



wwPDB X-ray Structure Validation Summary Report ⓘ

Jun 17, 2024 – 11:12 AM EDT

PDB ID : 2WYR
Title : 3-D structure of PhTET1-12s, dodecamer in the asymmetric unit
Authors : Vellieux, F.M.D.; Dura, M.A.; Franzetti, B.
Deposited on : 2009-11-20
Resolution : 2.25 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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	:	4.02b-467
Xtriage (Phenix)	:	1.20.1
EDS	:	2.37.1
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)	:	2.37.1

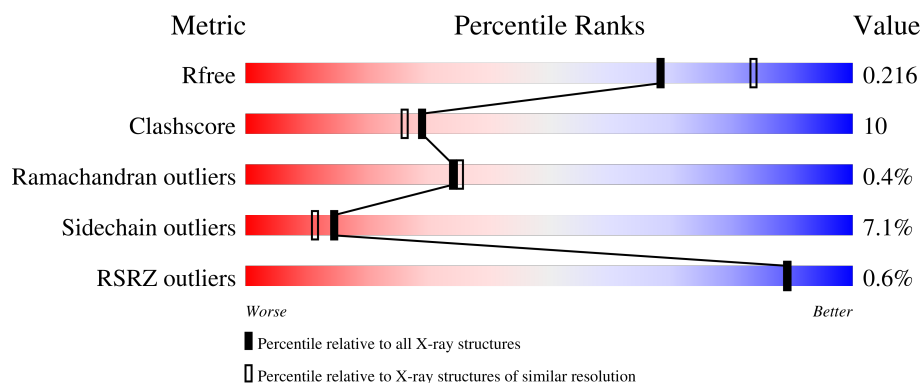
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.25 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	2391 (2.26-2.22)
Clashscore	141614	2539 (2.26-2.22)
Ramachandran outliers	138981	2489 (2.26-2.22)
Sidechain outliers	138945	2490 (2.26-2.22)
RSRZ outliers	127900	2353 (2.26-2.22)

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	332	<div> <div>%</div> <div> <div></div> <div>80%</div> <div>15%</div> <div>..</div> </div> </div>
1	B	332	<div> <div></div> <div>78%</div> <div>17%</div> <div>...</div> </div>
1	C	332	<div> <div>%</div> <div> <div></div> <div>80%</div> <div>17%</div> <div>..</div> </div> </div>
1	D	332	<div> <div></div> <div>72%</div> <div>21%</div> <div>5%</div> <div>.</div> </div>
1	E	332	<div> <div></div> <div>78%</div> <div>16%</div> <div>..</div> </div>

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Mol	Chain	Length	Quality of chain
1	F	332	<div><div><div>%</div><div><div></div><div></div><div></div></div><div>77%19%</div><div><div></div><div></div></div></div></div>
1	G	332	<div><div><div></div><div></div><div></div></div><div>80%16%</div><div><div></div><div></div></div></div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 32303 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 COBALT-ACTIVATED PEPTIDASE TET1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	326	Total	C	N	O	S	0	5	0
			2582	1665	426	485	6			
1	B	325	Total	C	N	O	S	0	5	0
			2579	1666	426	480	7			
1	C	326	Total	C	N	O	S	0	2	0
			2568	1656	428	478	6			
1	D	325	Total	C	N	O	S	0	2	0
			2560	1653	423	478	6			
1	E	326	Total	C	N	O	S	0	3	0
			2574	1662	425	481	6			
1	F	324	Total	C	N	O	S	0	2	0
			2554	1648	424	477	5			
1	G	325	Total	C	N	O	S	0	1	0
			2554	1648	422	478	6			
1	H	326	Total	C	N	O	S	0	4	0
			2579	1664	430	479	6			
1	I	325	Total	C	N	O	S	0	0	0
			2545	1640	422	477	6			
1	J	326	Total	C	N	O	S	0	1	0
			2560	1651	425	478	6			
1	K	325	Total	C	N	O	S	0	3	0
			2565	1656	423	480	6			
1	L	325	Total	C	N	O	S	0	1	0
			2553	1645	425	477	6			

