



# Full wwPDB X-ray Structure Validation Report ⓘ

May 26, 2020 – 05:57 am BST

PDB ID : 5Z2Q  
Title : Vgll1-TEAD4 core complex  
Authors : Pobbati, A.V.; Song, H.  
Deposited on : 2018-01-03  
Resolution : 2.74 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](mailto: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.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.11  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.11

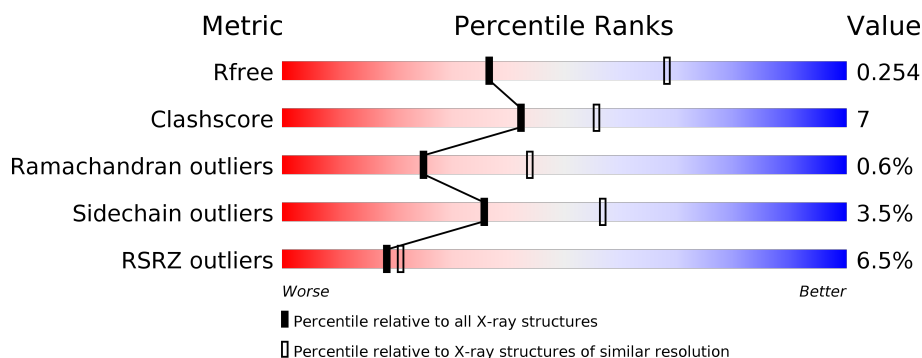
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.74 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))
$R_{free}$	130704	1271 (2.76-2.72)
Clashscore	141614	1322 (2.76-2.72)
Ramachandran outliers	138981	1297 (2.76-2.72)
Sidechain outliers	138945	1298 (2.76-2.72)
RSRZ outliers	127900	1243 (2.76-2.72)

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  $\geq 3$ , 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	C	48	<div> <div>2%</div> <div> <div></div> <div>60%</div> <div>10%</div> <div>•</div> <div>27%</div> </div> </div>
2	D	49	<div> <div>4%</div> <div> <div></div> <div>65%</div> <div>8%</div> <div>27%</div> </div> </div>
3	A	226	<div> <div>6%</div> <div> <div></div> <div>81%</div> <div>15%</div> <div>• •</div> </div> </div>
4	B	228	<div> <div>7%</div> <div> <div></div> <div>83%</div> <div>11%</div> <div>• 6%</div> </div> </div>

## 2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 4148 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 Transcription cofactor vestigial-like protein 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	C	35	Total	C	N	O	S	0	0	0
			287	183	49	54	1			

There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	6	MET	-	initiating methionine	UNP Q99NC0
C	7	GLY	-	expression tag	UNP Q99NC0
C	8	SER	-	expression tag	UNP Q99NC0
C	9	SER	-	expression tag	UNP Q99NC0
C	10	HIS	-	expression tag	UNP Q99NC0
C	11	HIS	-	expression tag	UNP Q99NC0
C	12	HIS	-	expression tag	UNP Q99NC0
C	13	HIS	-	expression tag	UNP Q99NC0
C	14	HIS	-	expression tag	UNP Q99NC0
C	15	HIS	-	expression tag	UNP Q99NC0
C	16	SER	-	expression tag	UNP Q99NC0
C	17	GLN	-	expression tag	UNP Q99NC0
C	18	ASP	-	expression tag	UNP Q99NC0
C	19	PRO	-	expression tag	UNP Q99NC0

- Molecule 2 is a protein called Transcription cofactor vestigial-like protein 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	D	36	Total	C	N	O	S	0	0	0
			294	187	53	53	1			

There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	6	MET	-	initiating methionine	UNP Q99NC0
D	7	GLY	-	expression tag	UNP Q99NC0

