



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 07:54 PM UTC

PDB ID : 3TIX / pdb_00003tix
Title : Crystal structure of the Chp1-Tas3 complex core
Authors : Schalch, T.; Joshua-Tor, L.
Deposited on : 2011-08-22
Resolution : 2.90 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
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

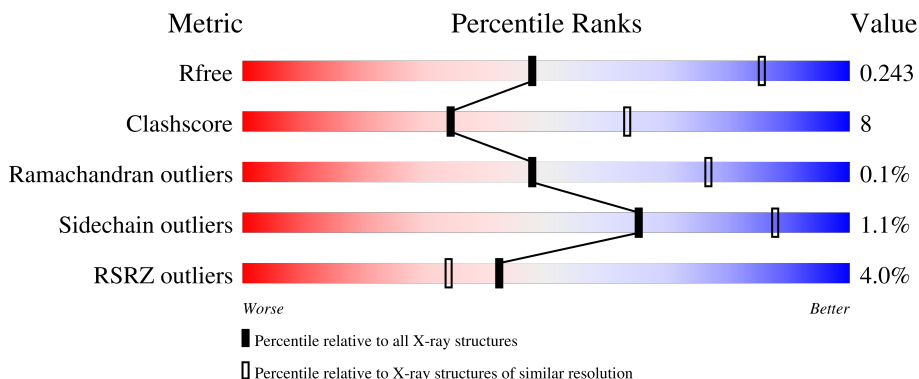
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.90 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	2481 (2.90-2.90)
Clashscore	190562	2690 (2.90-2.90)
Ramachandran outliers	187476	2623 (2.90-2.90)
Sidechain outliers	187428	2625 (2.90-2.90)
RSRZ outliers	180081	2481 (2.90-2.90)

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	207	2% 65% 8% 26%
1	C	207	% 60% 11% 29%
2	B	458	4% 74% 17% 8%
2	D	458	4% 74% 19% 7%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 9309 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 Ubiquitin-like protein SMT3, RNA-induced transcriptional silencing complex protein tas3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	153	Total	C	N	O	S	0	0	0
			1238	770	220	242	6			
1	C	147	Total	C	N	O	S	0	0	0
			1195	747	211	231	6			

There are 76 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-123	MET	-	initiating methionine	UNP Q12306
A	-122	SER	-	expression tag	UNP Q12306
A	-121	ALA	-	expression tag	UNP Q12306
A	-120	TRP	-	expression tag	UNP Q12306
A	-119	SER	-	expression tag	UNP Q12306
A	-118	HIS	-	expression tag	UNP Q12306
A	-117	PRO	-	expression tag	UNP Q12306
A	-116	GLN	-	expression tag	UNP Q12306
A	-115	PHE	-	expression tag	UNP Q12306
A	-114	GLU	-	expression tag	UNP Q12306
A	-113	LYS	-	expression tag	UNP Q12306
A	-112	GLY	-	expression tag	UNP Q12306
A	-111	GLY	-	expression tag	UNP Q12306
A	-110	GLY	-	expression tag	UNP Q12306
A	-109	SER	-	expression tag	UNP Q12306
A	-108	GLY	-	expression tag	UNP Q12306
A	-107	GLY	-	expression tag	UNP Q12306
A	-106	GLY	-	expression tag	UNP Q12306
A	-105	SER	-	expression tag	UNP Q12306
A	-104	GLY	-	expression tag	UNP Q12306
A	-103	GLY	-	expression tag	UNP Q12306
A	-102	SER	-	expression tag	UNP Q12306
A	-101	ALA	-	expression tag	UNP Q12306
A	-100	TRP	-	expression tag	UNP Q12306