- Molecule 2 is COBALT (II) ION (three-letter code: CO) (formula: Co).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	2	Total	Co	0	0
			2	2		
2	B	2	Total	Co	0	0
			2	2		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	C	2	Total 2	Co 2	0	0
2	D	2	Total 2	Co 2	0	0
2	E	2	Total 2	Co 2	0	0
2	F	2	Total 2	Co 2	0	0
2	G	2	Total 2	Co 2	0	0
2	H	2	Total 2	Co 2	0	0
2	I	2	Total 2	Co 2	0	0
2	J	2	Total 2	Co 2	0	0
2	K	2	Total 2	Co 2	0	0
2	L	2	Total 2	Co 2	0	0

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	140	Total 140	O 140	0	0
3	B	122	Total 122	O 122	0	0
3	C	146	Total 146	O 146	0	0
3	D	125	Total 125	O 125	0	0
3	E	143	Total 143	O 143	0	0
3	F	110	Total 110	O 110	0	0
3	G	142	Total 142	O 142	0	0
3	H	110	Total 110	O 110	0	0
3	I	84	Total 84	O 84	0	0

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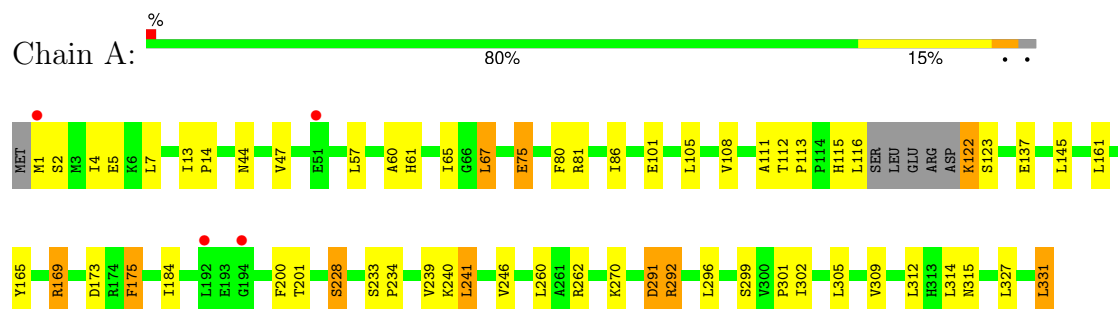
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	J	135	Total 135	O 135	0	0
3	K	122	Total 122	O 122	0	0
3	L	127	Total 127	O 127	0	0

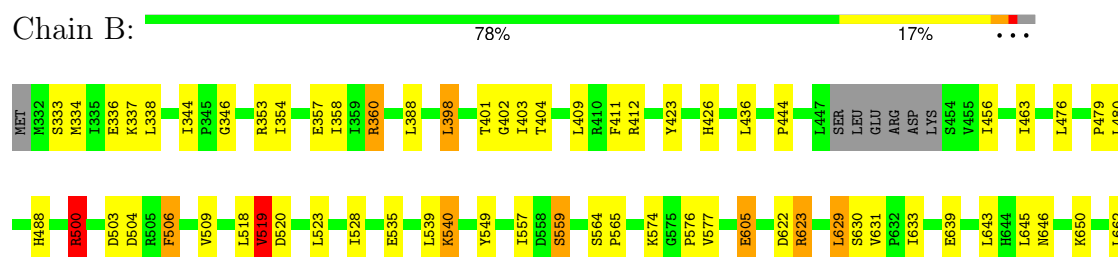
3 Residue-property plots [i](#)

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.

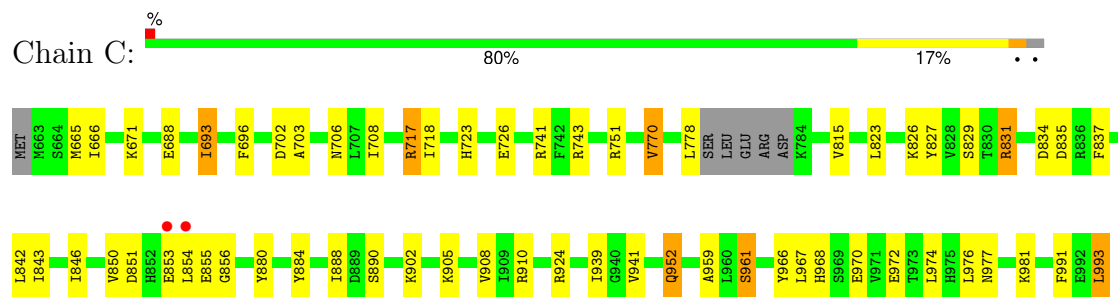
• Molecule 1: COBAL-T-ACTIVATED PEPTIDASE TET1



