



Full wwPDB X-ray Structure Validation Report ⓘ

May 26, 2020 – 11:48 am BST

PDB ID : 3A8P
Title : Crystal structure of the Tiam2 PHCCEX domain
Authors : Terawaki, S.; Kitano, K.; Mori, T.; Zhai, Y.; Higuchi, Y.; Itoh, N.; Watanabe, T.; Kaibuchi, K.; Hakoshima, T.
Deposited on : 2009-10-07
Resolution : 2.10 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
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

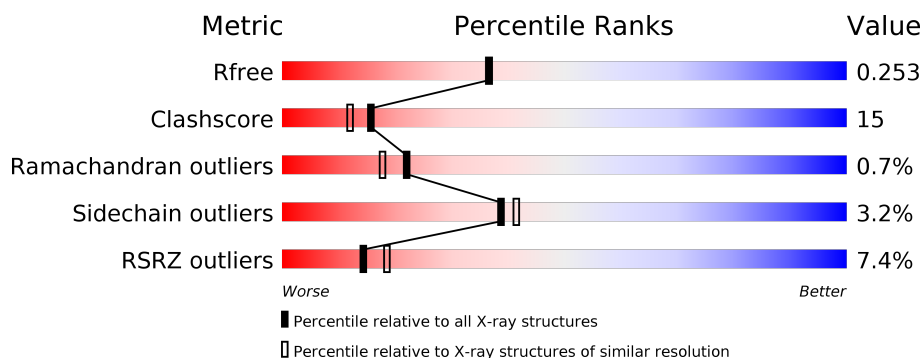
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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	5197 (2.10-2.10)
Clashscore	141614	5710 (2.10-2.10)
Ramachandran outliers	138981	5647 (2.10-2.10)
Sidechain outliers	138945	5648 (2.10-2.10)
RSRZ outliers	127900	5083 (2.10-2.10)

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 ≥ 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	263	<div> <div>5%</div> <div> <div></div> <div>66%</div> <div>21%</div> <div>•</div> <div>12%</div> </div> </div>
1	B	263	<div> <div>5%</div> <div> <div></div> <div>65%</div> <div>21%</div> <div>•</div> <div>12%</div> </div> </div>
1	C	263	<div> <div>8%</div> <div> <div></div> <div>66%</div> <div>19%</div> <div>•</div> <div>13%</div> </div> </div>
1	D	263	<div> <div>8%</div> <div> <div></div> <div>62%</div> <div>24%</div> <div>•</div> <div>13%</div> </div> </div>

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 7754 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 T-lymphoma invasion and metastasis-inducing protein 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	232	Total	C	N	O	S	0	0	0
			1856	1184	331	329	12			
1	B	231	Total	C	N	O	S	0	0	0
			1853	1182	330	329	12			
1	C	229	Total	C	N	O	S	0	0	0
			1839	1175	328	324	12			
1	D	228	Total	C	N	O	S	0	0	0
			1823	1163	327	321	12			

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	495	GLY	-	EXPRESSION TAG	UNP Q6ZPF3
A	496	PRO	-	EXPRESSION TAG	UNP Q6ZPF3
A	497	LEU	-	EXPRESSION TAG	UNP Q6ZPF3
A	498	GLY	-	EXPRESSION TAG	UNP Q6ZPF3
A	499	SER	-	EXPRESSION TAG	UNP Q6ZPF3
B	495	GLY	-	EXPRESSION TAG	UNP Q6ZPF3
B	496	PRO	-	EXPRESSION TAG	UNP Q6ZPF3
B	497	LEU	-	EXPRESSION TAG	UNP Q6ZPF3
B	498	GLY	-	EXPRESSION TAG	UNP Q6ZPF3
B	499	SER	-	EXPRESSION TAG	UNP Q6ZPF3
C	495	GLY	-	EXPRESSION TAG	UNP Q6ZPF3
C	496	PRO	-	EXPRESSION TAG	UNP Q6ZPF3
C	497	LEU	-	EXPRESSION TAG	UNP Q6ZPF3
C	498	GLY	-	EXPRESSION TAG	UNP Q6ZPF3
C	499	SER	-	EXPRESSION TAG	UNP Q6ZPF3
D	495	GLY	-	EXPRESSION TAG	UNP Q6ZPF3
D	496	PRO	-	EXPRESSION TAG	UNP Q6ZPF3
D	497	LEU	-	EXPRESSION TAG	UNP Q6ZPF3
D	498	GLY	-	EXPRESSION TAG	UNP Q6ZPF3
D	499	SER	-	EXPRESSION TAG	UNP Q6ZPF3

