



wwPDB X-ray Structure Validation Summary Report ⓘ

Dec 13, 2016 – 12:09 AM EST

PDB ID : 5K1I
Title : PDE4 crystal structure in complex with small molecule inhibitor
Authors : Segarra, V.; Hernandez, B.; Ferrer-Miralles, N.; Korndorfer, I.; Aymami, J.
Deposited on : 2016-05-18
Resolution : 2.61 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

<http://wwpdb.org/validation/2016/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
Mogul	:	1.7.1 (RC1), CSD as537be (2016)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20028442
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-20028442

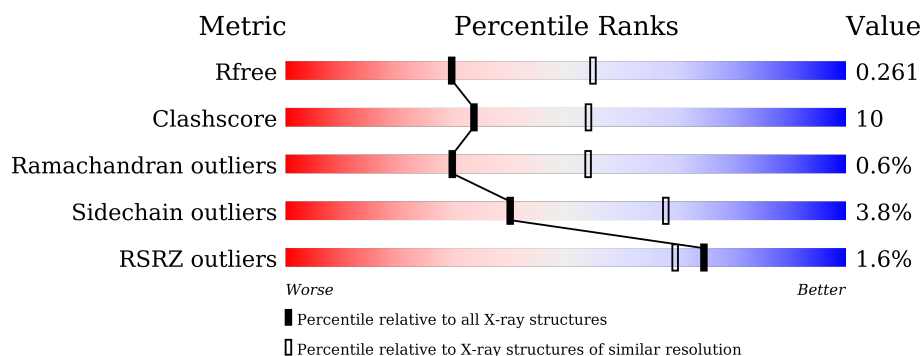
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.61 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	2700 (2.64-2.60)
Clashscore	102246	3065 (2.64-2.60)
Ramachandran outliers	100387	3015 (2.64-2.60)
Sidechain outliers	100360	3015 (2.64-2.60)
RSRZ outliers	91569	2706 (2.64-2.60)

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. 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	326	<div> <div>2%</div> <div> <div></div> <div>73%</div> <div>23%</div> <div>..</div> </div> </div>
1	B	326	<div> <div>%</div> <div> <div></div> <div>77%</div> <div>21%</div> <div>.</div> </div> </div>
1	C	326	<div> <div>%</div> <div> <div></div> <div>77%</div> <div>20%</div> <div>..</div> </div> </div>
1	D	326	<div> <div>%</div> <div> <div></div> <div>80%</div> <div>18%</div> <div>.</div> </div> </div>
1	E	326	<div> <div>%</div> <div> <div></div> <div>83%</div> <div>15%</div> <div>..</div> </div> </div>
1	F	326	<div> <div>4%</div> <div> <div></div> <div>70%</div> <div>27%</div> <div>.</div> </div> </div>

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Mol	Chain	Length	Quality of chain
1	G	326	
1	H	326	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	6PT	D	1001	-	-	-	X
2	6PT	G	1001	-	-	-	X
4	MG	A	1003	-	-	-	X
4	MG	B	1003	-	-	-	X
4	MG	C	1003	-	-	-	X
4	MG	D	1003	-	-	-	X
4	MG	E	1003	-	-	-	X
4	MG	F	1003	-	-	-	X
4	MG	G	1003	-	-	-	X
4	MG	H	1003	-	-	-	X

2 Entry composition

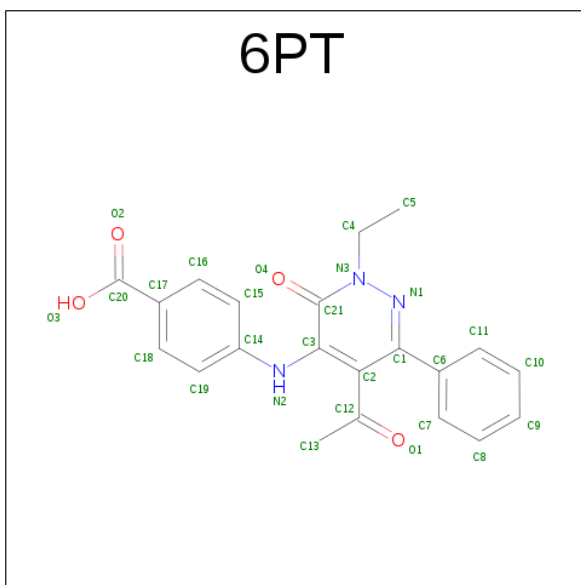
There are 5 unique types of molecules in this entry. The entry contains 21443 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 cAMP-specific 3',5'-cyclic phosphodiesterase 4D.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	322	Total	C	N	O	S	0	0	0
			2613	1655	446	498	14			
1	B	326	Total	C	N	O	S	0	0	0
			2637	1668	450	505	14			
1	C	321	Total	C	N	O	S	0	0	0
			2608	1652	445	497	14			
1	D	326	Total	C	N	O	S	0	0	0
			2638	1668	450	506	14			
1	E	321	Total	C	N	O	S	0	0	0
			2608	1652	445	497	14			
1	F	326	Total	C	N	O	S	0	0	0
			2638	1668	450	506	14			
1	G	322	Total	C	N	O	S	0	0	0
			2613	1655	446	498	14			
1	H	326	Total	C	N	O	S	0	0	0
			2638	1668	450	506	14			