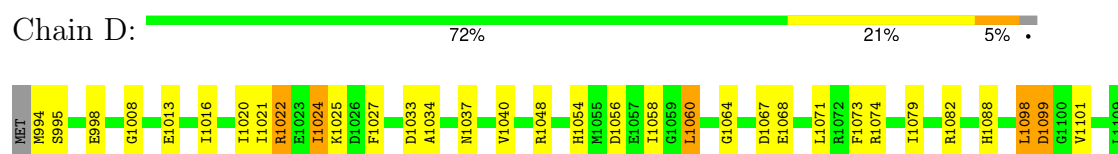
• Molecule 1: COBAL-T-ACTIVATED PEPTIDASE TET1

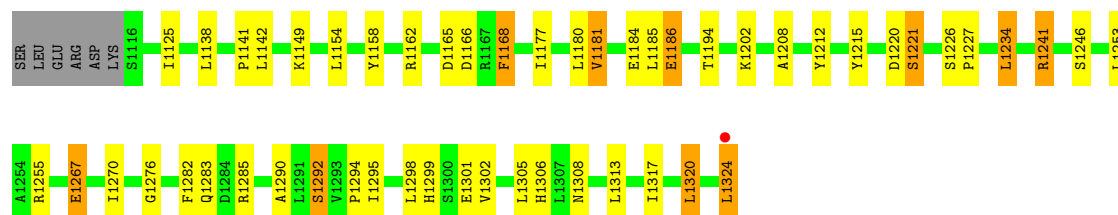


• Molecule 1: COBAL-T-ACTIVATED PEPTIDASE TET1



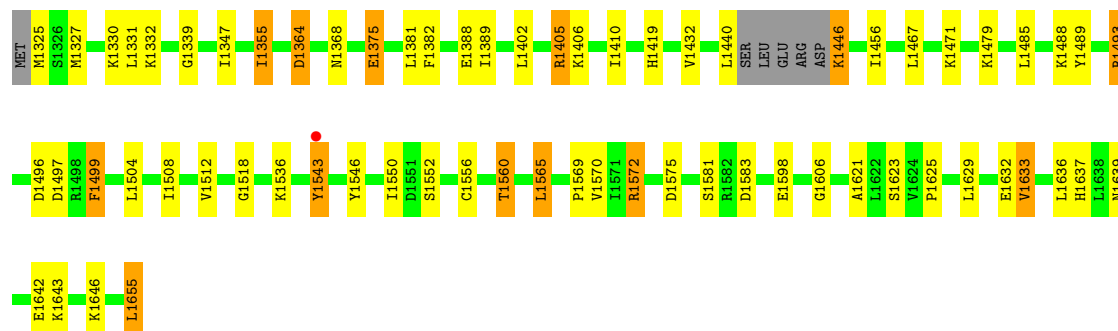
• Molecule 1: COBAL-T-ACTIVATED PEPTIDASE TET1





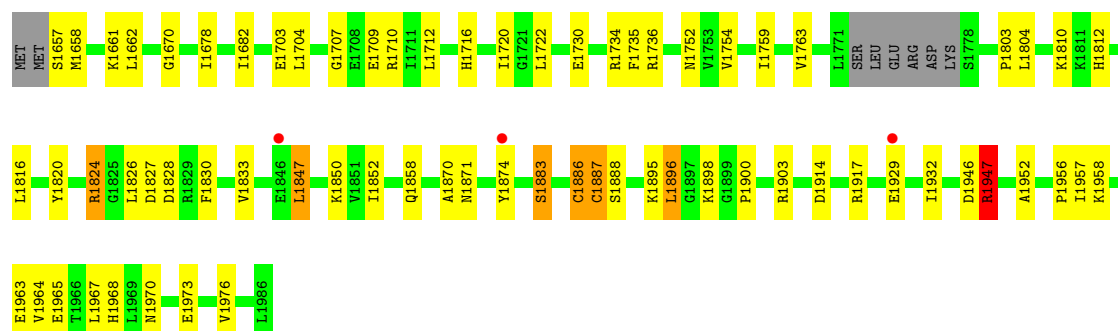
• Molecule 1: COBALT-ACTIVATED PEPTIDASE TET1