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Chain	Residue	Modelled	Actual	Comment	Reference
D	8	SER	-	expression tag	UNP Q99NC0
D	9	SER	-	expression tag	UNP Q99NC0
D	10	HIS	-	expression tag	UNP Q99NC0
D	11	HIS	-	expression tag	UNP Q99NC0
D	12	HIS	-	expression tag	UNP Q99NC0
D	13	HIS	-	expression tag	UNP Q99NC0
D	14	HIS	-	expression tag	UNP Q99NC0
D	15	HIS	-	expression tag	UNP Q99NC0
D	16	SER	-	expression tag	UNP Q99NC0
D	17	GLN	-	expression tag	UNP Q99NC0
D	18	ASP	-	expression tag	UNP Q99NC0
D	19	PRO	-	expression tag	UNP Q99NC0

- Molecule 3 is a protein called Transcriptional enhancer factor TEF-3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	A	219	Total	C	N	O	S	0	0	0
			1797	1155	295	337	10			

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	201	MET	-	initiating methionine	UNP Q62296
A	202	ALA	-	expression tag	UNP Q62296
A	203	ASP	-	expression tag	UNP Q62296
A	204	LEU	-	expression tag	UNP Q62296
A	205	ASN	-	expression tag	UNP Q62296
A	206	TRP	-	expression tag	UNP Q62296
A	207	ILE	-	expression tag	UNP Q62296
A	208	SER	-	expression tag	UNP Q62296
A	209	MET	-	expression tag	UNP Q62296

- Molecule 4 is a protein called Transcriptional enhancer factor TEF-3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	B	215	Total	C	N	O	S	0	0	0
			1756	1131	291	324	10			

There are 11 discrepancies between the modelled and reference sequences:

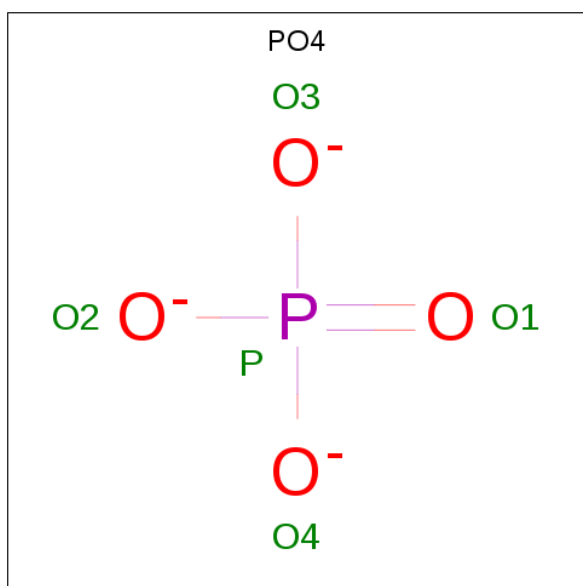
Chain	Residue	Modelled	Actual	Comment	Reference
B	199	MET	-	initiating methionine	UNP Q62296

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Chain	Residue	Modelled	Actual	Comment	Reference
B	200	ALA	-	expression tag	UNP Q62296
B	201	ASP	-	expression tag	UNP Q62296
B	202	LEU	-	expression tag	UNP Q62296
B	203	ASP	-	expression tag	UNP Q62296
B	204	LEU	-	expression tag	UNP Q62296
B	205	ASN	-	expression tag	UNP Q62296
B	206	TRP	-	expression tag	UNP Q62296
B	207	ILE	-	expression tag	UNP Q62296
B	208	SER	-	expression tag	UNP Q62296
B	209	MET	-	expression tag	UNP Q62296

- Molecule 5 is PHOSPHATE ION (three-letter code: PO4) (formula: O<sub>4</sub>P).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	B	1	Total O P 5 4 1	0	0

- Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	5	Total O 5 5	0	0
6	B	4	Total O 4 4	0	0

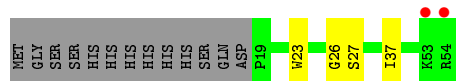
### 3 Residue-property plots [i](#)