- Molecule 2 is 4-[(5-acetyl-2-ethyl-3-oxo-6-phenyl-2,3-dihydropyridazin-4-yl)amino]benzoic acid (three-letter code: 6PT) (formula: C₂₁H₁₉N₃O₄).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			28	21	3	4		
2	B	1	Total	C	N	O	0	0
			28	21	3	4		
2	C	1	Total	C	N	O	0	0
			28	21	3	4		
2	D	1	Total	C	N	O	0	0
			28	21	3	4		
2	E	1	Total	C	N	O	0	0
			28	21	3	4		
2	F	1	Total	C	N	O	0	0
			28	21	3	4		
2	G	1	Total	C	N	O	0	0
			28	21	3	4		
2	H	1	Total	C	N	O	0	0
			28	21	3	4		

- Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	G	1	Total	Zn	0	0
			1	1		
3	D	1	Total	Zn	0	0
			1	1		
3	E	1	Total	Zn	0	0
			1	1		
3	H	1	Total	Zn	0	0
			1	1		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	1	Total 1	Zn 1	0	0
3	C	1	Total 1	Zn 1	0	0
3	A	1	Total 1	Zn 1	0	0
3	F	1	Total 1	Zn 1	0	0

- Molecule 4 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	G	1	Total 1	Mg 1	0	0
4	D	1	Total 1	Mg 1	0	0
4	E	1	Total 1	Mg 1	0	0
4	H	1	Total 1	Mg 1	0	0
4	B	1	Total 1	Mg 1	0	0
4	C	1	Total 1	Mg 1	0	0
4	A	1	Total 1	Mg 1	0	0
4	F	1	Total 1	Mg 1	0	0

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	18	Total 18	O 18	0	0
5	B	35	Total 35	O 35	0	0
5	C	33	Total 33	O 33	0	0
5	D	21	Total 21	O 21	0	0
5	E	32	Total 32	O 32	0	0

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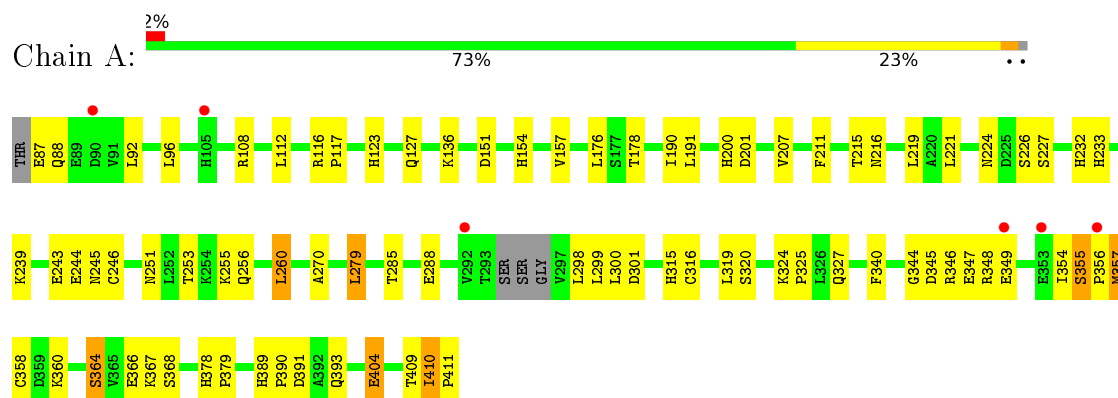
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	F	15	Total 15	O 15	0	0
5	G	33	Total 33	O 33	0	0
5	H	23	Total 23	O 23	0	0