Chain E: 78% 16%



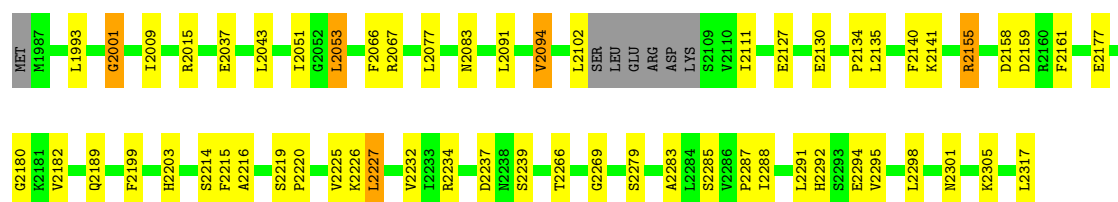
• Molecule 1: COBALT-ACTIVATED PEPTIDASE TET1

Chain F: 77% 19%



• Molecule 1: COBALT-ACTIVATED PEPTIDASE TET1

Chain G: 80% 16%



• Molecule 1: COBALT-ACTIVATED PEPTIDASE TET1

Chain H: 70% 23%

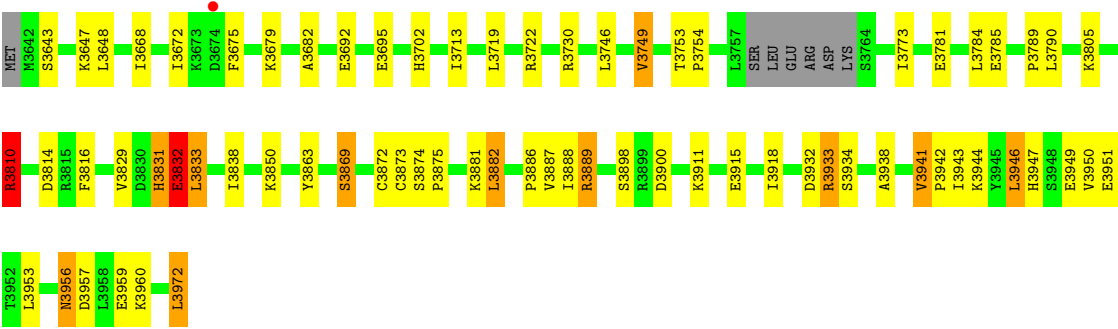
● Molecule 1: COBALT-ACTIVATED PEPTIDASE TET1

Chain L:

77%

17%

...



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	113.26Å 205.22Å 113.49Å 90.00° 100.78° 90.00°	Depositor
Resolution (Å)	49.68 – 2.25 49.68 – 2.25	Depositor EDS
% Data completeness (in resolution range)	99.8 (49.68-2.25) 99.8 (49.68-2.25)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.17 (at 2.25Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE)	Depositor
R, R_{free}	0.170 , 0.220 0.167 , 0.216	Depositor DCC
R_{free} test set	12098 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	30.9	Xtriage
Anisotropy	0.199	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 53.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.27$	Xtriage
Estimated twinning fraction	0.038 for l,-k,h	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	32303	wwPDB-VP
Average B, all atoms (Å ²)	35.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.97% 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

5.1 Standard geometry

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

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	0.39	0/2641	0.60	1/3559 (0.0%)
1	B	0.39	0/2639	0.61	1/3558 (0.0%)
1	C	0.42	0/2618	0.61	0/3527
1	D	0.40	0/2611	0.61	0/3521
1	E	0.42	0/2628	0.62	1/3543 (0.0%)
1	F	0.36	0/2605	0.60	1/3514 (0.0%)
1	G	0.44	0/2602	0.66	1/3510 (0.0%)
1	H	0.38	0/2635	0.62	1/3549 (0.0%)
1	I	0.36	0/2589	0.60	1/3491 (0.0%)
1	J	0.42	0/2607	0.62	0/3513
1	K	0.39	0/2619	0.61	1/3532 (0.0%)
1	L	0.41	0/2600	0.61	1/3505 (0.0%)
All	All	0.40	0/31394	0.61	9/42322 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	C	0	1
1	F	0	1
1	H	0	1
1	J	0	1
1	L	0	1
All	All	0	6

There are no bond length outliers.

