



wwPDB X-ray Structure Validation Summary Report ⓘ

Jun 22, 2024 – 04:37 PM EDT

PDB ID : 6HXG
Title : PDX1.2/PDX1.3 complex (intermediate)
Authors : Robinson, G.C.; Kaufmann, M.; Roux, C.; Martinez-Font, J.; Hothorn, M.;
Thore, S.; Fitzpatrick, T.B.
Deposited on : 2018-10-17
Resolution : 1.90 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
Mogul	:	2022.3.0, CSD as543be (2022)
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

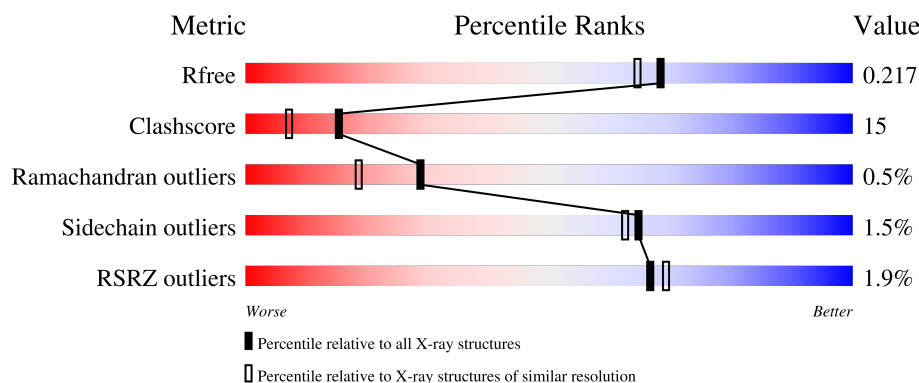
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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}	130704	6207 (1.90-1.90)
Clashscore	141614	6847 (1.90-1.90)
Ramachandran outliers	138981	6760 (1.90-1.90)
Sidechain outliers	138945	6760 (1.90-1.90)
RSRZ outliers	127900	6082 (1.90-1.90)

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	320	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 0%, red 1%, green 1%, green 67%, yellow 67%, yellow 81%, grey 81%);"></div> <div style="display: flex; justify-content: space-between; width: 90%; margin: 0 auto;"> 67% 14% • 18% </div> </div>
1	C	320	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 0%, red 3%, green 3%, green 66%, yellow 66%, yellow 81%, grey 81%);"></div> <div style="display: flex; justify-content: space-between; width: 90%; margin: 0 auto;"> 66% 15% • 19% </div> </div>
1	E	320	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 0%, red 1%, green 1%, green 66%, yellow 66%, yellow 79%, grey 79%);"></div> <div style="display: flex; justify-content: space-between; width: 90%; margin: 0 auto;"> 66% 13% • 20% </div> </div>
1	G	320	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 0%, red 3%, green 3%, green 66%, yellow 66%, yellow 80%, grey 80%);"></div> <div style="display: flex; justify-content: space-between; width: 90%; margin: 0 auto;"> 66% 14% • 19% </div> </div>
2	B	271	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 0%, red 1%, green 1%, green 76%, yellow 76%, yellow 99%, grey 99%);"></div> <div style="display: flex; justify-content: space-between; width: 90%; margin: 0 auto;"> 76% 24% • </div> </div>

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Mol	Chain	Length	Quality of chain
2	D	271	<div><div><div></div><div></div><div></div></div><div><div>2%</div><div>74%</div><div>21%</div><div>5%</div></div></div>
2	F	271	<div><div><div></div><div></div><div></div></div><div><div>%</div><div>72%</div><div>21%</div><div>• 6%</div></div></div>
2	H	271	<div><div><div></div><div></div><div></div></div><div><div>%</div><div>77%</div><div>18%</div><div>•</div></div></div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 14983 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 Pyridoxal 5'-phosphate synthase-like subunit PDX1.2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	264	Total	C	N	O	S	0	264	0
			1867	1166	329	358	14			
1	C	259	Total	C	N	O	S	0	259	0
			1836	1148	323	352	13			
1	E	255	Total	C	N	O	S	0	254	0
			1803	1130	314	346	13			
1	G	260	Total	C	N	O	S	0	260	0
			1836	1149	322	352	13			

