/103 (44%)	43 (96%)	2 (4%)	25	59
2	D	45/103 (44%)	44 (98%)	1 (2%)	45	78
All	All	468/602 (78%)	452 (97%)	16 (3%)	32	68

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

Mol	Chain	Res	Type
1	A	250	LYS
1	A	305	VAL
1	A	306	THR
1	A	312	CYS
1	A	318	VAL
1	A	331	ASN
1	A	343	MET
2	B	52	HIS
2	B	54	ILE
1	C	264	LYS
1	C	283	ILE
1	C	322	VAL
1	C	325	GLU
1	C	397	SER
1	C	404	HIS
2	D	87	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	212	GLN

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Mol	Chain	Res	Type
1	A	213	GLN
1	A	399	HIS
1	A	402	GLN
1	C	382	GLN
1	C	402	GLN
2	D	53	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	P1L	C	344	1	21,22,23	0.41	0	19,23,25	0.18	0
1	P1L	A	344	1	21,22,23	0.38	0	19,23,25	0.22	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
1	P1L	C	344	1	-	16/20/22/24	-
1	P1L	A	344	1	-	13/20/22/24	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (29) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	344	P1L	N-CA-CB-SG
1	A	344	P1L	C-CA-CB-SG
1	C	344	P1L	N-CA-CB-SG
1	C	344	P1L	C-CA-CB-SG
1	C	344	P1L	C7-C8-C9-C10
1	C	344	P1L	C10-C11-C12-C13
1	C	344	P1L	C14-C15-C16-C17
1	A	344	P1L	C12-C13-C14-C15
1	A	344	P1L	C14-C15-C16-C17
1	C	344	P1L	C17-C18-C19-C20
1	A	344	P1L	C11-C10-C9-C8
1	C	344	P1L	C18-C19-C20-C21
1	C	344	P1L	C13-C14-C15-C16
1	C	344	P1L	C15-C16-C17-C18
1	A	344	P1L	C17-C18-C19-C20
1	A	344	P1L	C15-C16-C17-C18
1	C	344	P1L	C11-C12-C13-C14
1	A	344	P1L	C9-C10-C11-C12
1	A	344	P1L	C19-C20-C21-C22
1	C	344	P1L	O7-C7-SG-CB
1	C	344	P1L	SG-C7-C8-C9
1	C	344	P1L	O7-C7-C8-C9
1	C	344	P1L	C8-C7-SG-CB
1	A	344	P1L	C16-C17-C18-C19
1	A	344	P1L	C7-C8-C9-C10
1	A	344	P1L	C18-C19-C20-C21
1	C	344	P1L	C12-C13-C14-C15
1	A	344	P1L	C11-C12-C13-C14
1	C	344	P1L	C11-C10-C9-C8

There are no ring outliers.

2 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	C	344	P1L	4	0
1	A	344	P1L	4	0

5.5 Carbohydrates

There are no oligosaccharides in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

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	207/219 (94%)	0.83	43 (20%) 2 2	35, 65, 113, 163	0
1	C	210/219 (95%)	0.26	16 (7%) 20 14	30, 60, 107, 148	0
2	B	50/125 (40%)	0.41	2 (4%) 42 33	45, 83, 135, 139	0
2	D	49/125 (39%)	0.07	1 (2%) 65 56	45, 75, 116, 123	0
All	All	516/688 (75%)	0.48	62 (12%) 9 6	30, 66, 123, 163	0

All (62) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	399	HIS	10.4
1	C	400	GLY	6.5
1	A	253	GLU	6.0
1	A	315	GLY	5.4
1	C	401	ALA	5.2
1	A	249	ASP	5.1
1	A	303	MET	4.9
1	A	265	GLY	4.8
1	A	254	LYS	4.6
1	C	238	LEU	4.5
1	A	331	ASN	4.3
1	C	326	TYR	4.2
1	A	399	HIS	4.0
1	A	298	GLU	3.8
1	A	197	GLY	3.8
1	A	258	LEU	3.8
1	A	196	ILE	3.6
1	A	263	GLY	3.6
1	A	317	GLN	3.4
1	A	213	GLN	3.4
1	A	199	THR	3.2

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Mol	Chain	Res	Type	RSRZ
1	A	205	GLU	3.2
1	C	254	LYS	3.2
1	A	296	GLN	3.2
1	A	252	PRO	3.1
1	A	307	CYS	3.0
1	A	202	ARG	2.8
1	A	411	ASP	2.8
1	A	286	ASP	2.8
1	A	200	LYS	2.8
1	A	304	THR	2.8
1	A	333	ARG	2.7
1	A	288	GLY	2.7
1	A	239	LEU	2.7
2	D	52	HIS	2.6
1	A	326	TYR	2.6
1	A	195	SER	2.6
1	C	284	GLN	2.6
1	A	264	LYS	2.5
1	C	253	GLU	2.4
1	A	255	LYS	2.4
1	C	327	ALA	2.4
1	A	312	CYS	2.4
2	B	76	LYS	2.4
1	C	398	GLU	2.4
2	B	61	SER	2.4
1	C	402	GLN	2.3
1	A	284	GLN	2.3
1	C	287	ALA	2.3
1	A	248	TYR	2.3
1	C	395	SER	2.2
1	A	337	ARG	2.2
1	C	411	ASP	2.2
1	A	300	SER	2.2
1	A	287	ALA	2.1
1	A	251	PHE	2.1
1	C	230	ALA	2.1
1	A	402	GLN	2.1
1	A	262	PHE	2.0
1	C	393	GLU	2.0
1	A	346	TYR	2.0
1	A	204	VAL	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($\text{\AA}^2$)	Q<0.9
1	P1L	A	344	23/24	0.88	0.23	52,79,111,124	0
1	P1L	C	344	23/24	0.91	0.18	48,61,97,148	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.