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
A	-99	SER	-	expression tag	UNP Q12306
A	-98	HIS	-	expression tag	UNP Q12306
A	-97	PRO	-	expression tag	UNP Q12306
A	-96	GLN	-	expression tag	UNP Q12306
A	-95	PHE	-	expression tag	UNP Q12306
A	-94	GLU	-	expression tag	UNP Q12306
A	-93	LYS	-	expression tag	UNP Q12306
A	-92	THR	-	expression tag	UNP Q12306
A	-91	GLY	-	expression tag	UNP Q12306
A	-90	SER	-	expression tag	UNP Q12306
A	-89	LEU	-	expression tag	UNP Q12306
A	-88	GLN	-	expression tag	UNP Q12306
A	-26	THR	ARG	conflict	UNP Q12306
A	-19	GLU	ARG	conflict	UNP Q12306
C	-123	MET	-	initiating methionine	UNP Q12306
C	-122	SER	-	expression tag	UNP Q12306
C	-121	ALA	-	expression tag	UNP Q12306
C	-120	TRP	-	expression tag	UNP Q12306
C	-119	SER	-	expression tag	UNP Q12306
C	-118	HIS	-	expression tag	UNP Q12306
C	-117	PRO	-	expression tag	UNP Q12306
C	-116	GLN	-	expression tag	UNP Q12306
C	-115	PHE	-	expression tag	UNP Q12306
C	-114	GLU	-	expression tag	UNP Q12306
C	-113	LYS	-	expression tag	UNP Q12306
C	-112	GLY	-	expression tag	UNP Q12306
C	-111	GLY	-	expression tag	UNP Q12306
C	-110	GLY	-	expression tag	UNP Q12306
C	-109	SER	-	expression tag	UNP Q12306
C	-108	GLY	-	expression tag	UNP Q12306
C	-107	GLY	-	expression tag	UNP Q12306
C	-106	GLY	-	expression tag	UNP Q12306
C	-105	SER	-	expression tag	UNP Q12306
C	-104	GLY	-	expression tag	UNP Q12306
C	-103	GLY	-	expression tag	UNP Q12306
C	-102	SER	-	expression tag	UNP Q12306
C	-101	ALA	-	expression tag	UNP Q12306
C	-100	TRP	-	expression tag	UNP Q12306
C	-99	SER	-	expression tag	UNP Q12306
C	-98	HIS	-	expression tag	UNP Q12306
C	-97	PRO	-	expression tag	UNP Q12306
C	-96	GLN	-	expression tag	UNP Q12306

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
C	-95	PHE	-	expression tag	UNP Q12306
C	-94	GLU	-	expression tag	UNP Q12306
C	-93	LYS	-	expression tag	UNP Q12306
C	-92	THR	-	expression tag	UNP Q12306
C	-91	GLY	-	expression tag	UNP Q12306
C	-90	SER	-	expression tag	UNP Q12306
C	-89	LEU	-	expression tag	UNP Q12306
C	-88	GLN	-	expression tag	UNP Q12306
C	-26	THR	ARG	conflict	UNP Q12306
C	-19	GLU	ARG	conflict	UNP Q12306

- Molecule 2 is a protein called Chromo domain-containing protein 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	421	Total	C	N	O	S	0	0	0
			3411	2216	553	631	11			
2	D	424	Total	C	N	O	S	0	0	0
			3428	2229	555	633	11			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	503	MET	-	initiating methionine	UNP Q10103
D	503	MET	-	initiating methionine	UNP Q10103

- Molecule 3 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	3	Total	Cl	0	0
			3	3		
3	B	1	Total	Cl	0	0
			1	1		
3	C	2	Total	Cl	0	0
			2	2		
3	D	2	Total	Cl	0	0
			2	2		

- Molecule 4 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	1	Total	K	0	0
			1	1		

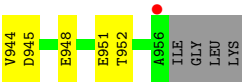
Continued on next page...

Continued from previous page...