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	315	HIS	-	expression tag	UNP Q9ZNR6
A	316	HIS	-	expression tag	UNP Q9ZNR6
A	317	HIS	-	expression tag	UNP Q9ZNR6
A	318	HIS	-	expression tag	UNP Q9ZNR6
A	319	HIS	-	expression tag	UNP Q9ZNR6
A	320	HIS	-	expression tag	UNP Q9ZNR6
C	315	HIS	-	expression tag	UNP Q9ZNR6
C	316	HIS	-	expression tag	UNP Q9ZNR6
C	317	HIS	-	expression tag	UNP Q9ZNR6
C	318	HIS	-	expression tag	UNP Q9ZNR6
C	319	HIS	-	expression tag	UNP Q9ZNR6
C	320	HIS	-	expression tag	UNP Q9ZNR6
E	315	HIS	-	expression tag	UNP Q9ZNR6
E	316	HIS	-	expression tag	UNP Q9ZNR6
E	317	HIS	-	expression tag	UNP Q9ZNR6
E	318	HIS	-	expression tag	UNP Q9ZNR6
E	319	HIS	-	expression tag	UNP Q9ZNR6
E	320	HIS	-	expression tag	UNP Q9ZNR6
G	315	HIS	-	expression tag	UNP Q9ZNR6
G	316	HIS	-	expression tag	UNP Q9ZNR6
G	317	HIS	-	expression tag	UNP Q9ZNR6

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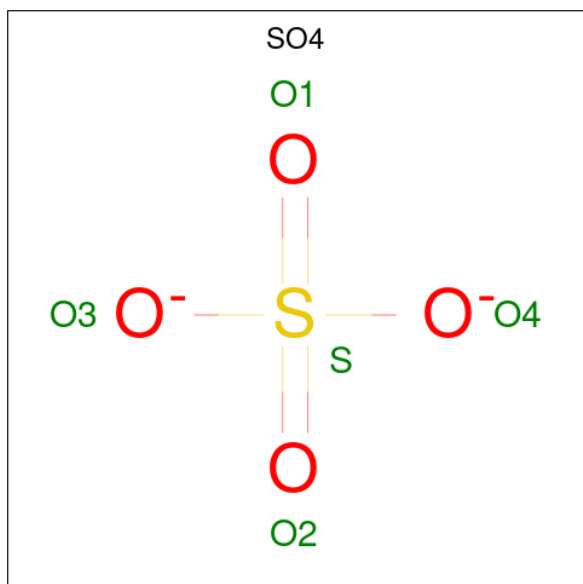
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Chain	Residue	Modelled	Actual	Comment	Reference
G	318	HIS	-	expression tag	UNP Q9ZNR6
G	319	HIS	-	expression tag	UNP Q9ZNR6
G	320	HIS	-	expression tag	UNP Q9ZNR6

- Molecule 2 is a protein called Pyridoxal 5'-phosphate synthase subunit PDX1.3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	269	Total	C	N	O	S	0	269	0
			1917	1202	338	359	18			
2	D	258	Total	C	N	O	S	0	258	0
			1833	1150	326	340	17			
2	F	254	Total	C	N	O	S	0	252	0
			1796	1125	318	337	16			
2	H	259	Total	C	N	O	S	0	259	0
			1838	1153	326	342	17			

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	O	S	0	0
			5	4	1		
3	C	1	Total	O	S	0	0
			5	4	1		
3	E	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	D	1	Total	O	S	0	0
			5	4	1		
3	F	1	Total	O	S	0	0
			5	4	1		
3	H	1	Total	O	S	0	0
			5	4	1		
3	H	1	Total	O	S	0	0
			5	4	1		

