



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 14, 2026 – 02:57 PM UTC

PDB ID : 4O5M / pdb_00004o5m
Title : X-ray Crystal Structure of Isovaleryl-CoA Dehydrogenase from Brucella suis
Authors : Seattle Structural Genomics Center for Infectious Disease (SSGCID)
Deposited on : 2013-12-19
Resolution : 2.20 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
Mogul : 2022.3.0, CSD as543be (2022)
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

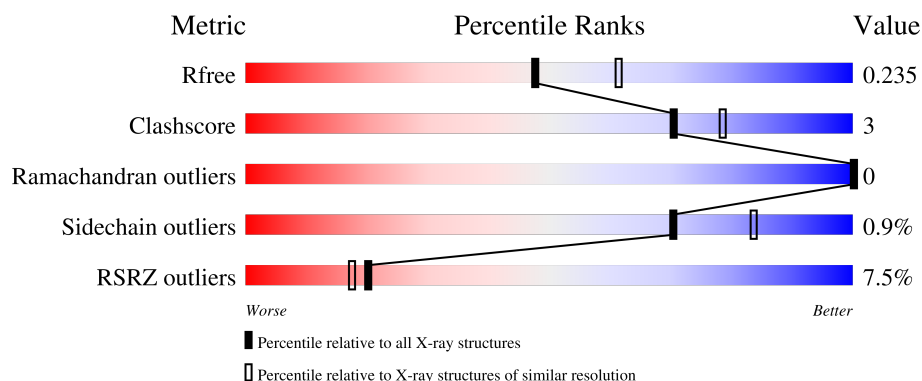
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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	6164 (2.20-2.20)
Clashscore	190562	6851 (2.20-2.20)
Ramachandran outliers	187476	6768 (2.20-2.20)
Sidechain outliers	187428	6769 (2.20-2.20)
RSRZ outliers	180081	6166 (2.20-2.20)

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	390	
1	B	390	
1	C	390	
1	D	390	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 10541 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 Isovaleryl-CoA dehydrogenase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	350	Total	C	N	O	S	0	0	0
			2523	1586	445	474	18			
1	B	342	Total	C	N	O	S	0	0	0
			2457	1546	431	462	18			
1	C	362	Total	C	N	O	S	0	0	0
			2650	1665	461	505	19			
1	D	358	Total	C	N	O	S	0	1	0
			2625	1651	458	496	20			

There are 32 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-7	MET	-	expression tag	UNP Q8G3C9
A	-6	ALA	-	expression tag	UNP Q8G3C9
A	-5	HIS	-	expression tag	UNP Q8G3C9
A	-4	HIS	-	expression tag	UNP Q8G3C9
A	-3	HIS	-	expression tag	UNP Q8G3C9
A	-2	HIS	-	expression tag	UNP Q8G3C9
A	-1	HIS	-	expression tag	UNP Q8G3C9
A	0	HIS	-	expression tag	UNP Q8G3C9
B	-7	MET	-	expression tag	UNP Q8G3C9
B	-6	ALA	-	expression tag	UNP Q8G3C9
B	-5	HIS	-	expression tag	UNP Q8G3C9
B	-4	HIS	-	expression tag	UNP Q8G3C9
B	-3	HIS	-	expression tag	UNP Q8G3C9
B	-2	HIS	-	expression tag	UNP Q8G3C9
B	-1	HIS	-	expression tag	UNP Q8G3C9
B	0	HIS	-	expression tag	UNP Q8G3C9
C	-7	MET	-	expression tag	UNP Q8G3C9
C	-6	ALA	-	expression tag	UNP Q8G3C9
C	-5	HIS	-	expression tag	UNP Q8G3C9
C	-4	HIS	-	expression tag	UNP Q8G3C9
C	-3	HIS	-	expression tag	UNP Q8G3C9