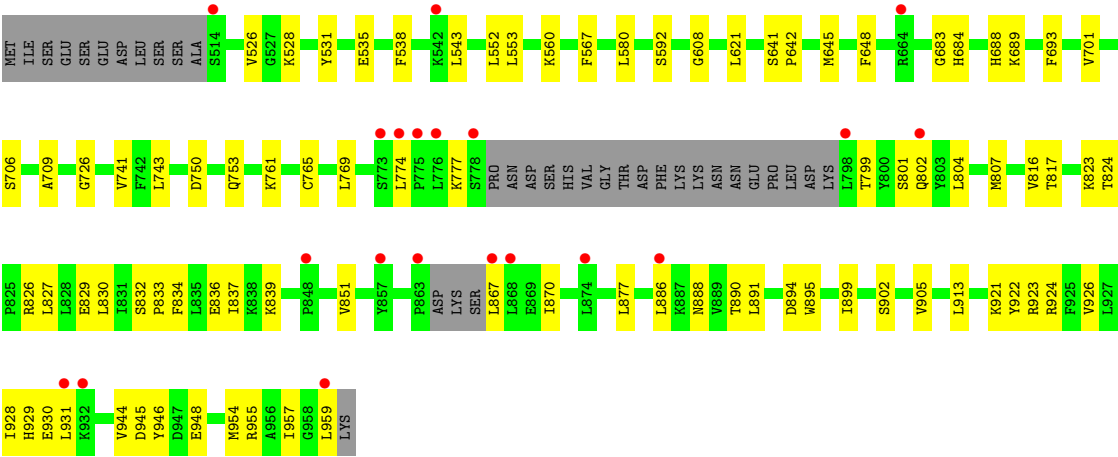
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	C	1	Total 1	K 1	0	0
4	D	1	Total 1	K 1	0	0

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	3	Total 3	O 3	0	0
5	B	16	Total 16	O 16	0	0
5	C	1	Total 1	O 1	0	0
5	D	6	Total 6	O 6	0	0



● Molecule 2: Chromo domain-containing protein 1



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	104.88Å 172.20Å 198.68Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	65.06 – 2.90 65.06 – 2.90	Depositor EDS
% Data completeness (in resolution range)	99.8 (65.06-2.90) 99.8 (65.06-2.90)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	0.07	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.25 (at 2.91Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7.1_743)	Depositor
R, R_{free}	0.211 , 0.243 0.211 , 0.243	Depositor DCC
R_{free} test set	1997 reflections (4.96%)	wwPDB-VP
Wilson B-factor (Å ²)	64.0	Xtriage
Anisotropy	0.345	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 65.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.020 for 1/2*h-1/2*k,-3/2*h-1/2*k,-l 0.031 for 1/2*h+1/2*k,3/2*h-1/2*k,-l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	9309	wwPDB-VP
Average B, all atoms (Å ²)	90.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.28% 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](#)

Bond lengths and bond angles in the following residue types are not validated in this section: K, CL

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	0.26	0/1258	0.58	0/1691
1	C	0.26	0/1213	0.61	0/1628
2	B	0.25	0/3485	0.63	0/4723
2	D	0.25	0/3501	0.64	0/4744
All	All	0.25	0/9457	0.62	0/12786