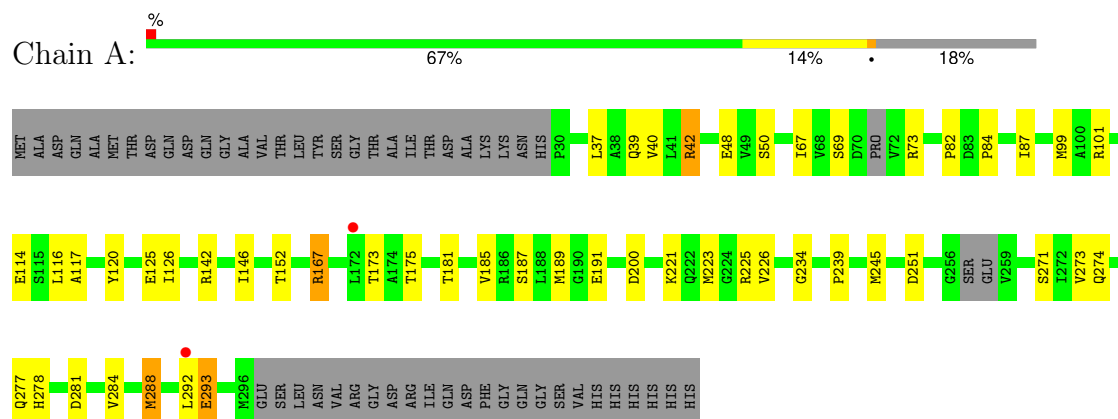
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	34	Total	O	0	0
			34	34		
4	C	30	Total	O	0	0
			30	30		
4	E	43	Total	O	0	0
			43	43		
4	G	30	Total	O	0	0
			30	30		
4	B	23	Total	O	0	0
			23	23		
4	D	17	Total	O	0	0
			17	17		
4	F	15	Total	O	0	0
			15	15		
4	H	25	Total	O	0	0
			25	25		

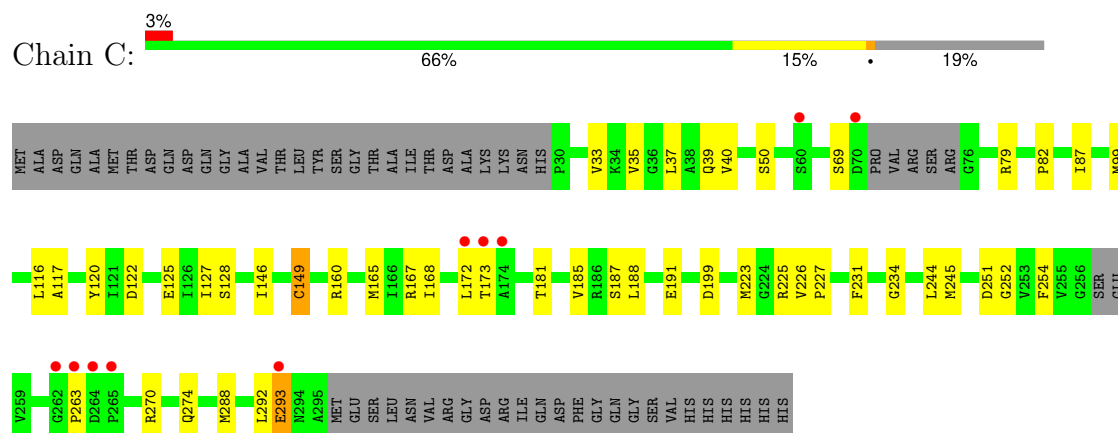
3 Residue-property plots [i](#)

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.