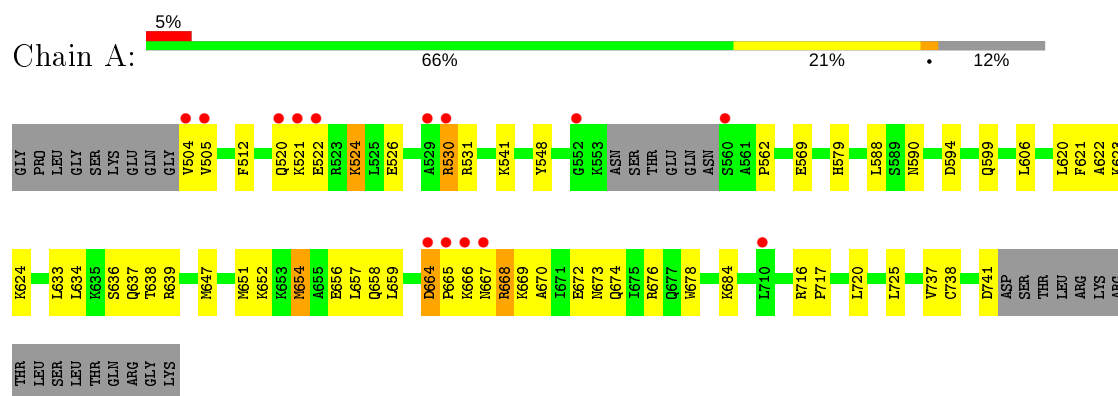
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	126	Total 126	O 126	0	0
2	B	75	Total 75	O 75	0	0
2	C	90	Total 90	O 90	0	0
2	D	92	Total 92	O 92	0	0

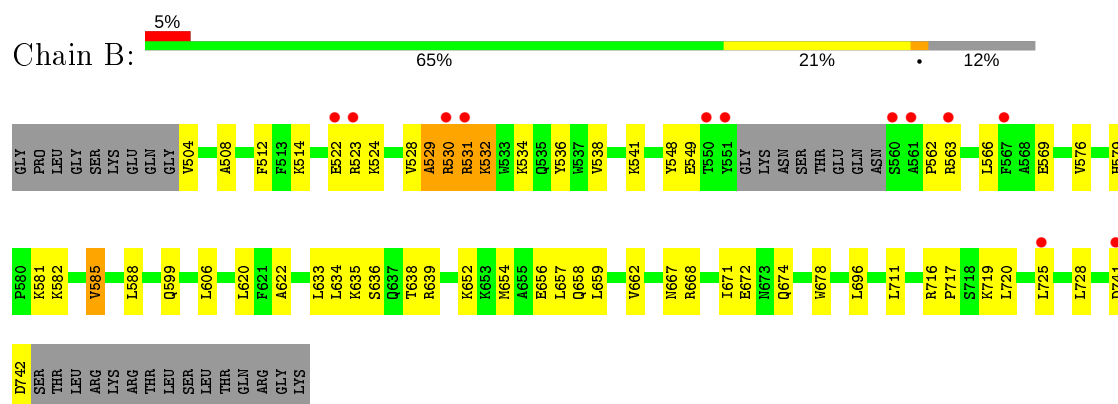
3 Residue-property plots [i](#)

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.

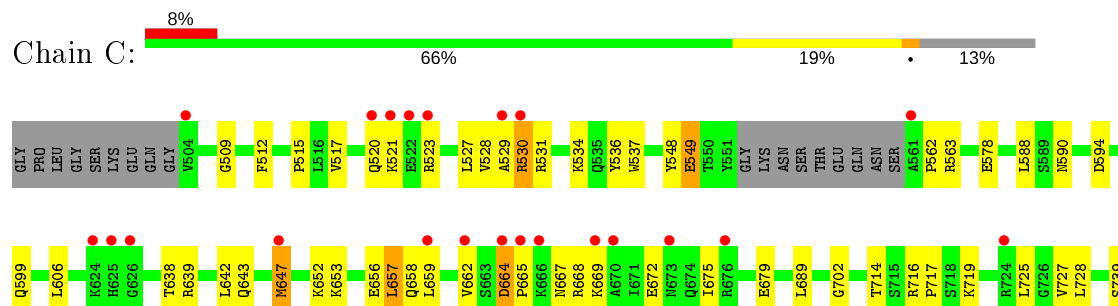
- Molecule 1: T-lymphoma invasion and metastasis-inducing protein 2



