WORLDWIDE wwPDB PROTEIN DATA BANK

Full wwPDB X-ray Structure Validation Report (i)

Sep 12, 2023 – 10:24 AM EDT

PDB ID	:	4OHL
Title	:	LEOPARD Syndrome-Associated SHP2/T468M mutant
Authors	:	Yu, Z.H.; Zhang, R.Y.; Walls, C.D.; Chen, L.; Zhang, S.; Wu, L.; Wang, L.; Liu, S.; Zhang, Z.Y.
Deposited on	:	2014-01-17
Resolution	:	2.40 Å(reported)

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

|		
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.35.1
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)	:	2.35.1

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 2.40 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	Percentile Ranks	Value
Rfree		0.258
Clashscore		8
Ramachandran outliers		1.2%
Sidechain outliers		4.6%
RSRZ outliers		3.8%

Worse ..... *Better*

▮ Percentile relative to all X-ray structures
▯ Percentile relative to X-ray structures of similar resolution
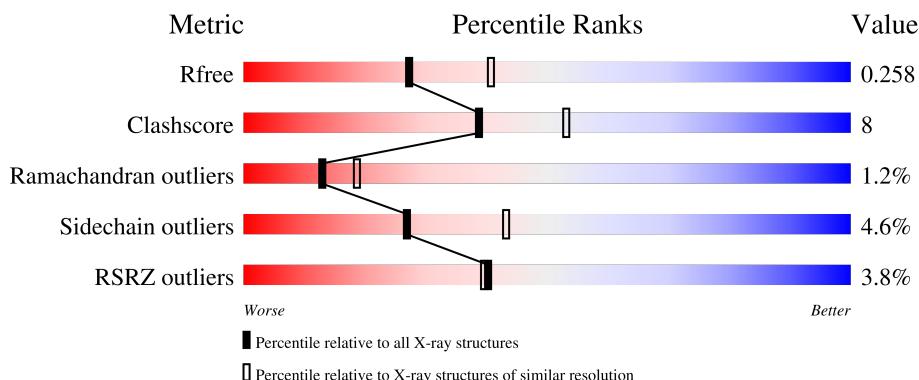
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R$_{free}$	130704	3907 (2.40-2.40)
Clashscore	141614	4398 (2.40-2.40)
Ramachandran outliers	138981	4318 (2.40-2.40)
Sidechain outliers	138945	4319 (2.40-2.40)
RSRZ outliers	127900	3811 (2.40-2.40)

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 <=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	536	3% — 69% 20% · 10%
1	B	536	4% — 71% 18% · 10%

WORLDWIDE PDB
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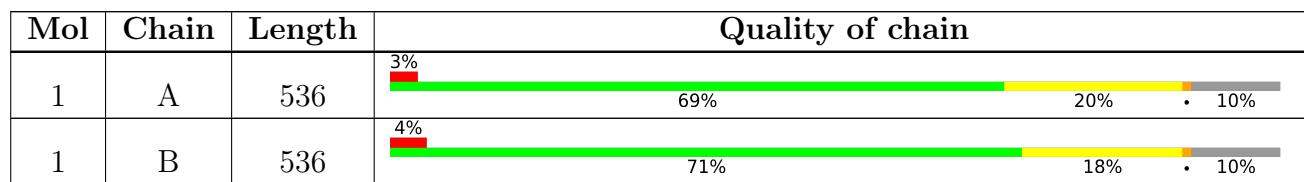
2 Entry composition ⓘ

There are 2 unique types of molecules in this entry. The entry contains 8154 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 Tyrosine-protein phosphatase non-receptor type 11.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	484	Total	C	N	O	S	0	0	0
			3912	2465	698	730	19			
1	B	485	Total	C	N	O	S	0	0	1
			3912	2464	699	730	19			