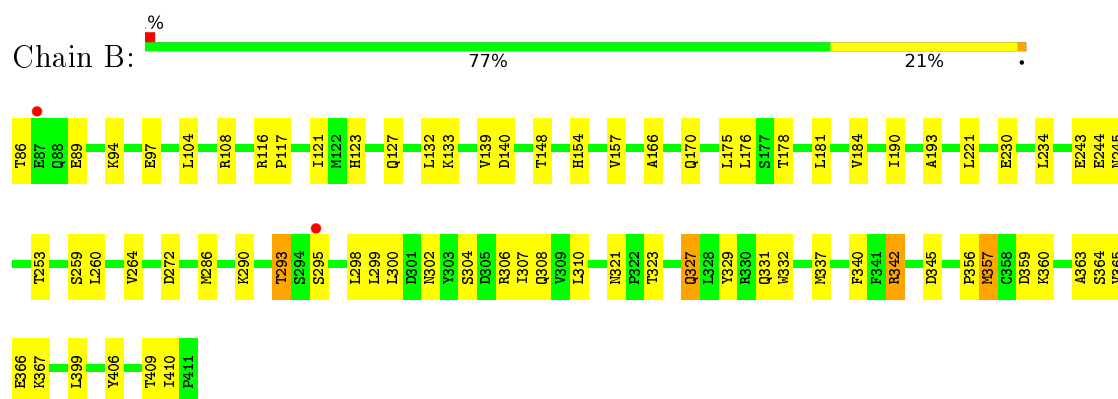
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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 ($RSRZ > 2$). 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.

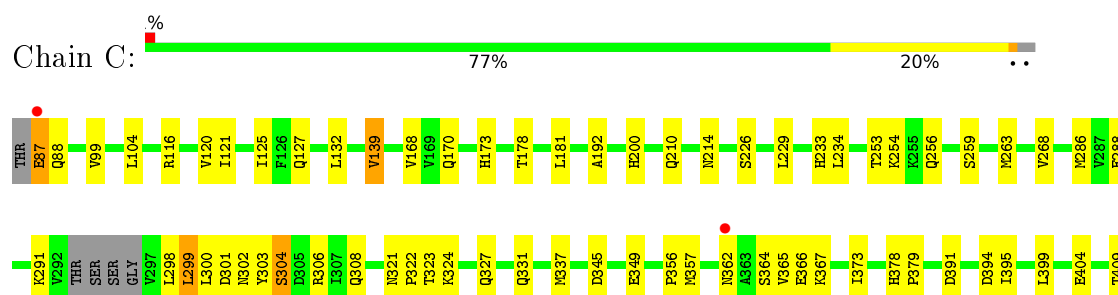
- Molecule 1: cAMP-specific 3',5'-cyclic phosphodiesterase 4D



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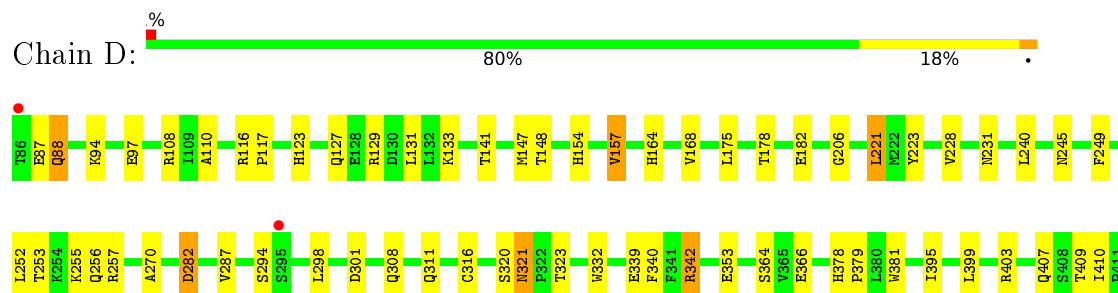