- Molecule 1: T-lymphoma invasion and metastasis-inducing protein 2



- Molecule 1: T-lymphoma invasion and metastasis-inducing protein 2



R740
D741
ASP
SER
THR
LEU
ARG
LYS
ARG
THR
LEU
SER
LEU
THR
GLN
ARG
GLY
LYS

- Molecule 1: T-lymphoma invasion and metastasis-inducing protein 2



GLY	PRO	LEU	GLY	SER	THR	LEU	ARG	LYS	GLU	Q502	F512	F513	K514	Q520	K521	E522	K523	K524	L525	E526	L527	V528	A529	K530	K533	K534	Q535	Y536	K537	C543	L546	F547	Y548	E549	THR	TYR	GLY	LYS	ASN	SER	THR	GLU	GLN	ASN	SER	ALA	P562	K563	C564	K582	L588	Q599	Q603
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L606	E607	A622	L633	L634	T638	R639	L642	Q643	K650	K651	K652	K653	M654	A655	E656	L657	Q658	L659	V662	S663	D664	P665	K666	M667	R668	K669	A670	I671	Q674	I675	R676	Q677	M678	E679	E683	K684	E703	K708	S709	L710	R716	P717	L720	R724	L725
------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------

Q726
V727
V730
D741
ASP
SER
THR
LEU
ARG
LYS
ARG
THR
LEU
SER
THR
GLN
ARG
GLY
LYS

4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	46.69 Å 104.79 Å 115.97 Å 90.00° 80.55° 90.00°	Depositor
Resolution (Å)	29.81 – 2.10 37.76 – 2.08	Depositor EDS
% Data completeness (in resolution range)	98.7 (29.81-2.10) 97.7 (37.76-2.08)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.15 (at 2.08 Å)	Xtriage
Refinement program	CNS 1.2	Depositor
R, R_{free}	0.211 , 0.253 0.211 , 0.253	Depositor DCC
R_{free} test set	6524 reflections (10.11%)	wwPDB-VP
Wilson B-factor (Å ²)	30.5	Xtriage
Anisotropy	0.546	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 53.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.024 for h,-k,h-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	7754	wwPDB-VP
Average B, all atoms (Å ²)	39.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.22% 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 [i](#)

5.1 Standard geometry [i](#)

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	0.35	0/1893	0.54	0/2548
1	B	0.34	0/1890	0.55	0/2544
1	C	0.33	0/1876	0.53	0/2525
1	D	0.33	0/1859	0.53	0/2500
All	All	0.34	0/7518	0.54	0/10117

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 [i](#)

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	1856	0	1901	49	0
1	B	1853	0	1901	62	0
1	C	1839	0	1892	49	0
1	D	1823	0	1875	62	0
2	A	126	0	0	2	0
2	B	75	0	0	0	0
2	C	90	0	0	2	0
2	D	92	0	0	3	0
All	All	7754	0	7569	219	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 15.