There are 26 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	GLN	deletion	UNP Q06124
A	?	-	ALA	deletion	UNP Q06124
A	?	-	LEU	deletion	UNP Q06124
A	?	-	LEU	deletion	UNP Q06124
A	468	MET	THR	engineered mutation	UNP Q06124
A	529	LEU	-	expression tag	UNP Q06124
A	530	GLU	-	expression tag	UNP Q06124
A	531	HIS	-	expression tag	UNP Q06124
A	532	HIS	-	expression tag	UNP Q06124
A	533	HIS	-	expression tag	UNP Q06124
A	534	HIS	-	expression tag	UNP Q06124
A	535	HIS	-	expression tag	UNP Q06124
A	536	HIS	-	expression tag	UNP Q06124
B	?	-	GLN	deletion	UNP Q06124
B	?	-	ALA	deletion	UNP Q06124
B	?	-	LEU	deletion	UNP Q06124
B	?	-	LEU	deletion	UNP Q06124
B	468	MET	THR	engineered mutation	UNP Q06124
B	529	LEU	-	expression tag	UNP Q06124
B	530	GLU	-	expression tag	UNP Q06124
B	531	HIS	-	expression tag	UNP Q06124
B	532	HIS	-	expression tag	UNP Q06124
B	533	HIS	-	expression tag	UNP Q06124
B	534	HIS	-	expression tag	UNP Q06124
B	535	HIS	-	expression tag	UNP Q06124

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Chain	Residue	Modelled	Actual	Comment	Reference
B	536	HIS	-	expression tag	UNP Q06124

• Molecule 2 is water.

| Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	183	Total O 183 183	0	0
2	B	147	Total O 147 147	0	0

3 Residue-property plots ⓘ

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density (RSRZ > 2). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: Tyrosine-protein phosphatase non-receptor type 11

Chain A:

• Molecule 1: Tyrosine-protein phosphatase non-receptor type 11

Chain B:
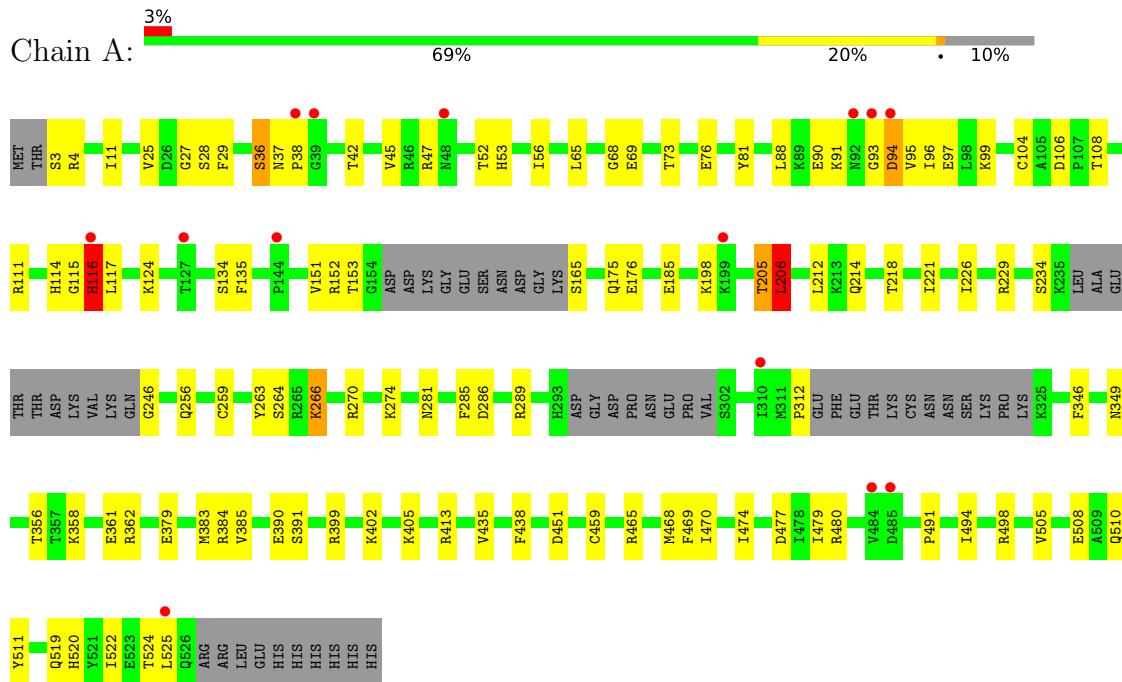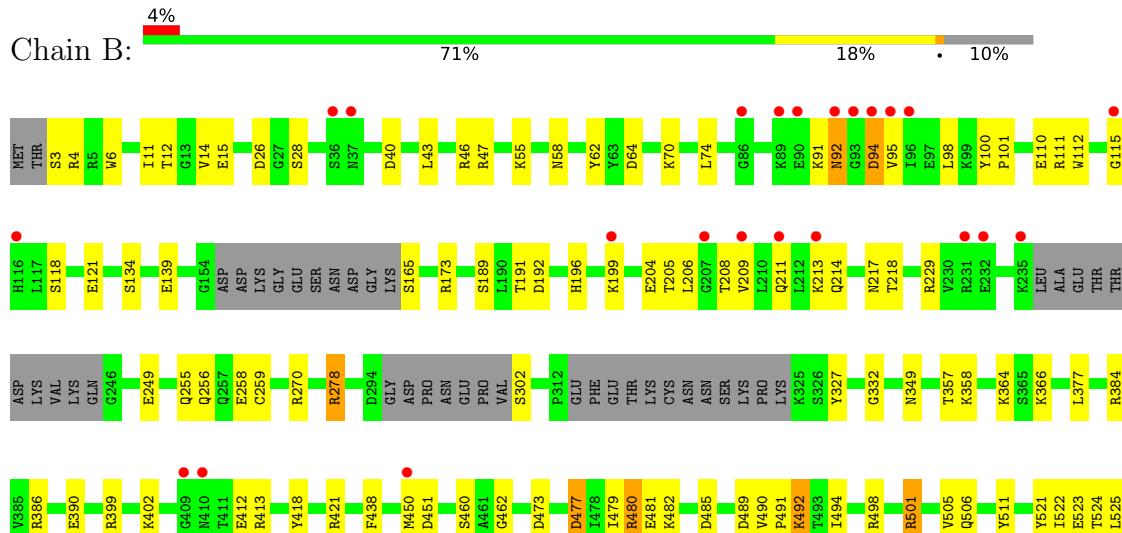
Q526 ARG ARG LEU GLU HIS HIS HIS HIS HIS HIS