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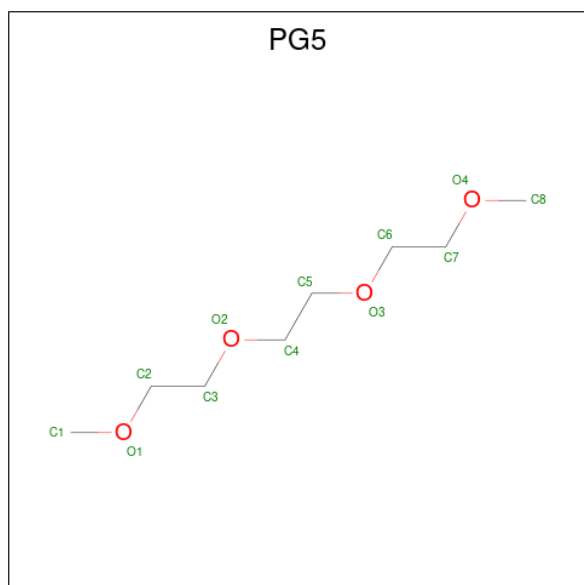
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Chain	Residue	Modelled	Actual	Comment	Reference
C	-2	HIS	-	expression tag	UNP Q8G3C9
C	-1	HIS	-	expression tag	UNP Q8G3C9
C	0	HIS	-	expression tag	UNP Q8G3C9
D	-7	MET	-	expression tag	UNP Q8G3C9
D	-6	ALA	-	expression tag	UNP Q8G3C9
D	-5	HIS	-	expression tag	UNP Q8G3C9
D	-4	HIS	-	expression tag	UNP Q8G3C9
D	-3	HIS	-	expression tag	UNP Q8G3C9
D	-2	HIS	-	expression tag	UNP Q8G3C9
D	-1	HIS	-	expression tag	UNP Q8G3C9
D	0	HIS	-	expression tag	UNP Q8G3C9

- Molecule 2 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total Ca 1 1	0	0

- Molecule 3 is 1-METHOXY-2-[2-(2-METHOXY-ETHOXY)]-ETHANE (CCD ID: PG5) (formula: C₈H₁₈O₄).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	B	1	Total C O 12 8 4	0	0
3	C	1	Total C O 12 8 4	0	0

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	D	1	Total	C	O	0	0
			12	8	4		

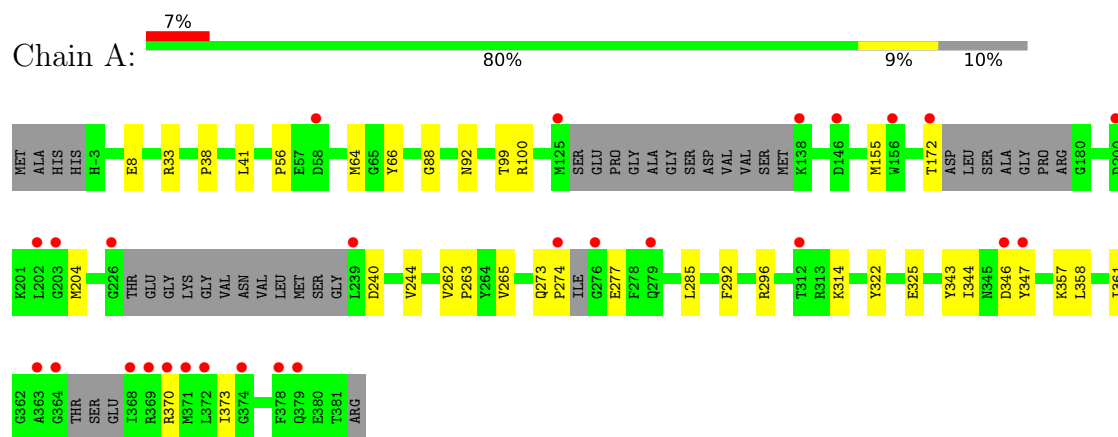
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	69	Total	O	0	0
			69	69		
4	B	37	Total	O	0	0
			37	37		
4	C	68	Total	O	0	0
			68	68		
4	D	75	Total	O	0	0
			75	75		

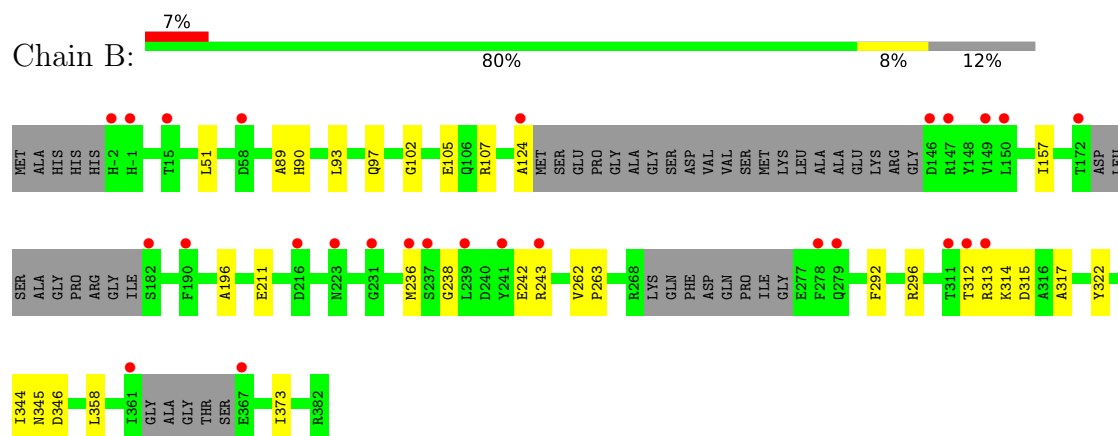
3 Residue-property plots [i](#)

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.