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	1238	0	1223	17	0
1	C	1195	0	1189	17	0
2	B	3411	0	3460	61	0
2	D	3428	0	3483	56	0
3	A	3	0	0	0	0
3	B	1	0	0	0	0
3	C	2	0	0	0	0
3	D	2	0	0	0	0
4	B	1	0	0	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	C	1	0	0	0	0
4	D	1	0	0	0	0
5	A	3	0	0	0	0
5	B	16	0	0	0	0
5	C	1	0	0	0	0
5	D	6	0	0	0	0
All	All	9309	0	9355	142	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 (142) 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)
2:D:765:CYS:O	2:D:923:ARG:NH2	2.20	0.74
2:B:832:SER:N	2:B:833:PRO:HD2	2.13	0.63
2:D:930:GLU:HG3	2:D:931:LEU:N	2.15	0.61
2:D:826:ARG:HG2	2:D:829:GLU:HB2	1.85	0.59
2:D:832:SER:N	2:D:833:PRO:HD2	2.18	0.59
1:C:-40:GLU:O	1:C:-36:LYS:HG2	2.02	0.59
2:D:837:ILE:HG21	2:D:957:ILE:CG2	2.33	0.58
1:C:9:LEU:N	1:C:10:PRO:HD2	2.19	0.58
2:B:800:TYR:CE1	2:B:806:PRO:HG3	2.40	0.57
2:B:849:SER:O	2:B:853:MET:HB2	2.05	0.57
2:B:701:VAL:HG12	2:B:747:LEU:CD1	2.35	0.57
2:B:774:LEU:HB3	2:B:777:LYS:HG2	1.87	0.56
1:C:-24:LEU:HD23	1:C:-19:GLU:HA	1.87	0.56
2:D:689:LYS:HG2	2:D:799:THR:HA	1.86	0.56
2:B:802:GLN:HA	2:D:895:TRP:HA	1.87	0.56
2:D:769:LEU:HG	2:D:807:MET:SD	2.47	0.55
2:B:928:ILE:HA	2:B:944:VAL:O	2.07	0.55
1:A:9:LEU:N	1:A:10:PRO:HD2	2.22	0.55
2:B:775:PRO:HB2	2:D:913:LEU:HD13	1.90	0.53
2:B:931:LEU:HB3	2:B:934:GLU:HB2	1.89	0.53
2:B:536:LEU:HD12	2:B:536:LEU:N	2.23	0.53
2:D:706:SER:HB2	2:D:709:ALA:HB3	1.91	0.53
2:D:641:SER:HB2	2:D:642:PRO:HD2	1.91	0.53
2:D:928:ILE:HA	2:D:944:VAL:O	2.08	0.53
2:B:638:GLN:NE2	2:B:640:ASN:OD1	2.42	0.53
1:C:-63:LYS:HD3	1:C:-56:GLU:HG3	1.91	0.52
2:B:596:MET:HE3	2:B:643:PHE:CZ	2.45	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:524:LEU:HD12	2:B:533:ALA:HB3	1.92	0.51
2:B:951:GLU:HG3	2:B:952:THR:HG23	1.93	0.51
2:D:851:VAL:HA	2:D:877:LEU:HD23	1.93	0.50
2:D:839:LYS:HG2	2:D:888:ASN:OD1	2.11	0.50
2:B:564:VAL:HG21	2:B:621:LEU:HD12	1.93	0.50
2:D:688:HIS:CE1	2:D:693:PHE:CD2	2.99	0.50
2:D:959:LEU:C	2:D:959:LEU:HD13	2.36	0.50
2:D:535:GLU:HB3	2:D:592:SER:HB3	1.94	0.50
2:B:706:SER:HB2	2:B:709:ALA:HB3	1.94	0.50
2:B:886:LEU:HB2	2:B:889:VAL:HG23	1.94	0.49
1:C:-62:VAL:HG21	1:C:-42:LEU:HD21	1.95	0.49
1:C:-42:LEU:C	1:C:-42:LEU:HD23	2.37	0.49
1:C:12:LEU:N	1:C:13:PRO:HD2	2.27	0.49
2:D:560:LYS:HA	2:D:560:LYS:HE2	1.95	0.49
2:B:811:GLY:HA3	2:B:841:SER:O	2.13	0.49