All (219) 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:C:520:GLN:HG3	1:C:521:LYS:H	1.30	0.94
1:A:664:ASP:HB2	1:A:667:ASN:HB2	1.51	0.93
1:D:650:LYS:O	1:D:653:LYS:HG2	1.78	0.82
1:B:662:VAL:HG13	1:B:668:ARG:NH1	1.95	0.80
1:C:520:GLN:CG	1:C:521:LYS:H	1.94	0.80
1:B:528:VAL:HB	1:B:531:ARG:HH11	1.46	0.79
1:B:514:LYS:HG3	1:B:531:ARG:HD3	1.67	0.77
1:B:514:LYS:CG	1:B:531:ARG:HD3	2.16	0.76
1:B:532:LYS:H	1:B:532:LYS:HD2	1.50	0.75
1:A:590:ASN:HD21	1:A:594:ASP:HB2	1.53	0.72
1:B:725:LEU:HD23	1:B:725:LEU:O	1.90	0.72
1:B:522:GLU:HB3	1:B:524:LYS:HE3	1.70	0.71
1:D:530:ARG:H	1:D:530:ARG:NE	1.88	0.71
1:D:659:LEU:HA	1:D:662:VAL:HG12	1.73	0.71
1:C:638:THR:O	1:C:642:LEU:HD13	1.91	0.71
1:D:684:LYS:HE2	2:D:239:HOH:O	1.89	0.71
1:D:703:GLU:CD	1:D:703:GLU:H	1.93	0.70
1:B:716:ARG:NH1	1:B:720:LEU:HD11	2.07	0.70
1:A:590:ASN:ND2	1:A:594:ASP:HB2	2.07	0.69
1:B:711:LEU:HD22	1:B:728:LEU:HD11	1.76	0.68
1:D:529:ALA:HB3	1:D:530:ARG:NH2	2.09	0.66
1:A:504:VAL:N	1:A:541:LYS:HZ2	1.94	0.66
1:C:669:LYS:HA	1:C:672:GLU:HG2	1.77	0.66
1:C:664:ASP:CB	1:C:667:ASN:HB3	2.26	0.66
1:B:652:LYS:O	1:B:656:GLU:HG3	1.97	0.65
1:C:664:ASP:HB2	1:C:667:ASN:HB3	1.78	0.65
1:C:520:GLN:HG3	1:C:521:LYS:N	2.07	0.64
1:A:654:MET:HE1	1:A:657:LEU:HD23	1.80	0.64
1:D:528:VAL:HG13	1:D:530:ARG:HH11	1.62	0.64
1:D:674:GLN:HG3	1:D:678:TRP:CZ3	2.32	0.63
1:D:634:LEU:O	1:D:638:THR:HG23	1.99	0.63
1:D:524:LYS:HE2	1:D:526:GLU:OE2	1.99	0.63
1:D:725:LEU:HD22	1:D:727:VAL:H	1.65	0.62
1:C:664:ASP:HB2	1:C:667:ASN:HD22	1.65	0.61
1:C:534:LYS:HD3	1:C:536:TYR:OH	2.00	0.61
1:A:716:ARG:O	1:A:720:LEU:HD13	2.01	0.60
1:A:673:ASN:HD22	1:A:676:ARG:NH1	1.99	0.60
1:A:530:ARG:HG2	1:A:530:ARG:O	2.00	0.60
1:B:662:VAL:HG13	1:B:668:ARG:HH11	1.63	0.60
1:D:725:LEU:C	1:D:725:LEU:HD23	2.21	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:520:GLN:CG	1:C:521:LYS:N	2.65	0.59
1:D:671:ILE:O	1:D:675:ILE:HG12	2.02	0.59
1:D:669:LYS:HD3	1:D:670:ALA:H	1.67	0.59
1:A:522:GLU:HB3	1:A:524:LYS:HD2	1.85	0.58
1:D:659:LEU:HA	1:D:662:VAL:CG1	2.33	0.58
1:B:582:LYS:HD3	1:B:599:GLN:NE2	2.18	0.58
1:D:548:TYR:CZ	1:D:562:PRO:HG3	2.39	0.58
1:C:657:LEU:H	1:C:657:LEU:HD22	1.68	0.57
1:A:664:ASP:CB	1:A:667:ASN:HD22	2.17	0.57
1:A:664:ASP:HB3	1:A:667:ASN:HD22	1.70	0.57
1:C:659:LEU:HD13	1:C:668:ARG:HH21	1.69	0.57
1:D:679:GLU:O	1:D:683:GLU:HG3	2.04	0.56
1:A:521:LYS:O	1:A:522:GLU:HB3	2.06	0.56
1:A:504:VAL:HG12	1:A:505:VAL:N	2.21	0.56
1:A:524:LYS:HD3	1:A:524:LYS:H	1.71	0.56
