



# Full wwPDB X-ray Structure Validation Report ⓘ

Jul 26, 2016 – 06:24 AM EDT

PDB ID : 5CIO  
Title : Crystal structure of PqqF  
Authors : Wei, Q.; Xu, D.; Ran, T.; Wang, W.  
Deposited on : 2015-07-13  
Resolution : 2.50 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

<http://wwpdb.org/validation/2016/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	:	unknown
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20027939
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	rb-20027939

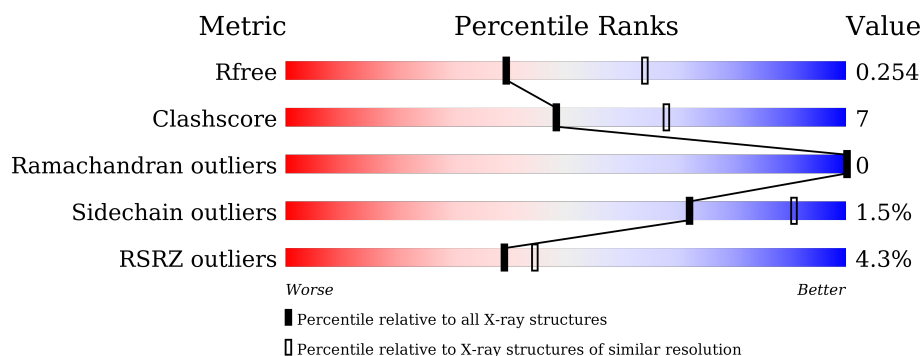
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.50 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	91344	3553 (2.50-2.50)
Clashscore	102246	4242 (2.50-2.50)
Ramachandran outliers	100387	4156 (2.50-2.50)
Sidechain outliers	100360	4158 (2.50-2.50)
RSRZ outliers	91569	3562 (2.50-2.50)

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. 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	793	<div> <div>5%</div> <div> <div></div> <div>81%</div> <div>16%</div> <div>.</div> </div> </div>
1	B	793	<div> <div>3%</div> <div> <div></div> <div>80%</div> <div>16%</div> <div>..</div> </div> </div>

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 12021 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 pyrroloquinoline quinone biosynthesis protein PqqF.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	770	Total	C	N	O	S	0	0	0
			5950	3755	1113	1065	17			
1	B	766	Total	C	N	O	S	0	0	0
			5922	3741	1105	1059	17			

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	2	Total	Zn	0	0
			2	2		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	75	Total	O	0	0
			75	75		
3	B	72	Total	O	0	0
			72	72		

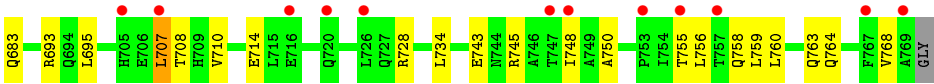
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ( $\text{RSRZ} > 2$ ). 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.

- Chain A:

81%

16%

- [illegible]



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	175.09Å 133.37Å 92.11Å 90.00° 119.40° 90.00°	Depositor
Resolution (Å)	47.51 – 2.50 47.51 – 2.50	Depositor EDS
% Data completeness (in resolution range)	99.4 (47.51-2.50) 99.4 (47.51-2.50)	Depositor EDS
$R_{merge}$	0.14	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.80 (at 2.51Å)	Xtriage
Refinement program	PHENIX (1.10.1_2155: ???)	Depositor
R, $R_{free}$	0.199 , 0.255 0.197 , 0.254	Depositor DCC
$R_{free}$ test set	3201 reflections (5.06%)	DCC
Wilson B-factor (Å <sup>2</sup> )	49.1	Xtriage
Anisotropy	0.466	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 45.3	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.064 for -h-2*k,l	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	12021	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	54.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.74% 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: ZN

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	0.52	8/6094 (0.1%)	0.64	2/8293 (0.0%)
1	B	0.46	0/6066	0.63	2/8256 (0.0%)
All	All	0.49	8/12160 (0.1%)	0.64	4/16549 (0.0%)