4 Data and refinement statistics ⓘ

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	45.34Å 209.26Å 56.08Å 90.00° 95.89° 90.00°	Depositor
Resolution (Å)	33.01 – 2.40 33.01 – 2.38	Depositor EDS
% Data completeness (in resolution range)	94.5 (33.01-2.40) 93.1 (33.01-2.38)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	0.09	Depositor
$< I/\sigma(I) >$ [1]	2.61 (at 2.36Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7.3_928)	Depositor
R, R_{free}	0.191 , 0.259 0.189 , 0.258	Depositor DCC
R_{free} test set	1889 reflections (4.88%)	wwPDB-VP
Wilson B-factor (Å^2)	34.8	Xtriage
Anisotropy	0.491	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.40 , 64.1	EDS
L-test for twinning[2]	$< |L| > = 0.47, < L^2 > = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	8154	wwPDB-VP
Average B, all atoms (Å^2)	41.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.73% of the height of the origin peak. No significant pseudotranslation is detected.*

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[1]Intensities estimated from amplitudes.
[2]Theoretical values of $< |L| >$, $< L^2 >$ 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 ⓘ

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	0.44	0/3993	0.58	0/5385
1	B	0.42	0/3993	0.58	1/5385 (0.0%)
All	All	0.43	0/7986	0.58	1/10770 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	501	ARG	NE-CZ-NH1	5.37	122.99	120.30

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	3912	0	3847	57	0
1	B	3912	0	3846	60	0
2	A	183	0	0	10	0
2	B	147	0	0	9	0
All	All	8154	0	7693	117	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 8.