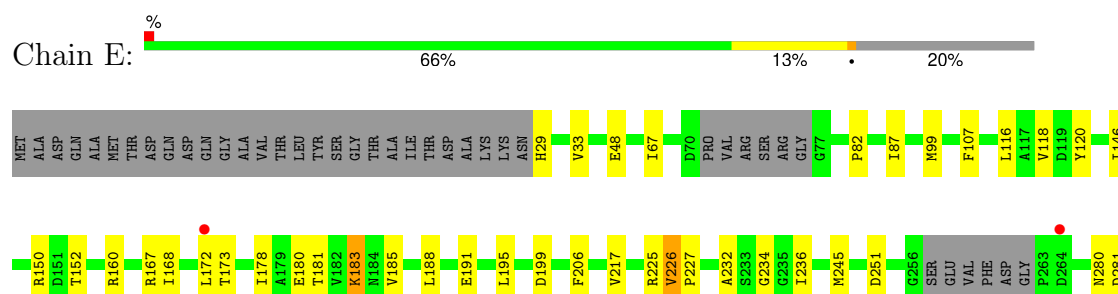
• Molecule 1: Pyridoxal 5'-phosphate synthase-like subunit PDX1.2

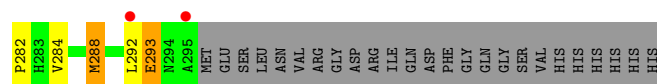


• Molecule 1: Pyridoxal 5'-phosphate synthase-like subunit PDX1.2

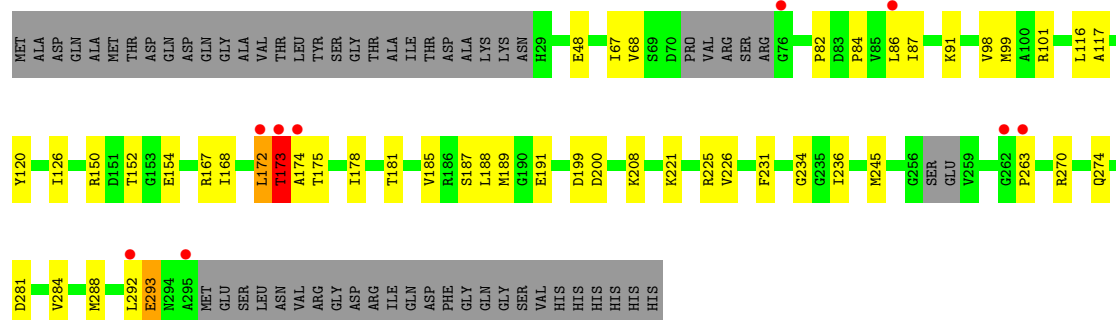


• Molecule 1: Pyridoxal 5'-phosphate synthase-like subunit PDX1.2

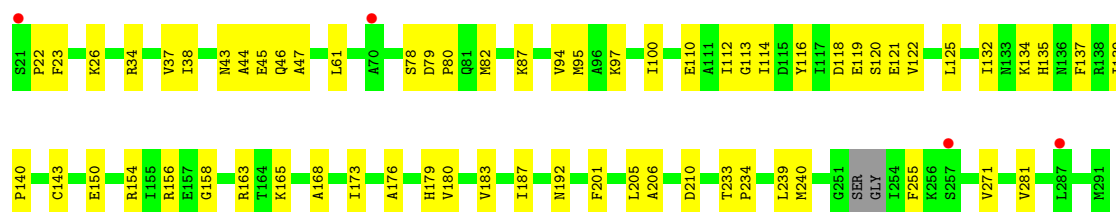
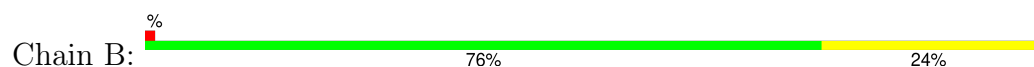