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	445	ARG	CZ-NH2	-9.89	1.20	1.33
1	A	445	ARG	NE-CZ	-9.79	1.20	1.33
1	A	445	ARG	CZ-NH1	-7.36	1.23	1.33
1	A	521	ARG	CZ-NH1	-7.04	1.23	1.33
1	A	521	ARG	NE-CZ	-6.74	1.24	1.33
1	A	445	ARG	CD-NE	-5.96	1.36	1.46
1	A	296	GLU	CD-OE2	-5.60	1.19	1.25
1	A	296	GLU	CD-OE1	-5.46	1.19	1.25

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	346	ARG	NE-CZ-NH2	-5.68	117.46	120.30
1	B	511	LEU	CA-CB-CG	-5.63	102.36	115.30
1	A	194	LEU	CA-CB-CG	5.44	127.81	115.30
1	A	1	MET	CG-SD-CE	5.10	108.36	100.20

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	5950	0	5881	88	1
1	B	5922	0	5862	91	1
2	A	2	0	0	0	0
3	A	75	0	0	5	0
3	B	72	0	0	2	0
All	All	12021	0	11743	173	1

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 (173) 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:B:756:LEU:HG	1:B:760:LEU:CD1	2.05	0.86
1:B:764:GLN:OE1	1:B:768:VAL:HG21	1.76	0.85
1:B:764:GLN:OE1	1:B:768:VAL:HG11	1.77	0.83
1:A:520:ASN:O	1:A:524:THR:HG23	1.79	0.82
1:B:755:THR:HG23	1:B:758:GLN:H	1.47	0.79
1:B:671:ARG:NH1	1:B:743:GLU:OE2	2.18	0.77
1:A:659:ARG:NH1	3:A:901:HOH:O	2.17	0.76
1:B:671:ARG:NH2	1:B:676:GLU:OE1	2.19	0.75
1:A:633:GLU:O	1:A:637:ARG:HG3	1.90	0.71
1:A:650:ARG:O	1:A:654:ARG:HG3	1.90	0.70
1:A:437:LEU:HD11	1:A:586:ARG:HD2	1.74	0.69
1:B:655:LEU:HD23	1:B:661:VAL:HG21	1.73	0.69
1:A:659:ARG:O	3:A:901:HOH:O	2.10	0.68
1:A:255:SER:HB3	1:B:370:HIS:CG	2.27	0.68
1:B:293:ARG:NH2	3:B:901:HOH:O	2.26	0.68
1:A:667:CYS:SG	1:A:678:LEU:HD21	2.34	0.68
1:A:123:ILE:HG23	1:A:166:PHE:HD2	1.59	0.68
1:A:342:GLN:OE1	1:B:6:SER:OG	2.08	0.67
1:A:121:GLN:HG2	1:A:660:ASN:HD21	1.58	0.66
1:A:756:LEU:CD2	1:A:760:LEU:HG	2.25	0.66
1:A:756:LEU:HD23	1:A:760:LEU:HG	1.75	0.66
1:A:293:ARG:NH2	3:A:902:HOH:O	2.29	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:186:ARG:HD3	1:A:217:GLY:O	1.97	0.65
1:A:346:ARG:HH22	1:A:489:GLU:CD	1.99	0.65
1:B:708:THR:HG22	1:B:760:LEU:HD21	1.77	0.64
1:A:582:GLU:CD	1:A:585:ARG:HH12	2.01	0.64
1:B:138:GLU:OE1	1:B:245:ARG:NH2	2.30	0.64
1:A:758:GLN:HA	1:A:761:HIS:HB3	1.80	0.63
1:B:346:ARG:HH22	1:B:489:GLU:CD	2.01	0.63