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	1493	ARG	NE-CZ-NH2	-6.93	116.84	120.30
1	F	1887	CYS	CA-CB-SG	-5.97	103.25	114.00
1	A	169	ARG	NE-CZ-NH2	-5.95	117.33	120.30
1	B	500	ARG	NE-CZ-NH1	-5.73	117.44	120.30
1	H	2580	LYS	N-CA-C	-5.59	95.90	111.00

There are no chirality outliers.

5 of 6 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	299	SER	Peptide
1	C	961	SER	Peptide
1	F	1886	CYS	Peptide
1	H	2548	CYS	Peptide
1	J	3278	SER	Peptide

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	2582	0	2642	38	0
1	B	2579	0	2642	61	0
1	C	2568	0	2631	48	0
1	D	2560	0	2614	80	0
1	E	2574	0	2631	54	0
1	F	2554	0	2605	50	0
1	G	2554	0	2601	41	0
1	H	2579	0	2650	73	0
1	I	2545	0	2592	75	0
1	J	2560	0	2618	39	0
1	K	2565	0	2618	43	0
1	L	2553	0	2605	55	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
2	C	2	0	0	0	0
2	D	2	0	0	0	0
2	E	2	0	0	0	0
2	F	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	G	2	0	0	0	0
2	H	2	0	0	0	0
2	I	2	0	0	0	0
2	J	2	0	0	0	0
2	K	2	0	0	0	0
2	L	2	0	0	0	0
3	A	140	0	0	4	0
3	B	122	0	0	3	0
3	C	146	0	0	5	0
3	D	125	0	0	8	0
3	E	143	0	0	3	0
3	F	110	0	0	5	0
3	G	142	0	0	4	0
3	H	110	0	0	6	0
3	I	84	0	0	4	0
3	J	135	0	0	1	0
3	K	122	0	0	2	0
3	L	127	0	0	5	0
All	All	32303	0	31449	598	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 10.

The worst 5 of 598 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:D:1220:ASP:O	1:D:1292:SER:HB3	1.43	1.18
1:I:2841:GLU:N	1:I:2842:GLY:HA3	1.56	1.10
1:B:559:SER:HB3	1:B:633:ILE:HD12	1.40	1.04
1:I:2875:ASP:O	1:I:2947:SER:HB3	1.57	1.03
1:B:334[A]:MET:HA	1:B:334[A]:MET:HE3	1.43	0.98

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	A	326/332 (98%)	316 (97%)	10 (3%)	0	100	100
1	B	326/332 (98%)	308 (94%)	17 (5%)	1 (0%)	41	44
1	C	324/332 (98%)	310 (96%)	14 (4%)	0	100	100
1	D	323/332 (97%)	307 (95%)	15 (5%)	1 (0%)	41	44
1	E	325/332 (98%)	314 (97%)	11 (3%)	0	100	100
1	F	322/332 (97%)	311 (97%)	10 (3%)	1 (0%)	41	44
1	G	322/332 (97%)	313 (97%)	8 (2%)	1 (0%)	41	44
1	H	326/332 (98%)	309 (95%)	14 (4%)	3 (1%)	17	13
1	I	321/332 (97%)	297 (92%)	18 (6%)	6 (2%)	8	3
1	J	323/332 (97%)	312 (97%)	10 (3%)	1 (0%)	41	44
1	K	324/332 (98%)	308 (95%)	15 (5%)	1 (0%)	41	44
1	L	322/332 (97%)	305 (95%)	16 (5%)	1 (0%)	41	44
All	All	3884/3984 (98%)	3710 (96%)	158 (4%)	16 (0%)	34	35

5 of 16 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	519	VAL
1	I	2841	GLU
1	K	3342	LYS
1	F	1947	ARG
1	I	2842	GLY

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	278/279 (100%)	259 (93%)	19 (7%)	16	13
1	B	277/279 (99%)	262 (95%)	15 (5%)	22	20

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	C	275/279 (99%)	261 (95%)	14 (5%)	24	23
1	D	274/279 (98%)	255 (93%)	19 (7%)	15	12
1	E	276/279 (99%)	254 (92%)	22 (8%)	12	8
1	F	273/279 (98%)	259 (95%)	14 (5%)	24	23
1	G	273/279 (98%)	258 (94%)	15 (6%)	21	20
1	H	277/279 (99%)	251 (91%)	26 (9%)	8	5
1	I	272/279 (98%)	248 (91%)	24 (9%)	10	6
1	J	274/279 (98%)	254 (93%)	20 (7%)	14	10
1	K	275/279 (99%)	253 (92%)	22 (8%)	12	8
1	L	273/279 (98%)	248 (91%)	25 (9%)	9	5
All	All	3297/3348 (98%)	3062 (93%)	235 (7%)	14	11