1:B:576:VAL:HB	1:B:585:VAL:CG2	2.36	0.56
1:B:636:SER:HA	1:B:639:ARG:NH1	2.21	0.56
1:B:523:ARG:HH22	1:B:741:ASP:C	2.10	0.55
1:D:709:SER:HB2	2:D:141:HOH:O	2.06	0.55
1:A:673:ASN:HD22	1:A:676:ARG:HH12	1.54	0.55
1:A:654:MET:CE	1:A:654:MET:HA	2.37	0.55
1:A:716:ARG:HB2	1:A:717:PRO:HD3	1.89	0.55
1:D:724:ARG:HH11	1:D:724:ARG:HG3	1.70	0.55
1:B:531:ARG:CD	1:B:531:ARG:H	2.20	0.55
1:B:512:PHE:HB2	1:B:599:GLN:HB3	1.88	0.55
1:C:669:LYS:HA	1:C:672:GLU:CG	2.37	0.54
1:C:725:LEU:HD23	1:C:725:LEU:C	2.26	0.54
1:B:531:ARG:HD2	1:B:531:ARG:N	2.21	0.54
1:D:665:PRO:HA	1:D:668:ARG:HG2	1.89	0.54
1:B:569:GLU:HG3	1:B:620:LEU:HD23	1.89	0.54
1:D:530:ARG:H	1:D:530:ARG:CD	2.19	0.54
1:B:534:LYS:HD3	1:B:536:TYR:OH	2.07	0.54
1:D:676:ARG:HG2	1:D:676:ARG:HH11	1.72	0.54
1:A:654:MET:HE2	1:A:654:MET:HA	1.89	0.53
1:D:671:ILE:O	1:D:671:ILE:HD13	2.08	0.53
1:A:668:ARG:O	1:A:672:GLU:HG3	2.08	0.53
1:A:521:LYS:O	1:A:522:GLU:CB	2.57	0.53
1:B:528:VAL:HB	1:B:531:ARG:NH1	2.19	0.53
1:B:531:ARG:H	1:B:531:ARG:HD2	1.72	0.53
1:C:530:ARG:HD3	1:C:530:ARG:C	2.29	0.52
1:A:579:HIS:O	1:B:719:LYS:HE2	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:702:GLY:HA3	2:C:278:HOH:O	2.10	0.52
1:C:662:VAL:O	1:C:668:ARG:HD3	2.09	0.52
1:D:603:GLN:O	1:D:607:GLU:HG3	2.09	0.52
1:D:652:LYS:HE3	1:D:679:GLU:HG2	1.92	0.52
1:D:659:LEU:HB2	1:D:671:ILE:HD12	1.90	0.52
1:D:669:LYS:HD3	1:D:670:ALA:N	2.25	0.52
1:D:520:GLN:HG3	1:D:526:GLU:OE1	2.10	0.51
1:B:711:LEU:HD22	1:B:728:LEU:CD1	2.40	0.51
1:D:622:ALA:HA	1:D:633:LEU:HD23	1.92	0.51
1:A:665:PRO:HG2	1:A:666:LYS:H	1.75	0.51
1:D:710:LEU:HD23	1:D:730:VAL:HG22	1.91	0.51
1:B:504:VAL:N	1:B:541:LYS:HE3	2.26	0.51
1:B:563:ARG:HD2	1:B:563:ARG:N	2.26	0.51
1:C:578:GLU:OE2	1:D:708:LYS:HE2	2.11	0.51
1:C:656:GLU:OE2	1:C:656:GLU:HA	2.11	0.51
1:C:662:VAL:HG13	1:C:664:ASP:OD1	2.10	0.51
1:D:671:ILE:C	1:D:671:ILE:HD13	2.30	0.51
1:B:548:TYR:CZ	1:B:562:PRO:HG3	2.46	0.50
1:D:653:LYS:HG3	1:D:654:MET:N	2.26	0.50
1:A:530:ARG:CG	1:A:530:ARG:O	2.59	0.50
1:B:667:ASN:O	1:B:671:ILE:HG13	2.12	0.50
1:A:673:ASN:ND2	1:A:676:ARG:HH12	2.09	0.50
1:B:549:GLU:HA	1:B:549:GLU:OE1	2.12	0.50
1:B:523:ARG:HH22	1:B:742:ASP:N	2.10	0.49
1:A:684:LYS:HD3	1:A:737:VAL:CG1	2.42	0.49
1:B:659:LEU:HA	1:B:662:VAL:HG12	1.94	0.49
1:C:509:GLY:HA2	1:C:537:TRP:CZ3	2.48	0.49
1:C:658:GLN:O	1:C:662:VAL:HG23	2.12	0.49
1:B:529:ALA:O	1:B:531:ARG:N	2.45	0.49
1:B:534:LYS:HG3	1:B:536:TYR:CE2	2.47	0.49
1:C:664:ASP:HB3	1:C:667:ASN:HB3	1.93	0.49
1:D:659:LEU:HD13	1:D:671:ILE:HG23	1.93	0.49