- Molecule 1: cAMP-specific 3',5'-cyclic phosphodiesterase 4D

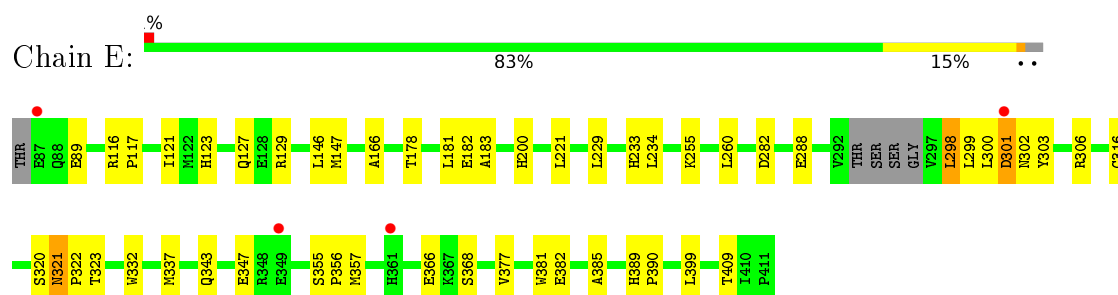


I410
P411

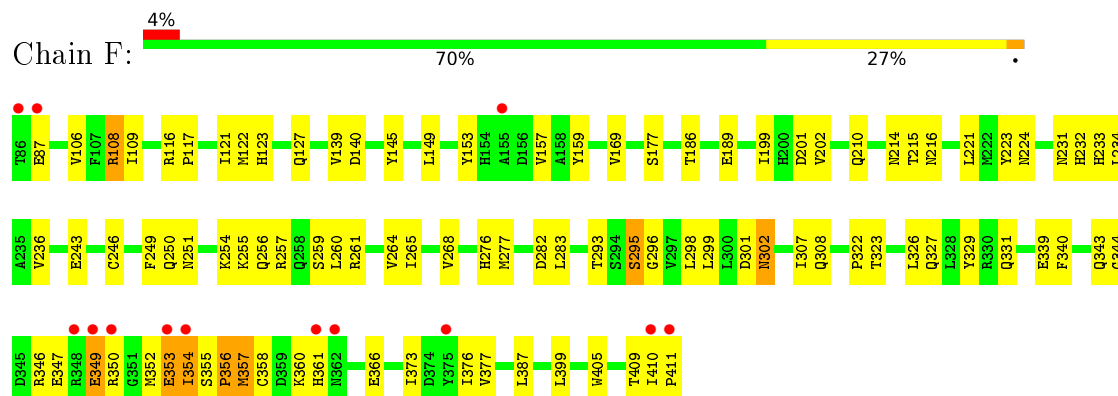
- Molecule 1: cAMP-specific 3',5'-cyclic phosphodiesterase 4D



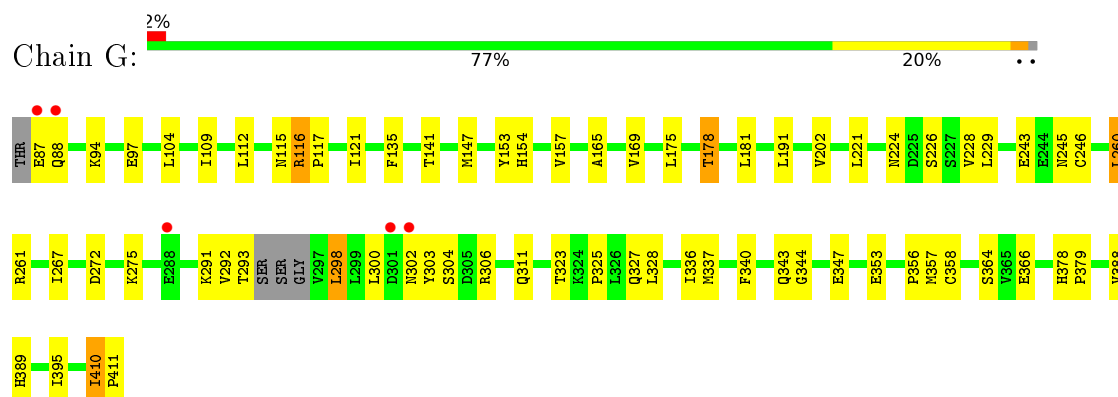
- Molecule 1: cAMP-specific 3',5'-cyclic phosphodiesterase 4D