All (117) 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:205:THR:HG23	1:B:206:LEU:HD22	1.70	0.73
1:B:94:ASP:OD1	1:B:94:ASP:N	2.25	0.68
1:B:196:HIS:HA	1:B:199:LYS:HE2	1.74	0.68
1:B:390:GLU:HG2	1:B:399:ARG:HG2	1.77	0.66
1:A:399:ARG:NE	2:A:685:HOH:O	2.29	0.65
1:B:477:ASP:HA	1:B:480:ARG:HG2	1.81	0.63
1:B:4:ARG:HG2	1:B:259:CYS:SG	2.39	0.62
1:A:65:LEU:HD12	1:A:68:GLY:HA3	1.80	0.61
1:A:3:SER:N	1:A:259:CYS:HG	1.97	0.61
1:B:58:ASN:ND2	1:B:506:GLN:OE1	2.26	0.60
1:A:312:PRO:HB3	1:A:474:ILE:HD13	1.84	0.59
1:B:278:ARG:NH1	1:B:332:GLY:O	2.35	0.59
1:A:90:GLU:N	1:A:94:ASP:O	2.29	0.59
1:B:189:SER:OG	1:B:192:ASP:OD2	2.19	0.59
1:B:270:ARG:NH1	2:B:630:HOH:O	2.28	0.59
1:B:377:LEU:HD13	1:B:386:ARG:HB3	1.83	0.59
1:A:99:LYS:NZ	2:A:768:HOH:O	2.37	0.58
1:A:256:GLN:NE2	2:A:689:HOH:O	2.37	0.57
1:A:111:ARG:NH1	2:A:758:HOH:O	2.33	0.57
1:A:520:HIS:O	1:A:524:THR:HG23	2.04	0.56
1:A:390:GLU:HG2	1:A:399:ARG:HG2	1.87	0.56
2:A:768:HOH:O	1:B:173:ARG:NH1	2.38	0.56
1:B:209:VAL:HG12	1:B:211:GLN:HG3	1.87	0.56
1:B:421:ARG:NH2	2:B:619:HOH:O	2.38	0.56
1:B:3:SER:OG	2:B:729:HOH:O	2.18	0.56
1:B:62:TYR:OH	1:B:364:LYS:NZ	2.37	0.55
1:A:399:ARG:NH2	2:A:685:HOH:O	2.40	0.55
1:B:218:THR:O	1:B:229:ARG:NH2	2.27	0.55
1:A:246:GLY:N	2:A:704:HOH:O	2.40	0.55
1:B:12:THR:HG22	1:B:14:VAL:H	1.73	0.54
1:A:134:SER:HA	1:A:214:GLN:O	2.07	0.54
1:B:64:ASP:OD1	2:B:637:HOH:O	2.18	0.54
1:B:3:SER:HB3	1:B:256:GLN:HG3	1.88	0.54
1:A:264:SER:HB2	1:A:266:LYS:CD	2.38	0.53
1:A:114:HIS:CE1	1:A:218:THR:HG21	2.43	0.53
1:B:349:ASN:ND2	1:B:451:ASP:O	2.40	0.53
1:A:379:GLU:HG2	1:A:384:ARG:HG3	1.90	0.52
1:B:480:ARG:NH2	2:B:737:HOH:O	2.43	0.52
1:B:115:GLY:HA2	1:B:139:GLU:HG3	1.92	0.52
1:B:4:ARG:HD3	1:B:258:GLU:HG2	1.92	0.51
1:B:110:GLU:OE1	1:B:112:TRP:NE1	2.43	0.51
1:A:385:VAL:HA	1:A:402:LYS:O	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:327:TYR:OH	1:B:473:ASP:OD2	2.21	0.51
1:A:205:THR:O	1:A:206:LEU:HB2	2.09	0.51
1:A:346:PHE:CE2	1:A:405:LYS:HE3	2.46	0.50
1:A:361:GLU:OE1	1:A:465:ARG:NH2	2.36	0.50
1:A:97:GLU:HG2	2:A:756:HOH:O	2.10	0.50
1:B:118:SER:HB3	1:B:121:GLU:HG3	1.94	0.50
1:B:489:ASP:OD1	1:B:491:PRO:HD2	2.12	0.50
1:B:6:TRP:HB3	1:B:101:PRO:HB3	1.93	0.50
1:B:479:ILE:HD13	1:B:522:ILE:HD11	1.93	0.50
1:A:56:ILE:HG12	1:A:65:LEU:HD23	1.93	0.49
1:A:135:PHE:HB3	1:A:151:VAL:HG13	1.92	0.49
1:A:264:SER:HB2	1:A:266:LYS:HD3	1.94	0.49
1:B:366:LYS:HD2	1:B:460:SER:HB3	1.94	0.49
1:A:356:THR:OG1	1:A:459:CYS:HB3	2.12	0.49
1:B:26:ASP:HA	1:B:46:ARG:HG2	1.93	0.49
1:B:62:TYR:CE1	1:B:70:LYS:HD3	2.48	0.49
1:A:205:THR:O	1:A:205:THR:OG1	2.29	0.48
1:B:249:GLU:N	1:B:249:GLU:OE1	2.46	0.48