1:C:714:THR:HG22	1:C:719:LYS:HG3	1.92	0.49
1:B:528:VAL:CB	1:B:531:ARG:HH11	2.20	0.49
1:B:716:ARG:HH12	1:B:720:LEU:HD11	1.75	0.49
1:C:725:LEU:HD22	1:C:727:VAL:H	1.77	0.49
1:D:512:PHE:HB2	1:D:599:GLN:HB3	1.95	0.49
1:A:520:GLN:HG3	1:A:526:GLU:CD	2.32	0.49
1:B:659:LEU:HA	1:B:662:VAL:CG1	2.42	0.49
1:C:653:LYS:O	1:C:657:LEU:HD22	2.13	0.49
1:D:662:VAL:O	1:D:662:VAL:HG13	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:647:MET:HA	1:C:647:MET:CE	2.43	0.48
1:C:652:LYS:O	1:C:656:GLU:HG2	2.13	0.48
1:D:675:ILE:O	1:D:679:GLU:HG3	2.14	0.48
1:B:532:LYS:H	1:B:532:LYS:CD	2.24	0.48
1:D:708:LYS:NZ	2:D:107:HOH:O	2.47	0.48
1:C:725:LEU:O	1:C:725:LEU:HD23	2.14	0.47
1:D:548:TYR:CE1	1:D:562:PRO:HG3	2.49	0.47
1:B:716:ARG:HB3	1:B:717:PRO:HD3	1.95	0.47
1:D:528:VAL:CG1	1:D:530:ARG:HH11	2.28	0.47
1:A:548:TYR:CZ	1:A:562:PRO:HG3	2.49	0.47
1:A:659:LEU:HD11	1:A:668:ARG:HD3	1.97	0.47
1:B:588:LEU:HD23	1:B:588:LEU:C	2.34	0.47
1:D:716:ARG:HB3	1:D:717:PRO:HD3	1.95	0.47
1:A:674:GLN:HE21	1:A:678:TRP:HE1	1.62	0.47
1:B:662:VAL:HG13	1:B:668:ARG:HH12	1.79	0.47
1:D:668:ARG:HA	1:D:671:ILE:HG22	1.97	0.47
1:B:531:ARG:C	1:B:531:ARG:HD2	2.35	0.46
1:D:546:LEU:HD22	1:D:562:PRO:HG2	1.96	0.46
1:A:654:MET:CE	1:A:657:LEU:HD23	2.43	0.46
1:C:659:LEU:O	1:C:659:LEU:HD13	2.15	0.46
1:A:620:LEU:HD12	1:A:623:LYS:HE3	1.97	0.46
1:A:669:LYS:HG3	1:A:670:ALA:N	2.30	0.46
1:B:606:LEU:C	1:B:606:LEU:HD23	2.36	0.46
1:A:652:LYS:O	1:A:656:GLU:HG3	2.15	0.46
1:C:664:ASP:CB	1:C:667:ASN:HD22	2.28	0.46
1:D:652:LYS:O	1:D:656:GLU:HG3	2.16	0.46
1:A:569:GLU:OE2	1:A:624:LYS:HD2	2.15	0.46
1:C:549:GLU:OE2	1:C:563:ARG:NH1	2.49	0.46
1:D:659:LEU:HD13	1:D:671:ILE:CG2	2.46	0.45
1:D:606:LEU:HD23	1:D:606:LEU:C	2.37	0.45
1:C:515:PRO:HB2	1:C:528:VAL:HG21	1.97	0.45
1:C:588:LEU:C	1:C:588:LEU:HD23	2.37	0.45
1:A:667:ASN:HB3	2:A:270:HOH:O	2.16	0.45
1:D:622:ALA:HA	1:D:633:LEU:CD2	2.46	0.45
1:B:532:LYS:N	1:B:532:LYS:HD2	2.27	0.45
1:A:621:PHE:HZ	1:A:637:GLN:HE21	1.65	0.44
1:C:606:LEU:C	1:C:606:LEU:HD23	2.38	0.44
1:A:531:ARG:HA	2:A:311:HOH:O	2.16	0.44
1:A:622:ALA:HA	1:A:633:LEU:CD2	2.48	0.44
1:B:711:LEU:HD13	1:B:728:LEU:HD13	1.98	0.44
1:B:579:HIS:CE1	1:B:581:LYS:HG3	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:512:PHE:HB2	1:A:599:GLN:HB3	1.99	0.44
1:B:576:VAL:HB	1:B:585:VAL:HG23	1.99	0.44
1:A:579:HIS:O	1:B:719:LYS:CE	2.66	0.44
1:C:639:ARG:O	1:C:643:GLN:HG3	2.18	0.44
1:D:665:PRO:C	1:D:667:ASN:H	2.19	0.44
1:A:634:LEU:O	1:A:638:THR:HG23	2.18	0.44