1:B:432:LEU:HD21	1:B:511:LEU:HA	1.80	0.62
1:A:707:LEU:HD23	1:A:760:LEU:HD23	1.81	0.61
1:B:116:ALA:O	1:B:170:ILE:HD11	2.00	0.61
1:A:413:GLY:HA2	3:A:930:HOH:O	2.02	0.60
1:B:55:PHE:CE1	1:B:78:LEU:HD21	2.36	0.60
1:B:620:GLU:OE2	1:B:683:GLN:NE2	2.35	0.60
1:B:756:LEU:HG	1:B:760:LEU:HD12	1.80	0.60
1:A:437:LEU:HD11	1:A:586:ARG:CD	2.32	0.60
1:B:260:ARG:HG2	1:B:344:ALA:HB1	1.84	0.59
1:A:528:PRO:O	1:A:532:ASN:ND2	2.34	0.59
1:B:633:GLU:O	1:B:637:ARG:HG3	2.03	0.59
1:B:102:LEU:HD11	1:B:194:LEU:HD21	1.85	0.58
1:B:346:ARG:NH2	1:B:489:GLU:OE2	2.30	0.57
1:B:432:LEU:HD11	1:B:514:HIS:ND1	2.19	0.57
1:A:124:GLU:OE1	1:A:163:ARG:NH2	2.38	0.57
1:A:553:ARG:NH1	1:A:616:GLU:OE2	2.38	0.57
1:B:764:GLN:OE1	1:B:768:VAL:CG2	2.52	0.56
1:A:120:ALA:HB2	1:A:170:ILE:HD12	1.88	0.56
1:A:659:ARG:O	1:A:659:ARG:HG3	2.06	0.56
1:B:756:LEU:O	1:B:760:LEU:HD12	2.05	0.55
1:B:707:LEU:O	1:B:710:VAL:HG12	2.07	0.55
1:B:98:LEU:HD23	1:B:206:LEU:HD13	1.88	0.55
1:A:121:GLN:CG	1:A:660:ASN:HD21	2.19	0.55
1:A:346:ARG:NH1	1:A:489:GLU:OE1	2.39	0.55
1:A:524:THR:OG1	1:A:525:ALA:N	2.39	0.55
1:B:119:ILE:O	1:B:123:ILE:HG13	2.06	0.55
1:B:421:GLU:HG2	1:B:422:PRO:HD2	1.89	0.54
1:A:-6:ARG:HH21	1:B:77:ARG:HD3	1.72	0.54
1:A:678:LEU:HD23	1:A:679:LEU:N	2.23	0.54
1:B:764:GLN:OE1	1:B:768:VAL:CG1	2.53	0.54
1:A:54:LEU:HD12	1:A:89:PHE:CZ	2.43	0.53
1:B:190:MET:HE1	1:B:214:LEU:HD22	1.90	0.53
1:A:201:GLU:HG3	1:B:507:GLY:HA2	1.91	0.53
1:A:626:PHE:O	1:A:628:PRO:HD3	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:114:LEU:HD12	1:B:178:ARG:HG3	1.90	0.53
1:B:654:ARG:O	1:B:659:ARG:HG3	2.09	0.53
1:A:754:ILE:HG23	1:A:758:GLN:HG2	1.90	0.52
1:A:678:LEU:HD23	1:A:679:LEU:H	1.74	0.52
1:B:426:PHE:HZ	1:B:429:SER:HB3	1.75	0.52
1:A:385:ARG:O	1:A:386:ARG:HD3	2.10	0.52
1:A:466:LEU:HD13	1:A:572:TRP:HZ2	1.74	0.52
1:A:446:HIS:CE1	1:A:584:LYS:HB2	2.44	0.51
1:B:54:LEU:HD12	1:B:89:PHE:CZ	2.45	0.51
1:A:754:ILE:CG2	1:A:758:GLN:HG2	2.39	0.51
1:B:157:ARG:NH1	3:B:903:HOH:O	2.27	0.50
1:A:764:GLN:O	1:A:768:VAL:HG22	2.11	0.50
1:A:55:PHE:CE1	1:A:78:LEU:HD21	2.47	0.50
1:B:252:HIS:CD2	1:B:293:ARG:HD2	2.47	0.50
1:A:722:LEU:O	1:A:726:LEU:HG	2.12	0.49