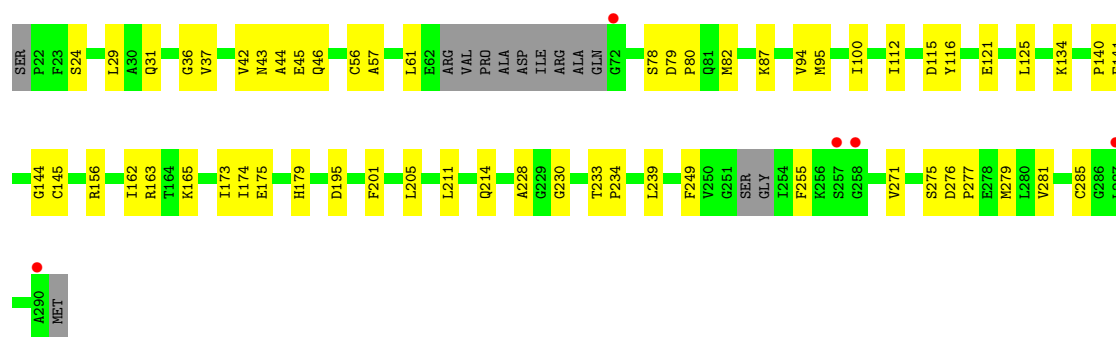
- Molecule 1: Pyridoxal 5'-phosphate synthase-like subunit PDX1.2



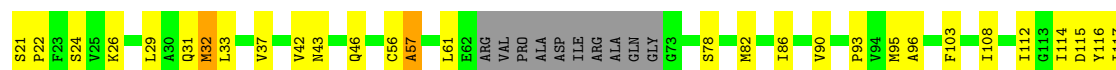
- Molecule 2: Pyridoxal 5'-phosphate synthase subunit PDX1.3

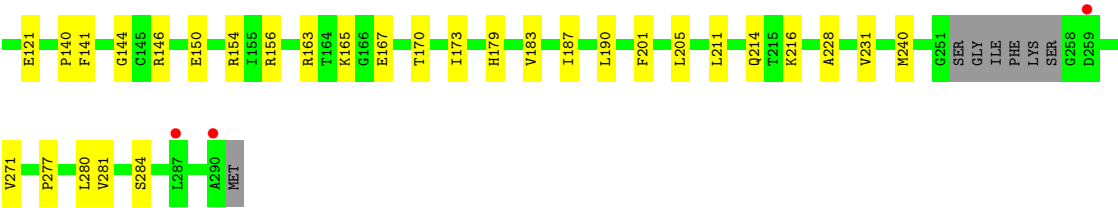


- Molecule 2: Pyridoxal 5'-phosphate synthase subunit PDX1.3

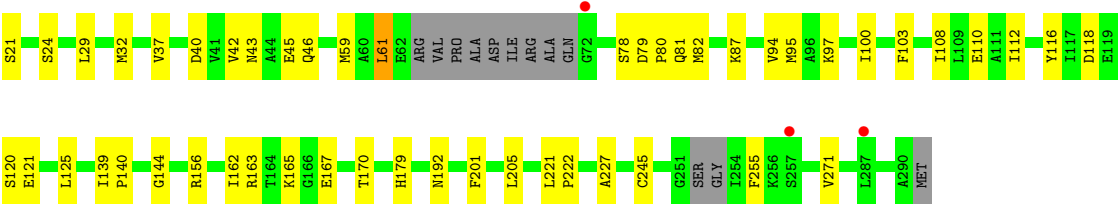
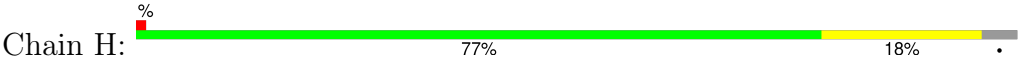