1:D:537:TRP:HB3	1:D:548:TYR:HB2	2.00	0.43
1:B:654:MET:HE1	1:B:657:LEU:HD22	2.01	0.43
1:C:728:LEU:HD23	1:C:728:LEU:C	2.38	0.43
1:B:634:LEU:HB2	1:B:696:LEU:HD13	1.99	0.43
1:C:590:ASN:ND2	1:C:594:ASP:HB2	2.33	0.43
1:C:668:ARG:HH11	1:C:668:ARG:HG2	1.82	0.43
1:A:520:GLN:HG2	1:A:526:GLU:HG2	2.01	0.43
1:A:588:LEU:C	1:A:588:LEU:HD23	2.39	0.43
1:D:520:GLN:HB2	1:D:524:LYS:HG3	2.00	0.43
1:D:725:LEU:HD22	1:D:727:VAL:N	2.32	0.43
1:B:674:GLN:HG3	1:B:678:TRP:CZ3	2.54	0.43
1:D:655:ALA:O	1:D:671:ILE:HD11	2.19	0.43
1:C:534:LYS:HD3	1:C:536:TYR:CZ	2.54	0.42
1:C:548:TYR:CZ	1:C:562:PRO:HG3	2.53	0.42
1:B:508:ALA:HA	1:B:538:VAL:O	2.19	0.42
1:B:674:GLN:HG3	1:B:678:TRP:CH2	2.55	0.42
1:A:606:LEU:HD23	1:A:606:LEU:C	2.40	0.42
1:C:523:ARG:HG2	1:C:739:SER:O	2.20	0.42
1:C:675:ILE:O	1:C:679:GLU:HG3	2.19	0.42
1:D:534:LYS:HE3	1:D:536:TYR:OH	2.20	0.42
1:A:738:CYS:HA	1:A:741:ASP:OD2	2.19	0.42
1:D:521:LYS:O	1:D:524:LYS:HG2	2.19	0.42
1:C:638:THR:HG23	1:C:689:LEU:HD11	2.01	0.42
1:C:512:PHE:HB2	1:C:599:GLN:HB3	2.02	0.41
1:D:724:ARG:HG3	1:D:724:ARG:NH1	2.35	0.41
1:B:529:ALA:O	1:B:530:ARG:C	2.58	0.41
1:D:716:ARG:O	1:D:720:LEU:HD13	2.20	0.41
1:B:654:MET:CE	1:B:657:LEU:HD22	2.50	0.41
1:B:548:TYR:CE2	1:B:562:PRO:HG3	2.55	0.41
1:C:531:ARG:HB3	2:C:314:HOH:O	2.20	0.41
1:D:659:LEU:CA	1:D:662:VAL:HG12	2.46	0.41
1:B:635:LYS:O	1:B:639:ARG:HG3	2.21	0.41
1:A:530:ARG:HH21	1:A:530:ARG:HG2	1.86	0.41
1:A:654:MET:O	1:A:658:GLN:HG2	2.21	0.41
1:B:579:HIS:HE1	1:B:581:LYS:HG3	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:634:LEU:O	1:B:638:THR:HG23	2.21	0.41
1:B:531:ARG:CD	1:B:531:ARG:N	2.82	0.41
1:D:668:ARG:HG3	1:D:668:ARG:HH11	1.85	0.41
1:C:716:ARG:HB2	1:C:717:PRO:HD3	2.02	0.41
1:B:522:GLU:HA	1:B:522:GLU:OE2	2.21	0.40
1:B:622:ALA:HA	1:B:633:LEU:HD23	2.03	0.40
1:A:636:SER:HA	1:A:639:ARG:CZ	2.51	0.40
1:A:647:MET:HE3	1:A:651:MET:CG	2.51	0.40
1:B:622:ALA:HA	1:B:633:LEU:CD2	2.51	0.40
1:C:517:VAL:HG22	1:C:527:LEU:HD23	2.02	0.40
1:C:668:ARG:HD2	1:C:668:ARG:HA	1.91	0.40
1:D:639:ARG:O	1:D:643:GLN:HG3	2.21	0.40
1:D:588:LEU:HD23	1:D:588:LEU:C	2.42	0.40
1:D:655:ALA:HB3	1:D:675:ILE:HD11	2.04	0.40
1:D:514:LYS:HE3	1:D:533:TRP:CD1	2.57	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	228/263 (87%)	225 (99%)	3 (1%)	0	100	100
1	B	227/263 (86%)	222 (98%)	3 (1%)	2 (1%)	17	12
1	C	225/263 (86%)	214 (95%)	9 (4%)	2 (1%)	17	12
1	D	224/263 (85%)	217 (97%)	5 (2%)	2 (1%)	17	12
All	All	904/1052 (86%)	878 (97%)	20 (2%)	6 (1%)	22	18