1:A:756:LEU:CD2	1:A:760:LEU:CD1	2.91	0.49
1:A:594:PHE:CD2	1:A:598:ILE:HD11	2.47	0.49
1:A:466:LEU:HD13	1:A:572:TRP:CZ2	2.48	0.49
1:B:624:LEU:HD11	1:B:679:LEU:HD11	1.94	0.49
1:A:44:PRO:HB2	1:A:165:ALA:HB1	1.95	0.48
1:A:756:LEU:CD2	1:A:760:LEU:CG	2.90	0.48
1:A:260:ARG:HG2	1:A:344:ALA:HB1	1.95	0.48
1:A:766:LEU:HD23	1:A:767:PHE:CZ	2.48	0.48
1:B:252:HIS:NE2	1:B:293:ARG:HD2	2.29	0.48
1:A:624:LEU:HD11	1:A:679:LEU:HD11	1.96	0.48
1:A:128:ALA:HB1	1:A:685:PRO:HG3	1.96	0.47
1:A:756:LEU:HD22	1:A:760:LEU:CD1	2.44	0.47
1:B:432:LEU:CD2	1:B:511:LEU:HA	2.43	0.47
1:B:637:ARG:HH21	1:B:748:ILE:CG1	2.27	0.47
1:A:703:MET:O	1:A:707:LEU:HB2	2.14	0.47
1:A:756:LEU:HD23	1:A:756:LEU:O	2.14	0.47
1:A:764:GLN:HG3	1:A:768:VAL:HG21	1.97	0.47
1:B:432:LEU:HD12	1:B:433:PRO:HD2	1.96	0.47
1:B:609:HIS:O	1:B:630:GLN:NE2	2.47	0.47
1:B:631:SER:OG	1:B:632:ASP:N	2.48	0.47
1:B:479:ARG:NH2	1:B:533:GLU:OE2	2.38	0.47
1:A:68:MET:HA	1:A:78:LEU:HD13	1.97	0.47
1:A:327:GLN:O	1:A:330:ASN:HB2	2.16	0.46
1:B:78:LEU:HD23	1:B:78:LEU:C	2.36	0.46
1:B:471:ALA:HA	1:B:474:LEU:HD12	1.98	0.46
1:B:631:SER:HG	1:B:633:GLU:H	1.57	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:72:GLN:NE2	1:B:652:PHE:CD1	2.83	0.46
1:A:611:PRO:HA	1:A:628:PRO:HD3	1.98	0.46
1:A:551:ILE:HG13	1:B:-9:LEU:HD13	1.98	0.46
1:B:71:THR:HG21	1:B:78:LEU:HB2	1.98	0.46
1:A:638:TRP:CH2	1:A:722:LEU:HB3	2.51	0.46
1:B:199:SER:OG	1:B:202:GLN:HG3	2.17	0.45
1:B:728:ARG:O	1:B:745:ARG:NH2	2.47	0.45
1:A:245:ARG:HG2	1:A:304:ILE:HG23	1.98	0.45
1:A:573:HIS:NE2	1:A:602:PRO:HD2	2.32	0.45
1:A:756:LEU:HD22	1:A:760:LEU:HD11	1.99	0.45
1:B:5:ALA:HB2	1:B:200:LEU:HD13	1.96	0.45
1:B:710:VAL:HG23	1:B:714:GLU:OE1	2.16	0.45
1:A:346:ARG:O	1:A:350:ARG:HG3	2.16	0.45
1:B:559:PRO:O	1:B:563:ASN:ND2	2.49	0.45
1:B:461:SER:OG	1:B:571:TYR:O	2.26	0.45
1:A:312:ALA:HB2	1:A:412:VAL:HG12	1.98	0.45
1:A:346:ARG:NH2	1:A:489:GLU:OE2	2.49	0.45
1:B:228:LEU:HD12	1:B:300:LEU:HD21	1.98	0.45
1:B:527:PRO:O	1:B:531:ILE:HD12	2.16	0.45
1:B:748:ILE:C	1:B:750:ALA:N	2.70	0.45
1:A:152:PHE:CD2	1:A:225:LEU:HD22	2.52	0.45
1:B:653:GLN:O	1:B:657:VAL:HG22	2.17	0.45