- Molecule 2: Pyridoxal 5'-phosphate synthase subunit PDX1.3





● Molecule 2: Pyridoxal 5'-phosphate synthase subunit PDX1.3



4 Data and refinement statistics

Property	Value	Source
Space group	H 3	Depositor
Cell constants a, b, c, α , β , γ	177.98Å 177.98Å 116.86Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	93.12 – 1.90 64.33 – 1.84	Depositor EDS
% Data completeness (in resolution range)	99.5 (93.12-1.90) 99.4 (64.33-1.84)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.37 (at 1.84Å)	Xtriage
Refinement program	REFMAC 5.8.0135	Depositor
R, R_{free}	0.216 , 0.231 0.222 , 0.217	Depositor DCC
R_{free} test set	5876 reflections (4.92%)	wwPDB-VP
Wilson B-factor (Å ²)	27.4	Xtriage
Anisotropy	0.577	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 38.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.025 for h,-h-k,-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	14983	wwPDB-VP
Average B, all atoms (Å ²)	31.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.22% 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](#)

Bond lengths and bond angles in the following residue types are not validated in this section: SO4

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	0.24	0/1891	0.43	0/2565
1	C	0.24	0/1860	0.42	0/2524
1	E	0.24	0/1826	0.42	0/2483
1	G	0.24	0/1860	0.42	0/2528
2	B	0.22	0/1943	0.40	0/2635
2	D	0.22	0/1857	0.39	0/2516
2	F	0.22	0/1818	0.39	0/2466
2	H	0.22	0/1862	0.38	0/2525
All	All	0.23	0/14917	0.41	0/20242

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	1867	0	1668	53	0
1	C	1836	0	1647	50	0
1	E	1803	0	1617	57	0
1	G	1836	0	1650	52	0
2	B	1917	0	1767	57	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	D	1833	0	1674	48	0
2	F	1796	0	1638	64	0
2	H	1838	0	1679	59	0
3	A	5	0	0	0	0
3	B	5	0	0	0	0
3	C	5	0	0	0	0
3	D	5	0	0	0	0
3	E	5	0	0	0	0
3	F	5	0	0	0	0
3	H	10	0	0	0	0
4	A	34	0	0	0	0
4	B	23	0	0	0	0
4	C	30	0	0	0	0
4	D	17	0	0	0	0
4	E	43	0	0	0	0
4	F	15	0	0	0	0
4	G	30	0	0	0	0
4	H	25	0	0	0	0
All	All	14983	0	13340	418	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.

The worst 5 of 418 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:E:178[A]:ILE:CD1	1:E:236[A]:ILE:HD13	1.46	1.46
1:E:178[A]:ILE:CD1	1:E:236[A]:ILE:CD1	2.05	1.33
1:E:180[A]:GLU:OE1	1:E:183[A]:LYS:NZ	1.63	1.29
1:E:178[A]:ILE:HD11	1:E:236[A]:ILE:CD1	1.58	1.28
2:F:173[B]:ILE:HD11	2:F:240[B]:MET:CE	1.62	1.27

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	258/320 (81%)	252 (98%)	5 (2%)	1 (0%)	34	24
1	C	253/320 (79%)	244 (96%)	8 (3%)	1 (0%)	34	24
1	E	249/320 (78%)	244 (98%)	3 (1%)	2 (1%)	19	9
1	G	254/320 (79%)	243 (96%)	7 (3%)	4 (2%)	9	2
2	B	265/271 (98%)	254 (96%)	11 (4%)	0	100	100
2	D	252/271 (93%)	239 (95%)	13 (5%)	0	100	100
2	F	248/271 (92%)	236 (95%)	10 (4%)	2 (1%)	19	9
2	H	253/271 (93%)	246 (97%)	7 (3%)	0	100	100
All	All	2032/2364 (86%)	1958 (96%)	64 (3%)	10 (0%)	29	18

5 of 10 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	293[A]	GLU
1	G	173[A]	THR
1	E	293[A]	GLU
1	G	172[A]	LEU
1	G	293[A]	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	180/262 (69%)	176 (98%)	4 (2%)	52	47
1	C	181/262 (69%)	178 (98%)	3 (2%)	60	57
1	E	177/262 (68%)	172 (97%)	5 (3%)	43	36
1	G	179/262 (68%)	176 (98%)	3 (2%)	60	57
2	B	183/210 (87%)	182 (100%)	1 (0%)	88	89
2	D	174/210 (83%)	171 (98%)	3 (2%)	60	57