2:D:816:VAL:HG12	2:D:817:THR:N	2.28	0.48
2:D:834:PHE:HB2	2:D:954:MET:HE3	1.95	0.48
2:D:543:LEU:HD23	2:D:543:LEU:O	2.13	0.48
2:B:869:GLU:O	2:B:873:LEU:HG	2.13	0.48
2:B:870:ILE:O	2:B:874:LEU:HD23	2.13	0.48
2:B:689:LYS:HE2	2:B:799:THR:HA	1.96	0.48
1:C:-40:GLU:HB2	1:C:-30:MET:HE2	1.95	0.48
1:A:-55:ILE:CD1	1:A:-35:ARG:HD3	2.44	0.48
1:A:52:LYS:HA	2:B:777:LYS:HD2	1.96	0.47
2:D:955:ARG:HD2	2:D:955:ARG:C	2.39	0.47
2:D:580:LEU:HB3	2:D:648:PHE:CD2	2.50	0.47
2:B:838:LYS:HB3	2:B:842:TRP:CD1	2.50	0.47
2:B:543:LEU:HD21	2:B:549:HIS:HB2	1.97	0.47
2:B:686:ASP:CG	2:B:689:LYS:HG2	2.40	0.46
2:D:823:LYS:HD2	2:D:930:GLU:HB2	1.97	0.46
2:B:832:SER:N	2:B:833:PRO:CD	2.78	0.46
1:C:-63:LYS:HE2	1:C:-2:ILE:HG12	1.96	0.46
1:C:9:LEU:N	1:C:10:PRO:CD	2.79	0.46
1:C:-63:LYS:HD3	1:C:-56:GLU:CG	2.45	0.46
2:B:862:ASN:HB3	2:B:865:LYS:HG2	1.97	0.46
1:A:-43:ARG:HG3	1:A:-42:LEU:N	2.31	0.46
2:D:830:LEU:HD23	2:D:946:TYR:CZ	2.51	0.46
1:A:13:PRO:HA	1:A:36:LEU:HD13	1.97	0.45
2:B:621:LEU:HD23	2:B:645:MET:HG3	1.98	0.45
2:B:641:SER:HB2	2:B:642:PRO:CD	2.47	0.45
2:D:851:VAL:HA	2:D:877:LEU:CD2	2.46	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:-63:LYS:HD2	1:C:-63:LYS:C	2.41	0.45
1:A:-49:LYS:O	1:A:-11:GLU:HB2	2.16	0.45
2:B:862:ASN:HB3	2:B:865:LYS:CG	2.47	0.45
2:B:538:PHE:CD1	2:B:645:MET:HE2	2.53	0.44
2:B:774:LEU:HB3	2:B:777:LYS:CG	2.46	0.44
2:B:895:TRP:HB3	2:D:801:SER:O	2.17	0.44
1:C:-41:MET:CE	1:C:-18:ILE:HB	2.47	0.44
2:D:538:PHE:CG	2:D:645:MET:HE2	2.52	0.44
2:D:837:ILE:HG21	2:D:957:ILE:HG21	2.00	0.44
2:D:836:GLU:HB2	2:D:886:LEU:HD11	2.00	0.44
1:A:-62:VAL:HG21	1:A:-42:LEU:HD21	1.99	0.44
2:B:866:SER:O	2:B:870:ILE:HG12	2.17	0.44
2:D:944:VAL:HB	2:D:948:GLU:HB2	1.98	0.44
2:D:750:ASP:HB3	2:D:753:GLN:HG3	1.98	0.44
2:D:683:GLY:O	2:D:684:HIS:HB2	2.18	0.44
2:B:777:LYS:N	2:B:777:LYS:HD3	2.33	0.44
1:C:-44:ARG:HB2	1:C:-16:ALA:HB1	2.00	0.44
2:D:802:GLN:H	2:D:802:GLN:CD	2.26	0.44
2:B:524:LEU:HB2	2:B:536:LEU:HD13	2.00	0.43
2:B:886:LEU:N	2:B:886:LEU:HD12	2.33	0.43
2:B:523:VAL:HG22	2:B:535:GLU:HG2	2.01	0.43
1:C:56:GLU:OE1	1:C:56:GLU:N	2.49	0.43
2:B:802:GLN:OE1	2:D:899:ILE:HG13	2.19	0.43
2:B:641:SER:CB	2:B:642:PRO:CD	2.96	0.43
2:B:862:ASN:CB	2:B:865:LYS:HG3	2.49	0.43
2:D:867:LEU:HA	2:D:870:ILE:HB	2.00	0.42
1:A:14:PHE:HB2	2:B:576:PHE:O	2.18	0.42