1:A:494:ILE:O	1:A:498:ARG:HG3	2.15	0.47
1:B:364:LYS:HE2	1:B:364:LYS:HB3	1.64	0.47
1:B:386:ARG:HG2	1:B:402:LYS:HB2	1.96	0.47
1:A:470:ILE:O	1:A:474:ILE:HG13	2.14	0.47
1:A:4:ARG:HG2	1:A:259:CYS:SG	2.55	0.47
1:A:25:VAL:H	1:A:28:SER:HG	1.61	0.47
1:B:191:THR:OG1	2:B:641:HOH:O	2.20	0.46
1:B:217:ASN:ND2	1:B:492:LYS:HE3	2.30	0.46
1:A:90:GLU:HB3	1:A:91:LYS:H	1.57	0.46
1:B:491:PRO:HG3	1:B:511:TYR:OH	2.15	0.45
1:A:358:LYS:NZ	2:A:767:HOH:O	2.25	0.45
1:A:399:ARG:CZ	2:A:685:HOH:O	2.64	0.45
1:B:204:GLU:HB2	1:B:208:THR:HB	1.98	0.45
1:A:152:ARG:HG2	1:A:153:THR:N	2.31	0.45
1:A:491:PRO:HG3	1:A:511:TYR:OH	2.16	0.45
1:B:473:ASP:OD1	2:B:737:HOH:O	2.21	0.45
1:A:198:LYS:HG2	1:A:212:LEU:HB2	1.99	0.45
1:B:134:SER:HA	1:B:214:GLN:O	2.16	0.45
1:A:479:ILE:HD13	1:A:522:ILE:HD11	1.99	0.45
1:B:134:SER:OG	1:B:214:GLN:NE2	2.49	0.45
1:A:27:GLY:HA3	1:A:99:LYS:HD2	1.97	0.44
1:B:357:THR:HG22	2:B:720:HOH:O	2.16	0.44
1:A:106:ASP:OD1	1:A:108:THR:HG23	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:42:THR:HG21	1:A:53:HIS:HB3	1.99	0.43
1:A:69:GLU:HG2	1:A:281:ASN:OD1	2.17	0.43
1:A:270:ARG:O	1:A:274:LYS:HG3	2.17	0.43
1:B:28:SER:HA	1:B:100:TYR:O	2.18	0.43
1:B:211:GLN:NE2	1:B:213:LYS:HE2	2.33	0.43
1:A:263:TYR:HB2	1:A:285:PHE:CD1	2.53	0.43
1:B:418:TYR:HB3	1:B:438:PHE:CE1	2.54	0.43
1:B:40:ASP:HB3	1:B:55:LYS:HE2	2.01	0.43
1:B:462:GLY:O	1:B:501:ARG:HD3	2.18	0.43
1:B:481:GLU:HG3	1:B:482:LYS:N	2.34	0.43
1:B:43:LEU:HD21	1:B:98:LEU:HD11	2.01	0.43
1:A:383:MET:HE1	1:A:405:LYS:HG2	2.01	0.43
1:A:29:PHE:HB3	1:A:45:VAL:HG13	1.99	0.42
1:A:115:GLY:O	1:A:116:HIS:CG	2.73	0.42
1:A:73:THR:OG1	1:A:76:GLU:HG3	2.20	0.42
1:A:104:CYS:SG	1:A:106:ASP:HB3	2.59	0.42
1:B:377:LEU:HD11	1:B:384:ARG:HG2	2.01	0.42
1:A:286:ASP:O	1:A:289:ARG:HG2	2.20	0.42
1:B:11:ILE:HG12	1:B:15:GLU:HB2	2.02	0.42
1:B:523:GLU:C	1:B:525:LEU:H	2.23	0.42
1:A:4:ARG:O	1:A:256:GLN:NE2	2.53	0.41
1:A:465:ARG:O	1:A:469:PHE:HD2	2.04	0.41
1:B:74:LEU:HD23	1:B:74:LEU:HA	1.85	0.41
1:B:255:GLN:OE1	1:B:498:ARG:NH1	2.49	0.41
1:B:490:VAL:O	1:B:494:ILE:HG13	2.20	0.41
1:A:81:TYR:CD1	1:A:88:LEU:HB2	2.55	0.41
1:B:521:TYR:O	1:B:525:LEU:HD13	2.20	0.41
1:B:91:LYS:HD3	2:B:723:HOH:O	2.20	0.41
1:A:226:ILE:HG21	1:A:519:GLN:HA	2.03	0.41
1:A:221:ILE:HG22	1:A:229:ARG:HH11	1.86	0.40
1:A:349:ASN:ND2	1:A:451:ASP:O	2.54	0.40
1:A:468:MET:HG3	1:A:510:GLN:HB3	2.04	0.40
1:B:358:LYS:HE3	1:B:421:ARG:O	2.21	0.40
1:A:435:VAL:O	1:A:438:PHE:HB3	2.22	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	474/536 (88%)	445 (94%)	21 (4%)	8 (2%)	9	11
1	B	475/536 (89%)	447 (94%)	25 (5%)	3 (1%)	25	36
All	All	949/1072 (88%)	892 (94%)	46 (5%)	11 (1%)	13	19