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

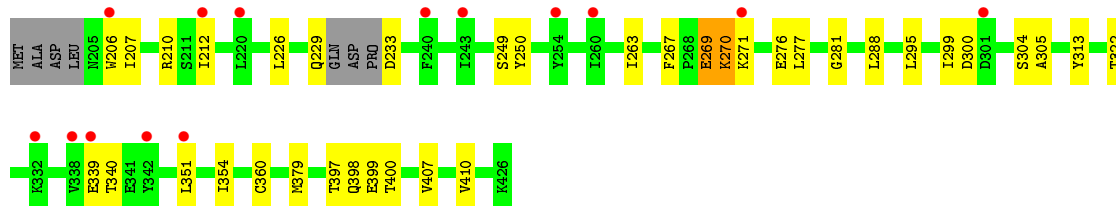
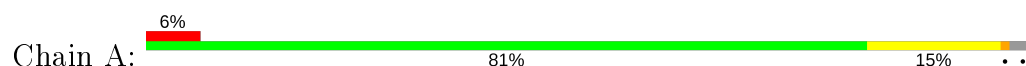
- Molecule 1: Transcription cofactor vestigial-like protein 1



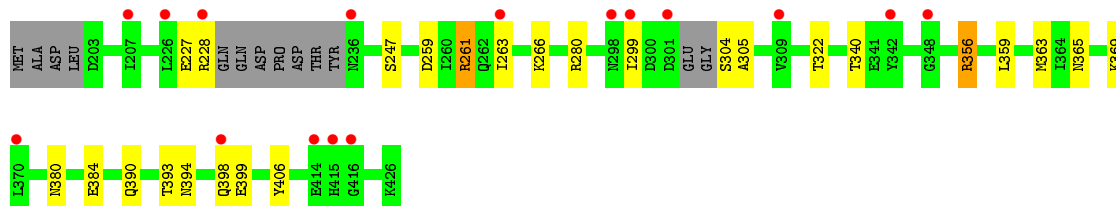
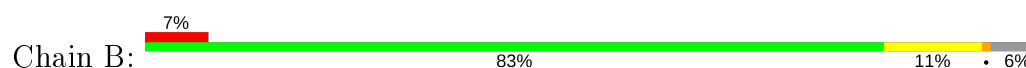
- Molecule 2: Transcription cofactor vestigial-like protein 1



- Molecule 3: Transcriptional enhancer factor TEF-3



- Molecule 4: Transcriptional enhancer factor TEF-3



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	113.93Å 113.93Å 144.36Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	98.67 – 2.74 98.67 – 2.74	Depositor EDS
% Data completeness (in resolution range)	99.7 (98.67-2.74) 94.6 (98.67-2.74)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.64 (at 2.73Å)	Xtriage
Refinement program	REFMAC 5.8.0189	Depositor
R, $R_{free}$	0.201 , 0.246 0.225 , 0.254	Depositor DCC
$R_{free}$ test set	1475 reflections (5.09%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	73.7	Xtriage
Anisotropy	0.165	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 52.7	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.025 for -h,-k,l	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	4148	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	83.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.05% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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: PO4

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	C	0.76	0/294	0.81	0/395
2	D	0.69	0/301	0.84	0/404
3	A	0.80	0/1844	0.84	0/2495
4	B	0.74	0/1801	0.88	0/2437
All	All	0.77	0/4240	0.86	0/5731

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	287	0	272	6	0
2	D	294	0	281	3	0
3	A	1797	0	1721	31	0
4	B	1756	0	1683	21	0
5	B	5	0	0	0	0
6	A	5	0	0	0	0
6	B	4	0	0	0	0
All	All	4148	0	3957	56	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 7.