2:B:802:GLN:HG2	2:D:894:ASP:O	2.19	0.42
1:A:-66:ILE:HG23	1:A:-49:LYS:CE	2.49	0.42
1:A:-42:LEU:C	1:A:-42:LEU:HD23	2.44	0.42
2:B:944:VAL:HB	2:B:948:GLU:HB2	2.01	0.42
2:D:902:SER:HB3	2:D:905:VAL:HB	2.00	0.42
2:D:567:PHE:CZ	2:D:608:GLY:HA3	2.54	0.42
2:D:741:VAL:HG12	2:D:743:LEU:CD1	2.50	0.42
2:B:670:HIS:O	2:B:673:GLN:HG2	2.20	0.42
2:B:919:TYR:C	2:B:919:TYR:CD1	2.98	0.42
2:D:823:LYS:CD	2:D:930:GLU:HB2	2.50	0.42
1:A:-34:GLN:N	1:A:-34:GLN:OE1	2.53	0.42
2:D:890:THR:HG22	2:D:891:LEU:N	2.35	0.42
2:D:923:ARG:HG2	2:D:924:ARG:HG2	2.02	0.42
1:C:61:LEU:HD12	2:D:774:LEU:HD11	2.02	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:12:LEU:N	1:A:13:PRO:HD2	2.35	0.41
2:B:596:MET:HE3	2:B:643:PHE:CE1	2.55	0.41
2:B:618:THR:HB	2:B:648:PHE:HB2	2.01	0.41
2:B:799:THR:OG1	2:B:800:TYR:N	2.50	0.41
2:B:800:TYR:CZ	2:B:806:PRO:HG3	2.55	0.41
1:A:17:CYS:HB3	2:B:572:TYR:CD2	2.56	0.41
2:D:824:THR:O	2:D:827:LEU:HB2	2.20	0.41
2:D:929:HIS:O	2:D:945:ASP:HA	2.21	0.41
2:D:761:LYS:O	2:D:923:ARG:NH1	2.54	0.41
1:A:-66:ILE:HG23	1:A:-49:LYS:HE3	2.02	0.41
1:A:9:LEU:N	1:A:10:PRO:CD	2.83	0.41
2:B:752:ASP:O	2:B:939:ASN:HB2	2.20	0.41
1:C:8:GLY:C	1:C:10:PRO:HD2	2.45	0.41
2:B:805:ARG:HA	2:B:806:PRO:HD3	1.93	0.41
2:B:847:PRO:HA	2:B:848:PRO:HD3	1.97	0.41
2:B:850:ILE:HG21	2:B:881:LEU:HD11	2.03	0.41
2:B:945:ASP:OD1	2:B:945:ASP:C	2.64	0.41
2:D:552:LEU:C	2:D:552:LEU:HD23	2.46	0.41
2:D:839:LYS:HD2	2:D:839:LYS:C	2.46	0.41
2:B:719:ALA:O	2:B:720:ALA:HB3	2.22	0.40
2:B:855:LYS:HB2	2:B:874:LEU:HD11	2.03	0.40
2:D:526:VAL:HB	2:D:531:TYR:CZ	2.56	0.40
2:D:837:ILE:HG21	2:D:957:ILE:HG23	2.03	0.40
1:A:-66:ILE:CG2	1:A:-49:LYS:HE2	2.50	0.40
2:B:858:PHE:CD1	2:B:870:ILE:CD1	3.05	0.40
1:A:-66:ILE:HD11	1:A:-12:PRO:HB3	2.03	0.40
2:B:543:LEU:HB3	2:B:553:LEU:HD12	2.03	0.40
2:D:701:VAL:HG12	2:D:726:GLY:O	2.20	0.40
2:D:921:LYS:CD	2:D:922:TYR:CE2	3.05	0.40
2:D:621:LEU:HD23	2:D:645:MET:HG3	2.04	0.40
2:D:774:LEU:HD13	2:D:777:LYS:HE3	2.03	0.40
2:B:768:PHE:HE1	2:B:800:TYR:HE1	1.70	0.40
2:D:553:LEU:HD23	2:D:553:LEU:C	2.46	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	151/207 (73%)	149 (99%)	2 (1%)	0	100	100
1	C	143/207 (69%)	142 (99%)	1 (1%)	0	100	100
2	B	417/458 (91%)	407 (98%)	9 (2%)	1 (0%)	43	72
2	D	418/458 (91%)	405 (97%)	13 (3%)	0	100	100
All	All	1129/1330 (85%)	1103 (98%)	25 (2%)	1 (0%)	48	77