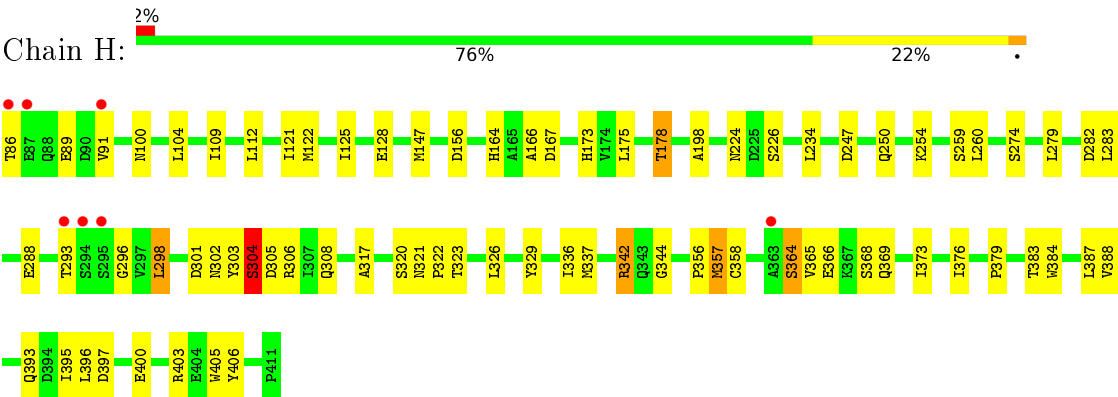
- Molecule 1: cAMP-specific 3',5'-cyclic phosphodiesterase 4D



- Molecule 1: cAMP-specific 3',5'-cyclic phosphodiesterase 4D



● Molecule 1: cAMP-specific 3',5'-cyclic phosphodiesterase 4D



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	61.44Å 78.35Å 161.76Å 91.01° 92.79° 90.08°	Depositor
Resolution (Å)	25.00 – 2.61 24.98 – 2.61	Depositor EDS
% Data completeness (in resolution range)	94.8 (25.00-2.61) 94.5 (24.98-2.61)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.98 (at 2.60Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.191 , 0.258 0.197 , 0.261	Depositor DCC
R_{free} test set	4408 reflections (5.33%)	DCC
Wilson B-factor (Å ²)	26.7	Xtriage
Anisotropy	0.214	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 44.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.27$	Xtriage
Estimated twinning fraction	0.077 for h,-k,-l 0.069 for -h,k,-l 0.065 for -h,-k,l	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	21443	wwPDB-VP
Average B, all atoms (Å ²)	30.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.95% 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: 6PT, ZN, MG

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	0.56	0/2666	0.66	0/3621
1	B	0.62	0/2691	0.71	0/3656
1	C	0.61	0/2661	0.72	0/3614
1	D	0.61	0/2692	0.71	1/3658 (0.0%)
1	E	0.64	0/2661	0.74	1/3614 (0.0%)
1	F	0.54	0/2692	0.65	0/3658
1	G	0.60	0/2666	0.69	0/3621
1	H	0.61	0/2692	0.70	0/3658
All	All	0.60	0/21421	0.70	2/29100 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	221	LEU	CA-CB-CG	-5.66	102.28	115.30
1	E	282	ASP	CB-CG-OD1	5.26	123.03	118.30

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	2613	0	2565	56	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	2637	0	2589	54	0
1	C	2608	0	2563	50	0
1	D	2638	0	2591	47	0
1	E	2608	0	2563	38	0
1	F	2638	0	2591	82	0
1	G	2613	0	2565	48	0
1	H	2638	0	2591	49	0
2	A	28	0	0	1	0
2	B	28	0	0	3	0
2	C	28	0	0	1	0
2	D	28	0	0	2	0
2	E	28	0	0	1	0
2	F	28	0	0	3	0
2	G	28	0	0	4	0
2	H	28	0	0	1	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
3	E	1	0	0	0	0
3	F	1	0	0	0	0
3	G	1	0	0	0	0
3	H	1	0	0	0	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
4	C	1	0	0	0	0
4	D	1	0	0	0	0
4	E	1	0	0	0	0
4	F	1	0	0	0	0
4	G	1	0	0	0	0
4	H	1	0	0	0	0
5	A	18	0	0	6	0
5	B	35	0	0	3	0
5	C	33	0	0	3	0
5	D	21	0	0	2	0
5	E	32	0	0	3	0
5	F	15	0	0	11	0
5	G	33	0	0	0	0
5	H	23	0	0	4	0
All	All	21443	0	20618	425	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 425 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:F:301:ASP:HB3	5:F:1109:HOH:O	1.18	1.27
1:C:411:PRO:HB3	5:C:1125:HOH:O	1.35	1.26
1:F:358:CYS:HB3	5:F:1103:HOH:O	1.02	1.17
1:F:331:GLN:HB3	5:F:1104:HOH:O	1.40	1.16
1:F:108:ARG:HH11	1:F:108:ARG:CG	1.57	1.14