All (56) 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)
3:A:322:THR:HG22	3:A:340:THR:HG22	1.30	1.07
3:A:271:LYS:HA	3:A:276:GLU:OE1	1.55	1.07
2:D:27:SER:HB3	3:A:339:GLU:HG2	1.54	0.90
4:B:322:THR:HG22	4:B:340:THR:HG22	1.59	0.82
3:A:322:THR:HG22	3:A:340:THR:CG2	2.10	0.82
1:C:38:ASN:ND2	4:B:365:ASN:HD21	1.85	0.74
2:D:27:SER:HB3	3:A:339:GLU:CG	2.17	0.73
4:B:380:ASN:O	4:B:384:GLU:HG3	1.92	0.70
3:A:379:MET:HE1	3:A:410:VAL:HG21	1.76	0.65
3:A:379:MET:CE	3:A:410:VAL:HG21	2.26	0.64
4:B:322:THR:HG22	4:B:340:THR:CG2	2.29	0.63
3:A:277:LEU:CD1	3:A:400:THR:HG21	2.29	0.63
3:A:397:THR:O	3:A:397:THR:OG1	2.16	0.63
3:A:206:TRP:O	3:A:210:ARG:NH1	2.30	0.63
4:B:394:ASN:O	4:B:398:GLN:HA	1.99	0.61
4:B:259:ASP:OD1	4:B:261:ARG:HG3	2.01	0.61
3:A:271:LYS:O	3:A:276:GLU:CD	2.42	0.58
3:A:233:ASP:OD1	3:A:233:ASP:O	2.22	0.57
3:A:322:THR:CG2	3:A:340:THR:HG22	2.20	0.57
4:B:227:GLU:CD	4:B:356:ARG:HH12	2.09	0.55
1:C:36:ASP:OD1	1:C:37:ILE:N	2.41	0.54
3:A:299:ILE:O	3:A:299:ILE:HG22	2.09	0.52
3:A:206:TRP:CD2	3:A:250:TYR:CE1	2.97	0.52
3:A:226:LEU:HD11	3:A:305:ALA:HB1	1.91	0.52
4:B:228:ARG:HG3	4:B:299:ILE:CG2	2.39	0.52
1:C:33:PHE:CD1	1:C:40:MET:HG2	2.45	0.52
4:B:322:THR:CG2	4:B:340:THR:HG22	2.36	0.51
4:B:228:ARG:HG3	4:B:299:ILE:HG23	1.92	0.50
3:A:313:TYR:O	3:A:351:LEU:HD12	2.12	0.50
3:A:267:PHE:O	3:A:269:GLU:OE2	2.31	0.48
3:A:206:TRP:CD2	3:A:250:TYR:HE1	2.32	0.48
1:C:41:VAL:HG11	4:B:369:LYS:HD2	1.95	0.47
4:B:228:ARG:HG2	4:B:305:ALA:HB2	1.96	0.47
3:A:295:LEU:HD12	3:A:379:MET:CE	2.45	0.47
3:A:226:LEU:CD1	3:A:305:ALA:HB1	2.45	0.46
4:B:394:ASN:O	4:B:398:GLN:CA	2.64	0.45
3:A:277:LEU:HD12	3:A:400:THR:HG21	1.98	0.45
3:A:271:LYS:CA	3:A:276:GLU:OE1	2.46	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:288:LEU:HD11	3:A:407:VAL:HG21	1.99	0.45
2:D:23:TRP:CH2	2:D:26:GLY:HA2	2.52	0.44
4:B:228:ARG:CD	4:B:299:ILE:HG23	2.47	0.44
3:A:207:ILE:O	3:A:207:ILE:HG22	2.17	0.44
3:A:339:GLU:OE1	3:A:354:ILE:CG2	2.65	0.44
4:B:394:ASN:O	4:B:398:GLN:N	2.50	0.44
4:B:359:LEU:HG	4:B:363:MET:HB2	2.00	0.44
3:A:397:THR:O	3:A:399:GLU:N	2.44	0.43
3:A:339:GLU:OE1	3:A:354:ILE:HG23	2.19	0.43
3:A:269:GLU:O	3:A:270:LYS:CB	2.66	0.42
3:A:379:MET:HE2	3:A:410:VAL:HG21	2.00	0.42
1:C:33:PHE:CG	1:C:40:MET:HG2	2.53	0.42
4:B:261:ARG:H	4:B:261:ARG:HG3	1.57	0.42
1:C:41:VAL:HG21	4:B:365:ASN:HB3	2.02	0.41
4:B:390:GLN:NE2	4:B:406:TYR:OH	2.53	0.41
4:B:399:GLU:HG2	4:B:399:GLU:O	2.19	0.41
4:B:393:THR:HG22	4:B:398:GLN:HA	2.03	0.40
3:A:281:GLY:HA3	3:A:400:THR:OG1	2.21	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	C	33/48 (69%)	32 (97%)	1 (3%)	0	100	100
2	D	34/49 (69%)	33 (97%)	1 (3%)	0	100	100
3	A	215/226 (95%)	206 (96%)	6 (3%)	3 (1%)	11	20
4	B	209/228 (92%)	196 (94%)	13 (6%)	0	100	100
All	All	491/551 (89%)	467 (95%)	21 (4%)	3 (1%)	25	44