1:B:728:ARG:HE	1:B:728:ARG:HB3	1.64	0.44
1:B:756:LEU:HG	1:B:760:LEU:HD11	1.97	0.44
1:A:652:PHE:CZ	1:A:656:ARG:HG2	2.52	0.44
1:B:237:SER:HA	1:B:391:LEU:O	2.17	0.44
1:A:327:GLN:HG3	1:A:381:MET:HE3	1.99	0.44
1:A:71:THR:HG21	1:A:78:LEU:HB2	2.00	0.44
1:B:512:ILE:HG22	1:B:587:LEU:HD21	2.00	0.44
1:B:90:PHE:HD2	1:B:354:LEU:HD11	1.82	0.44
1:A:498:GLN:HB2	3:A:915:HOH:O	2.18	0.44
1:B:346:ARG:NH1	1:B:489:GLU:OE1	2.39	0.44
1:B:432:LEU:HD13	1:B:488:ARG:HD3	2.00	0.43
1:A:2:THR:O	1:A:3:LEU:HD23	2.18	0.43
1:B:72:GLN:NE2	1:B:652:PHE:CG	2.86	0.43
1:A:275:LEU:HD23	1:A:275:LEU:HA	1.80	0.43
1:B:145:GLN:OE1	1:B:245:ARG:HD3	2.18	0.43
1:A:337:LEU:HD21	1:A:373:TRP:CD1	2.54	0.43
1:B:475:GLN:O	1:B:479:ARG:HB2	2.19	0.43
1:B:655:LEU:HD21	1:B:695:LEU:HB3	2.01	0.43
1:A:502:LEU:HD11	1:A:742:LEU:HD11	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:647:TYR:OH	1:B:763:GLN:NE2	2.47	0.42
1:A:723:GLN:O	1:A:727:GLN:HG2	2.18	0.42
1:A:756:LEU:CD2	1:A:760:LEU:HD11	2.49	0.42
1:B:93:VAL:HG23	1:B:94:GLY:O	2.19	0.42
1:A:114:LEU:HD12	1:A:178:ARG:HG2	2.01	0.42
1:A:654:ARG:NH1	1:A:702:GLN:OE1	2.51	0.42
1:B:401:ILE:HB	1:B:406:LEU:HD12	2.02	0.42
1:B:457:LEU:CD2	1:B:504:GLN:HG2	2.50	0.42
1:B:756:LEU:O	1:B:760:LEU:CD1	2.67	0.42
1:A:688:THR:OG1	1:A:691:GLN:HG3	2.20	0.42
1:B:525:ALA:O	1:B:527:PRO:HD3	2.19	0.42
1:B:637:ARG:NH2	1:B:748:ILE:HD11	2.35	0.42
1:A:764:GLN:NE2	1:A:768:VAL:HG11	2.35	0.42
1:A:715:LEU:HD21	1:A:719:GLN:HE21	1.84	0.41
1:B:643:LEU:HG	1:B:759:LEU:HD11	2.00	0.41
1:A:-6:ARG:HH21	1:B:77:ARG:CD	2.33	0.41
1:B:550:ALA:O	1:B:554:LEU:HG	2.20	0.41
1:B:488:ARG:O	1:B:489:GLU:HB2	2.19	0.41
1:B:132:LEU:HD22	1:B:663:TYR:CE1	2.55	0.41
1:B:663:TYR:HD1	1:B:664:VAL:HG23	1.85	0.41
1:A:100:GLU:O	1:A:103:ALA:HB3	2.20	0.41
1:A:743:GLU:O	1:A:744:ASN:HB2	2.20	0.41
1:A:542:GLN:O	1:A:546:GLN:HG2	2.20	0.41
1:B:148:MET:CE	1:B:388:LEU:HB2	2.51	0.41
1:B:491:HIS:CG	1:B:734:LEU:HD11	2.57	0.40
1:B:558:LEU:HB3	1:B:559:PRO:HD3	2.03	0.40
1:B:609:HIS:HA	1:B:610:PRO:HD3	1.95	0.40
1:A:119:ILE:O	1:A:122:GLU:N	2.55	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:213:GLY:CA	1:B:693:ARG:NH2[4_748]	2.15	0.05