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	F	170/210 (81%)	169 (99%)	1 (1%)	86	87
2	H	175/210 (83%)	174 (99%)	1 (1%)	86	87
All	All	1419/1888 (75%)	1398 (98%)	21 (2%)	65	62

5 of 21 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	G	226[A]	VAL
2	D	195[B]	ASP
2	H	61[B]	LEU
2	D	285[B]	CYS
2	D	24[B]	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 15 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	197[A]	ASN
2	F	242[B]	GLN
1	E	278[A]	HIS
2	H	172[B]	ASN
2	F	31[B]	GLN

5.3.3 RNA [i](#)

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](#)

8 ligands are modelled in this entry.

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	$\# Z > 2$
3	SO4	C	401	-	4,4,4	0.32	0	6,6,6	0.13	0
3	SO4	D	301	-	4,4,4	0.44	0	6,6,6	0.05	0
3	SO4	H	302	-	4,4,4	0.43	0	6,6,6	0.10	0
3	SO4	H	301	-	4,4,4	0.35	0	6,6,6	0.11	0
3	SO4	A	401	-	4,4,4	0.34	0	6,6,6	0.09	0
3	SO4	E	401	-	4,4,4	0.26	0	6,6,6	0.26	0
3	SO4	B	301	-	4,4,4	0.40	0	6,6,6	0.24	0
3	SO4	F	301	-	4,4,4	0.42	0	6,6,6	0.16	0

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 ⓘ

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	264/320 (82%)	-0.14	2 (0%) 86 87	15, 24, 40, 49	264 (100%)
1	C	259/320 (80%)	-0.10	10 (3%) 39 42	16, 23, 43, 64	259 (100%)
1	E	255/320 (79%)	-0.15	4 (1%) 72 74	16, 24, 41, 63	255 (100%)
1	G	260/320 (81%)	-0.10	9 (3%) 44 47	15, 24, 44, 56	260 (100%)
2	B	269/271 (99%)	-0.12	4 (1%) 73 76	22, 33, 61, 67	269 (100%)
2	D	258/271 (95%)	-0.10	5 (1%) 66 69	24, 34, 67, 113	258 (100%)
2	F	254/271 (93%)	-0.17	3 (1%) 79 81	25, 36, 58, 92	254 (100%)
2	H	259/271 (95%)	-0.12	3 (1%) 79 81	24, 34, 60, 85	259 (100%)
All	All	2078/2364 (87%)	-0.12	40 (1%) 66 69	15, 29, 55, 113	2078 (100%)

The worst 5 of 40 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	F	287	LEU	6.6
1	E	292	LEU	5.9
2	D	257[B]	SER	5.8
1	A	172[A]	LEU	5.1
1	C	262[A]	GLY	4.9

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

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

6.3 Carbohydrates ⓘ

There are no monosaccharides in this entry.

6.4 Ligands [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(Å ²)	Q<0.9
3	SO4	F	301	5/5	0.95	0.16	67,68,70,70	0
3	SO4	H	302	5/5	0.95	0.14	62,64,65,67	0
3	SO4	D	301	5/5	0.96	0.22	66,66,68,70	0
3	SO4	B	301	5/5	0.97	0.14	55,55,57,57	0
3	SO4	C	401	5/5	0.99	0.13	33,34,36,37	0
3	SO4	E	401	5/5	0.99	0.11	33,35,36,36	0
3	SO4	H	301	5/5	0.99	0.12	33,34,35,36	0
3	SO4	A	401	5/5	0.99	0.11	31,32,33,35	0

6.5 Other polymers [i](#)

There are no such residues in this entry.