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	A	270	LYS
3	A	398	GLN
3	A	212	ILE

### 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	C	31/43 (72%)	30 (97%)	1 (3%)	39	59
2	D	31/44 (70%)	30 (97%)	1 (3%)	39	59
3	A	199/208 (96%)	192 (96%)	7 (4%)	36	57
4	B	193/210 (92%)	186 (96%)	7 (4%)	35	55
All	All	454/505 (90%)	438 (96%)	16 (4%)	36	57

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

Mol	Chain	Res	Type
1	C	40	MET
2	D	37	ILE
3	A	229	GLN
3	A	249	SER
3	A	263	ILE
3	A	269	GLU
3	A	300	ASP
3	A	304	SER
3	A	360	CYS
4	B	247	SER
4	B	261	ARG
4	B	263	ILE
4	B	266	LYS
4	B	280	ARG
4	B	304	SER
4	B	356	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	C	38	ASN
4	B	385	ASN
4	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 ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

## 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

1 ligand is 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	$\# Z  > 2$
5	PO4	B	501	-	4,4,4	0.71	0	6,6,6	0.70	0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	C	35/48 (72%)	0.81	1 (2%) 51 58	57, 79, 102, 113	0
2	D	36/49 (73%)	0.95	2 (5%) 24 27	51, 82, 103, 127	0
3	A	219/226 (96%)	0.83	14 (6%) 19 22	30, 85, 120, 153	0
4	B	215/228 (94%)	0.89	16 (7%) 14 16	61, 77, 113, 145	0
All	All	505/551 (91%)	0.86	33 (6%) 18 21	30, 80, 118, 153	0

All (33) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
4	B	228	ARG	4.8
4	B	415	HIS	4.7
4	B	298	ASN	4.0
2	D	54	ARG	3.5
3	A	342	TYR	3.4
2	D	53	LYS	3.2
3	A	332	LYS	3.2
3	A	206	TRP	3.0
3	A	212	ILE	2.7
4	B	226	LEU	2.5
4	B	299	ILE	2.5
3	A	254	TYR	2.5
4	B	263	ILE	2.4
3	A	271	LYS	2.4
3	A	260	ILE	2.4
4	B	414	GLU	2.3
4	B	370	LEU	2.3
4	B	236	ASN	2.3
3	A	220	LEU	2.3
1	C	41	VAL	2.3
3	A	301	ASP	2.3

*Continued on next page...*

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Mol	Chain	Res	Type	RSRZ
4	B	398	GLN	2.2
3	A	339	GLU	2.2
4	B	348	GLY	2.2
4	B	416	GLY	2.2
4	B	342	TYR	2.1
3	A	338	VAL	2.1
4	B	301	ASP	2.1
3	A	240	PHE	2.1
4	B	309	VAL	2.1
3	A	243	ILE	2.0
3	A	351	LEU	2.0
4	B	207	ILE	2.0

## 6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

## 6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
5	PO4	B	501	5/5	0.89	0.17	104,113,127,128	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.