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	809	PRO

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	137/179 (76%)	136 (99%)	1 (1%)	76	92
1	C	132/179 (74%)	130 (98%)	2 (2%)	57	84
2	B	389/423 (92%)	383 (98%)	6 (2%)	57	84
2	D	391/423 (92%)	388 (99%)	3 (1%)	73	90
All	All	1049/1204 (87%)	1037 (99%)	12 (1%)	65	88

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	52	LYS
2	B	524	LEU
2	B	718	GLU
2	B	727	LEU
2	B	736	SER
2	B	776	LEU
2	B	874	LEU
1	C	-47	THR
1	C	-26	THR
2	D	528	LYS
2	D	804	LEU
2	D	926	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	-4	ASN
2	B	681	GLN
2	B	872	ASN
1	C	-34	GLN
2	D	550	GLN
2	D	681	GLN
2	D	704	GLN
2	D	802	GLN
2	D	878	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 oligosaccharides in this entry.

5.6 Ligand geometry

Of 11 ligands modelled in this entry, 11 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, 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	153/207 (73%)	0.40	4 (2%) 57 48	50, 98, 145, 166	0
1	C	147/207 (71%)	0.23	2 (1%) 73 65	49, 93, 144, 170	0
2	B	421/458 (91%)	0.17	20 (4%) 35 28	45, 72, 140, 184	0
2	D	424/458 (92%)	0.28	20 (4%) 36 28	51, 83, 161, 199	0
All	All	1145/1330 (86%)	0.25	46 (4%) 42 34	45, 81, 151, 199	0

All (46) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	27	THR	4.1
2	D	514	SER	4.1
2	D	959	LEU	4.0
2	D	857	TYR	3.5
2	D	776	LEU	3.5
2	B	868	LEU	3.4
2	B	867	LEU	3.4
2	B	873	LEU	3.3
2	B	857	TYR	3.2
2	D	778	SER	3.2
2	D	798	LEU	2.9
2	D	931	LEU	2.8
2	B	956	ALA	2.8
1	A	29	ARG	2.8
2	B	870	ILE	2.8
2	D	867	LEU	2.7
2	B	589	CYS	2.7
2	B	885	ALA	2.6
1	A	58	ARG	2.5
2	D	773	SER	2.5
2	D	848	PRO	2.5

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
2	D	802	GLN	2.5
2	B	749	ASP	2.5
2	D	774	LEU	2.4
2	B	846	LEU	2.4
2	D	664	ARG	2.3
2	B	801	SER	2.3
2	B	671	LYS	2.3
2	D	775	PRO	2.3
2	B	664	ARG	2.3
2	D	874	LEU	2.2
2	B	777	LYS	2.2
2	D	542	LYS	2.2
2	D	868	LEU	2.2
2	D	932	LYS	2.2
2	B	869	GLU	2.2
2	B	515	THR	2.2
2	B	826	ARG	2.1
2	B	874	LEU	2.1
2	B	799	THR	2.1
1	A	-20	ILE	2.1
2	B	871	GLN	2.1
2	D	863	PRO	2.1
1	C	-34	GLN	2.1
2	D	886	LEU	2.1
1	C	-47	THR	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 oligosaccharides in this entry.

6.4 Ligands ⓘ

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
4	K	C	1001	1/1	0.48	0.24	109,109,109,109	0
4	K	D	1001	1/1	0.69	0.17	118,118,118,118	0
3	CL	A	1001	1/1	0.83	0.23	77,77,77,77	0
3	CL	C	1002	1/1	0.89	0.25	85,85,85,85	0
3	CL	A	1002	1/1	0.92	0.11	68,68,68,68	0
3	CL	B	1002	1/1	0.94	0.09	62,62,62,62	0
3	CL	C	1003	1/1	0.94	0.10	74,74,74,74	0
3	CL	A	1003	1/1	0.95	0.08	76,76,76,76	0
3	CL	D	1002	1/1	0.95	0.11	64,64,64,64	0
3	CL	D	1004	1/1	0.96	0.11	65,65,65,65	0
4	K	B	1001	1/1	0.98	0.04	63,63,63,63	0

6.5 Other polymers [i](#)

There are no such residues in this entry.