## 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	762/793 (96%)	719 (94%)	43 (6%)	0	100	100
1	B	758/793 (96%)	732 (97%)	26 (3%)	0	100	100
All	All	1520/1586 (96%)	1451 (96%)	69 (4%)	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	595/616 (97%)	586 (98%)	9 (2%)	72	91
1	B	593/616 (96%)	584 (98%)	9 (2%)	72	91
All	All	1188/1232 (96%)	1170 (98%)	18 (2%)	72	91

All (18) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	296	GLU
1	A	358	ARG
1	A	437	LEU
1	A	571	TYR
1	A	609	HIS
1	A	630	GLN
1	A	671	ARG
1	A	701	GLN

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Mol	Chain	Res	Type
1	A	732	GLU
1	B	-4	SER
1	B	96	ASP
1	B	138	GLU
1	B	147	GLN
1	B	369	GLN
1	B	511	LEU
1	B	548	ASP
1	B	663	TYR
1	B	707	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	121	GLN
1	A	660	ASN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

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

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, 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	A	770/793 (97%)	0.27	40 (5%) 31 35	29, 53, 93, 105	0
1	B	766/793 (96%)	0.13	26 (3%) 49 54	28, 48, 86, 102	0
All	All	1536/1586 (96%)	0.20	66 (4%) 39 44	28, 51, 91, 105	0

All (66) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	754	ILE	5.3
1	A	756	LEU	5.3
1	A	707	LEU	5.0
1	A	445	ARG	4.4
1	B	769	ALA	4.2
1	A	748	ILE	4.1
1	A	751	ALA	4.1
1	A	713	GLY	3.8
1	A	769	ALA	3.7
1	A	571	TYR	3.7
1	A	440	GLY	3.5
1	A	718	THR	3.4
1	A	712	VAL	3.4
1	A	750	ALA	3.3
1	A	768	VAL	3.3
1	A	463	HIS	3.2
1	A	528	PRO	3.2
1	A	726	LEU	3.2
1	A	522	ALA	3.1
1	A	757	THR	3.1
1	A	596	TYR	3.0
1	A	720	GLN	3.0
1	A	758	GLN	3.0
1	B	757	THR	2.9

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Mol	Chain	Res	Type	RSRZ
1	B	707	LEU	2.9
1	B	399	ARG	2.8
1	A	419	THR	2.8
1	B	753	PRO	2.7
1	A	397	GLU	2.7
1	B	571	TYR	2.7
1	A	439	ALA	2.6
1	B	720	GLN	2.6
1	B	528	PRO	2.6
1	A	603	GLN	2.5
1	B	748	ILE	2.5
1	A	449	PRO	2.5
1	A	418	PRO	2.5
1	A	686	THR	2.5
1	B	661	VAL	2.4
1	A	727	GLN	2.4
1	A	705	HIS	2.4
1	B	663	TYR	2.4
1	A	762	TRP	2.4
1	A	722	LEU	2.4
1	B	716	GLU	2.3
1	A	576	LEU	2.3
1	B	396	GLY	2.3
1	A	642	VAL	2.3
1	B	755	THR	2.3
1	B	635	GLU	2.3
1	B	463	HIS	2.2
1	B	633	GLU	2.2
1	A	755	THR	2.2
1	B	705	HIS	2.2
1	A	759	LEU	2.2
1	B	395	GLY	2.2
1	B	529	ALA	2.1
1	B	-7	PRO	2.1
1	B	168	SER	2.1
1	B	747	THR	2.0
1	B	767	PHE	2.0
1	A	752	ALA	2.0
1	A	446	HIS	2.0
1	A	451	GLU	2.0
1	B	726	LEU	2.0
1	B	449	PRO	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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 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	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
2	ZN	A	801	1/1	0.99	0.14	-	53,53,53,53	0
2	ZN	A	802	1/1	0.95	0.16	-	54,54,54,54	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.