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	530	ARG
1	C	529	ALA
1	C	665	PRO
1	B	529	ALA
1	D	664	ASP
1	D	666	LYS

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	204/233 (88%)	198 (97%)	6 (3%)	42	46
1	B	205/233 (88%)	199 (97%)	6 (3%)	42	46
1	C	203/233 (87%)	198 (98%)	5 (2%)	47	52
1	D	201/233 (86%)	192 (96%)	9 (4%)	27	27
All	All	813/932 (87%)	787 (97%)	26 (3%)	39	41

All (26) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	524	LYS
1	A	530	ARG
1	A	654	MET
1	A	664	ASP
1	A	668	ARG
1	A	725	LEU
1	B	531	ARG
1	B	532	LYS
1	B	566	LEU
1	B	585	VAL
1	B	658	GLN
1	B	672	GLU
1	C	530	ARG
1	C	549	GLU
1	C	647	MET
1	C	657	LEU

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Mol	Chain	Res	Type
1	C	664	ASP
1	D	530	ARG
1	D	543	CYS
1	D	582	LYS
1	D	642	LEU
1	D	657	LEU
1	D	658	GLN
1	D	664	ASP
1	D	669	LYS
1	D	671	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (21) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	574	GLN
1	A	658	GLN
1	A	667	ASN
1	A	673	ASN
1	A	674	GLN
1	A	680	GLN
1	B	574	GLN
1	B	599	GLN
1	B	637	GLN
1	B	658	GLN
1	B	667	ASN
1	B	673	ASN
1	C	637	GLN
1	C	667	ASN
1	C	674	GLN
1	C	680	GLN
1	C	686	HIS
1	D	574	GLN
1	D	599	GLN
1	D	643	GLN
1	D	686	HIS

5.3.3 RNA ⓘ

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](#)

There are no ligands in this entry.

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	232/263 (88%)	0.32	14 (6%) 21 27	22, 32, 59, 72	0
1	B	231/263 (87%)	0.37	12 (5%) 27 32	20, 37, 66, 80	0
1	C	229/263 (87%)	0.51	22 (9%) 8 10	24, 37, 73, 88	0
1	D	228/263 (86%)	0.47	20 (8%) 10 12	22, 35, 68, 83	0
All	All	920/1052 (87%)	0.42	68 (7%) 14 18	20, 35, 68, 88	0

All (68) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	659	LEU	6.8
1	D	665	PRO	6.7
1	A	504	VAL	6.6
1	C	665	PRO	6.1
1	D	666	LYS	5.8
1	C	669	LYS	5.5
1	B	550	THR	5.5
1	C	530	ARG	4.9
1	A	665	PRO	4.7
1	D	563	ARG	4.6
1	C	522	GLU	4.6
1	B	551	TYR	4.3
1	B	531	ARG	4.2
1	A	666	LYS	4.2
1	C	504	VAL	4.2
1	A	530	ARG	4.1
1	D	522	GLU	4.0
1	C	666	LYS	3.9
1	D	521	LYS	3.9
1	D	663	SER	3.8
1	C	664	ASP	3.7

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Mol	Chain	Res	Type	RSRZ
1	C	625	HIS	3.6
1	C	662	VAL	3.6
1	A	552	GLY	3.5
1	A	521	LYS	3.4
1	D	562	PRO	3.2
1	C	529	ALA	3.2
1	D	523	ARG	3.2
1	B	522	GLU	3.2
1	D	669	LYS	3.2
1	C	521	LYS	3.1
1	D	662	VAL	3.1
1	B	530	ARG	3.1
1	D	664	ASP	3.0
1	D	671	ILE	3.0
1	A	522	GLU	2.9
1	B	741	ASP	2.9
1	D	548	TYR	2.8
1	A	667	ASN	2.8
1	D	667	ASN	2.8
1	C	523	ARG	2.8
1	D	524	LYS	2.7
1	C	520	GLN	2.6
1	D	678	TRP	2.6
1	A	560	SER	2.5
1	B	523	ARG	2.5
1	B	560	SER	2.5
1	C	624	LYS	2.5
1	D	725	LEU	2.5
1	B	567	PHE	2.5
1	C	647	MET	2.5
1	A	505	VAL	2.4
1	B	563	ARG	2.4
1	D	564	CYS	2.4
1	C	561	ALA	2.4
1	B	561	ALA	2.4
1	A	664	ASP	2.4
1	D	676	ARG	2.3
1	C	673	ASN	2.3
1	A	529	ALA	2.3
1	B	725	LEU	2.3
1	C	626	GLY	2.2
1	D	520	GLN	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	520	GLN	2.2
1	C	676	ARG	2.1
1	C	670	ALA	2.0
1	A	710	LEU	2.0
1	C	724	ARG	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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.