5 of 235 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	G	2279	SER
1	L	3831	HIS
1	H	2648	LEU
1	L	3810	ARG
1	K	3485	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 48 such sidechains are listed below:

Mol	Chain	Res	Type
1	H	2607	GLN
1	I	2963	ASN
1	I	2745	ASN
1	I	2851	GLN
1	J	3200	GLN

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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 24 ligands modelled in this entry, 24 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 [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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	326/332 (98%)	-0.44	4 (1%) 79 80	17, 29, 58, 83	0
1	B	325/332 (97%)	-0.48	0 100 100	18, 32, 60, 85	0
1	C	326/332 (98%)	-0.52	2 (0%) 89 89	15, 28, 53, 82	0
1	D	325/332 (97%)	-0.46	1 (0%) 94 94	20, 35, 60, 83	0
1	E	326/332 (98%)	-0.55	1 (0%) 94 94	19, 29, 51, 73	0
1	F	324/332 (97%)	-0.37	3 (0%) 84 84	24, 35, 62, 81	0
1	G	325/332 (97%)	-0.51	0 100 100	17, 27, 48, 70	0
1	H	326/332 (98%)	-0.39	3 (0%) 84 84	23, 36, 62, 85	0
1	I	325/332 (97%)	-0.25	7 (2%) 62 63	25, 41, 70, 94	0
1	J	326/332 (98%)	-0.52	1 (0%) 94 94	19, 28, 53, 74	0
1	K	325/332 (97%)	-0.39	1 (0%) 94 94	20, 33, 57, 81	0
1	L	325/332 (97%)	-0.58	1 (0%) 94 94	16, 29, 53, 78	1 (0%)
All	All	3904/3984 (97%)	-0.45	24 (0%) 89 89	15, 32, 59, 94	1 (0%)

The worst 5 of 24 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	I	2840	LEU	3.5
1	E	1543[A]	TYR	3.4
1	H	2509	LEU	3.3
1	C	853	GLU	3.2
1	C	854	LEU	3.2

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 monosaccharides 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, 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(\AA^2)	Q<0.9
2	CO	B	1663	1/1	0.98	0.12	30,30,30,30	0
2	CO	B	1664	1/1	0.98	0.12	25,25,25,25	0
2	CO	D	2325	1/1	0.98	0.08	35,35,35,35	0
2	CO	E	2656	1/1	0.98	0.10	30,30,30,30	0
2	CO	H	3649	1/1	0.98	0.12	39,39,39,39	0
2	CO	I	3980	1/1	0.98	0.12	38,38,38,38	0
2	CO	K	4642	1/1	0.98	0.13	35,35,35,35	0
2	CO	F	2987	1/1	0.99	0.09	35,35,35,35	0
2	CO	A	1332	1/1	0.99	0.11	28,28,28,28	0
2	CO	H	3650	1/1	0.99	0.12	29,29,29,29	0
2	CO	D	2326	1/1	0.99	0.11	28,28,28,28	0
2	CO	I	3981	1/1	0.99	0.13	33,33,33,33	0
2	CO	J	4311	1/1	0.99	0.12	28,28,28,28	0
2	CO	J	4312	1/1	0.99	0.14	23,23,23,23	0
2	CO	A	1333	1/1	0.99	0.13	24,24,24,24	0
2	CO	L	4974	1/1	0.99	0.12	23,23,23,23	0
2	CO	C	1995	1/1	1.00	0.13	22,22,22,22	0
2	CO	F	2988	1/1	1.00	0.13	29,29,29,29	0
2	CO	G	3318	1/1	1.00	0.11	27,27,27,27	0
2	CO	G	3319	1/1	1.00	0.12	24,24,24,24	0
2	CO	C	1994	1/1	1.00	0.10	30,30,30,30	0
2	CO	K	4643	1/1	1.00	0.12	26,26,26,26	0
2	CO	L	4973	1/1	1.00	0.09	29,29,29,29	0
2	CO	E	2657	1/1	1.00	0.12	27,27,27,27	0

6.5 Other polymers [i](#)

There are no such residues in this entry.