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	318/326 (98%)	286 (90%)	29 (9%)	3 (1%)	21	41
1	B	324/326 (99%)	306 (94%)	17 (5%)	1 (0%)	46	70
1	C	317/326 (97%)	299 (94%)	18 (6%)	0	100	100
1	D	324/326 (99%)	306 (94%)	18 (6%)	0	100	100
1	E	317/326 (97%)	301 (95%)	16 (5%)	0	100	100
1	F	324/326 (99%)	284 (88%)	35 (11%)	5 (2%)	13	24
1	G	318/326 (98%)	293 (92%)	22 (7%)	3 (1%)	21	41
1	H	324/326 (99%)	301 (93%)	20 (6%)	3 (1%)	21	41
All	All	2566/2608 (98%)	2376 (93%)	175 (7%)	15 (1%)	30	54

5 of 15 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	F	353	GLU
1	F	357	MET
1	G	410	ILE

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Mol	Chain	Res	Type
1	H	304	SER
1	F	349	GLU

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	294/298 (99%)	280 (95%)	14 (5%)	31	57
1	B	297/298 (100%)	287 (97%)	10 (3%)	44	71
1	C	294/298 (99%)	284 (97%)	10 (3%)	44	71
1	D	298/298 (100%)	283 (95%)	15 (5%)	30	55
1	E	294/298 (99%)	285 (97%)	9 (3%)	47	75
1	F	298/298 (100%)	289 (97%)	9 (3%)	48	75
1	G	294/298 (99%)	285 (97%)	9 (3%)	47	75
1	H	298/298 (100%)	283 (95%)	15 (5%)	30	55
All	All	2367/2384 (99%)	2276 (96%)	91 (4%)	40	68

5 of 91 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	287	VAL
1	E	221	LEU
1	H	304	SER
1	D	294	SER
1	D	353	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 46 such sidechains are listed below:

Mol	Chain	Res	Type
1	E	123	HIS
1	E	308	GLN
1	H	242	GLN

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Mol	Chain	Res	Type
1	E	210	GLN
1	E	245	ASN

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 carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 24 ligands modelled in this entry, 16 are monoatomic - leaving 8 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	6PT	A	1001	-	24,30,30	0.77	1 (4%)	25,42,42	1.33	3 (12%)
2	6PT	B	1001	-	24,30,30	0.85	2 (8%)	25,42,42	1.41	2 (8%)
2	6PT	C	1001	-	24,30,30	0.67	0	25,42,42	1.44	4 (16%)
2	6PT	D	1001	-	24,30,30	0.65	1 (4%)	25,42,42	1.60	7 (28%)
2	6PT	E	1001	-	24,30,30	0.94	1 (4%)	25,42,42	1.69	7 (28%)
2	6PT	F	1001	-	24,30,30	0.63	0	25,42,42	1.57	4 (16%)
2	6PT	G	1001	-	24,30,30	0.82	1 (4%)	25,42,42	1.56	5 (20%)
2	6PT	H	1001	-	24,30,30	0.89	1 (4%)	25,42,42	1.88	6 (24%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral

centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	6PT	A	1001	-	-	0/13/18/18	0/3/3/3
2	6PT	B	1001	-	-	0/13/18/18	0/3/3/3
2	6PT	C	1001	-	-	0/13/18/18	0/3/3/3
2	6PT	D	1001	-	-	0/13/18/18	0/3/3/3
2	6PT	E	1001	-	-	0/13/18/18	0/3/3/3
2	6PT	F	1001	-	-	0/13/18/18	0/3/3/3
2	6PT	G	1001	-	-	0/13/18/18	0/3/3/3
2	6PT	H	1001	-	-	0/13/18/18	0/3/3/3

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	G	1001	6PT	C21-C3	-3.05	1.37	1.41
2	B	1001	6PT	C21-C3	-2.05	1.38	1.41
2	D	1001	6PT	C1-N1	2.02	1.35	1.33
2	B	1001	6PT	C1-N1	2.12	1.35	1.33
2	E	1001	6PT	C1-N1	2.87	1.36	1.33