All (11) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	206	LEU
1	B	92	ASN
1	A	116	HIS
1	A	36	SER
1	A	38	PRO
1	A	205	THR
1	A	37	ASN
1	A	93	GLY
1	A	505	VAL
1	B	505	VAL
1	B	524	THR

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	428/478 (90%)	404 (94%)	24 (6%)	21	34
1	B	428/478 (90%)	413 (96%)	15 (4%)	36	55

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	856/956 (90%)	817 (95%)	39 (5%)	27 43

All (39) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	11	ILE
1	A	36	SER
1	A	47	ARG
1	A	52	THR
1	A	94	ASP
1	A	95	VAL
1	A	96	ILE
1	A	116	HIS
1	A	117	LEU
1	A	124	LYS
1	A	165	SER
1	A	175	GLN
1	A	176	GLU
1	A	185	GLU
1	A	206	LEU
1	A	234	SER
1	A	266	LYS
1	A	362	ARG
1	A	391	SER
1	A	413	ARG
1	A	477	ASP
1	A	480	ARG
1	A	508	GLU
1	A	525	LEU
1	B	47	ARG
1	B	92	ASN
1	B	94	ASP
1	B	95	VAL
1	B	111	ARG
1	B	165	SER
1	B	278	ARG
1	B	302	SER
1	B	412	GLU
1	B	413	ARG
1	B	450	MET
1	B	477	ASP
1	B	480	ARG

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Mol	Chain	Res	Type
1	B	485	ASP
1	B	492	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	114	HIS
1	A	256	GLN
1	B	211	GLN
1	B	214	GLN
1	B	287	HIS

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 monosaccharides 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	484/536 (90%)	0.01	14 (2%)	51	50	20, 39, 61, 82	0
1	B	485/536 (90%)	0.05	23 (4%)	31	30	19, 43, 64, 87	0
All	All	969/1072 (90%)	0.03	37 (3%)	40	39	19, 40, 63, 87	0

All (37) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	93	GLY	7.0
1	A	92	ASN	6.0
1	B	116	HIS	5.4
1	B	93	GLY	5.2
1	A	116	HIS	4.6
1	B	92	ASN	4.4
1	B	90	GLU	4.4
1	B	94	ASP	4.0
1	B	86	GLY	3.6
1	B	232	GLU	3.5
1	B	410	ASN	3.4
1	B	409	GLY	3.2
1	B	209	VAL	3.2
1	B	231	ARG	3.2
1	A	48	ASN	3.0
1	B	36	SER	3.0
1	A	525	LEU	3.0
1	A	484	VAL	2.8
1	B	96	ILE	2.6
1	B	37	ASN	2.6
1	A	144	PRO	2.5
1	B	95	VAL	2.5
1	B	213	LYS	2.4
1	B	115	GLY	2.4

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Mol	Chain	Res	Type	RSRZ
1	B	450	MET	2.3
1	A	38	PRO	2.3
1	A	39	GLY	2.3
1	A	94	ASP	2.3
1	B	211	GLN	2.2
1	A	199	LYS	2.2
1	B	235	LYS	2.2
1	B	89	LYS	2.1
1	B	199	LYS	2.1
1	A	127	THR	2.1
1	A	310	ILE	2.1
1	B	207	GLY	2.0
1	A	485	ASP	2.0

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

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

6.3 Carbohydrates ⓘ

There are no monosaccharides in this entry.

6.4 Ligands ⓘ

There are no ligands in this entry.

6.5 Other polymers ⓘ

There are no such residues in this entry.