The worst 5 of 38 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	1001	6PT	C7-C6-C1	-4.43	113.69	120.60
2	H	1001	6PT	C2-C1-C6	-3.90	118.07	123.51
2	F	1001	6PT	C7-C6-C1	-3.83	114.63	120.60
2	D	1001	6PT	O1-C12-C2	-3.44	113.29	119.97
2	F	1001	6PT	O1-C12-C2	-3.39	113.39	119.97

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

8 monomers are involved in 16 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1001	6PT	1	0
2	B	1001	6PT	3	0
2	C	1001	6PT	1	0
2	D	1001	6PT	2	0
2	E	1001	6PT	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	F	1001	6PT	3	0
2	G	1001	6PT	4	0
2	H	1001	6PT	1	0

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	322/326 (98%)	-0.12	6 (1%) 70 65	22, 36, 59, 82	0
1	B	326/326 (100%)	-0.31	2 (0%) 90 88	15, 27, 48, 63	0
1	C	321/326 (98%)	-0.27	3 (0%) 85 83	17, 26, 44, 55	0
1	D	326/326 (100%)	-0.35	2 (0%) 90 88	17, 26, 45, 65	0
1	E	321/326 (98%)	-0.33	4 (1%) 81 77	14, 24, 42, 52	0
1	F	326/326 (100%)	-0.04	13 (3%) 42 35	22, 37, 63, 83	0
1	G	322/326 (98%)	-0.36	5 (1%) 74 69	16, 27, 43, 63	0
1	H	326/326 (100%)	-0.16	7 (2%) 67 61	17, 30, 50, 71	0
All	All	2590/2608 (99%)	-0.24	42 (1%) 74 69	14, 29, 52, 83	0

The worst 5 of 42 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	411	PRO	5.2
1	H	86	THR	4.9
1	H	295	SER	4.3
1	F	353	GLU	4.0
1	F	86	THR	3.5

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 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, 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	LLDF	B-factors(Å ²)	Q<0.9
4	MG	H	1003	1/1	0.87	0.62	55.18	38,38,38,38	0
4	MG	B	1003	1/1	0.94	0.64	46.70	37,37,37,37	0
4	MG	F	1003	1/1	0.96	0.55	27.80	37,37,37,37	0
4	MG	D	1003	1/1	0.95	0.63	26.80	34,34,34,34	0
4	MG	C	1003	1/1	0.95	0.59	23.77	38,38,38,38	0
4	MG	G	1003	1/1	0.94	0.67	21.32	35,35,35,35	0
4	MG	A	1003	1/1	0.89	0.41	19.65	42,42,42,42	0
4	MG	E	1003	1/1	0.85	0.38	15.13	38,38,38,38	0
2	6PT	G	1001	28/28	0.95	0.20	2.75	27,28,30,30	0
2	6PT	D	1001	28/28	0.95	0.18	2.17	28,29,30,31	0
2	6PT	E	1001	28/28	0.93	0.18	1.94	27,29,30,31	0
2	6PT	B	1001	28/28	0.94	0.18	1.70	28,29,29,29	0
2	6PT	C	1001	28/28	0.93	0.19	1.26	27,29,30,31	0
2	6PT	A	1001	28/28	0.93	0.18	0.50	28,30,31,32	0
2	6PT	F	1001	28/28	0.92	0.17	0.42	29,30,31,32	0
2	6PT	H	1001	28/28	0.95	0.14	-0.10	28,29,30,31	0
3	ZN	C	1002	1/1	0.97	0.12	-0.65	32,32,32,32	0
3	ZN	B	1002	1/1	0.99	0.12	-1.01	29,29,29,29	0
3	ZN	G	1002	1/1	0.98	0.12	-1.30	26,26,26,26	0
3	ZN	D	1002	1/1	0.98	0.10	-1.53	33,33,33,33	0
3	ZN	F	1002	1/1	0.99	0.11	-1.79	37,37,37,37	0
3	ZN	E	1002	1/1	0.99	0.10	-1.83	31,31,31,31	0
3	ZN	H	1002	1/1	0.97	0.08	-1.87	36,36,36,36	0
3	ZN	A	1002	1/1	0.98	0.10	-2.01	37,37,37,37	0

6.5 Other polymers [i](#)

There are no such residues in this entry.