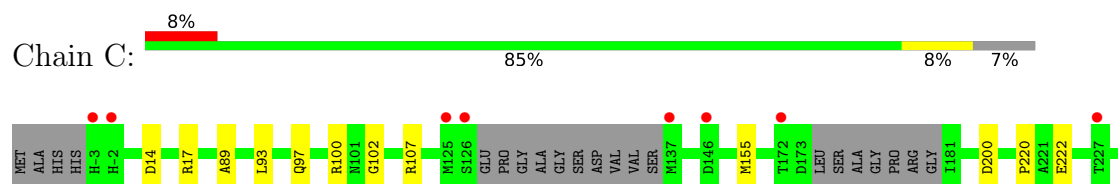
- Molecule 1: Isovaleryl-CoA dehydrogenase

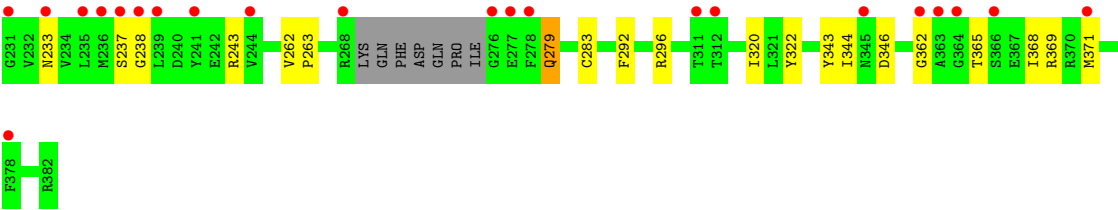


- Molecule 1: Isovaleryl-CoA dehydrogenase

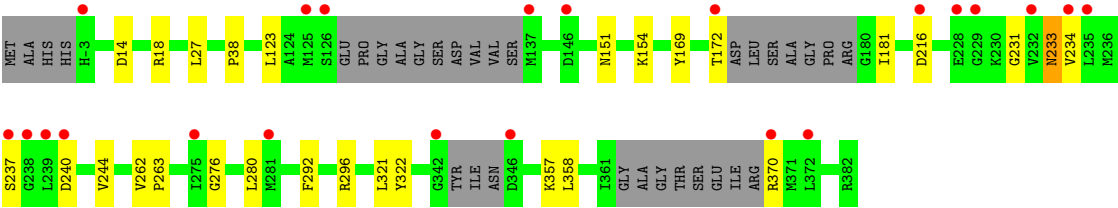
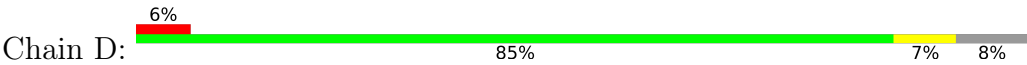


- Molecule 1: Isovaleryl-CoA dehydrogenase





● Molecule 1: Isovaleryl-CoA dehydrogenase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	82.21Å 91.07Å 102.14Å 90.00° 99.25° 90.00°	Depositor
Resolution (Å)	46.28 – 2.20 46.28 – 2.20	Depositor EDS
% Data completeness (in resolution range)	98.8 (46.28-2.20) 98.8 (46.28-2.20)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.64 (at 2.20Å)	Xtriage
Refinement program	PHENIX 1.8.4_1496	Depositor
R, R_{free}	0.200 , 0.234 0.202 , 0.235	Depositor DCC
R_{free} test set	3752 reflections (4.96%)	wwPDB-VP
Wilson B-factor (Å ²)	40.0	Xtriage
Anisotropy	0.350	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 60.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	10541	wwPDB-VP
Average B, all atoms (Å ²)	59.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.85% 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: PG5, CA

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	0.30	0/2565	0.73	1/3477 (0.0%)
1	B	0.29	0/2498	0.75	0/3390
1	C	0.29	0/2694	0.73	0/3649
1	D	0.30	0/2672	0.74	0/3617
All	All	0.29	0/10429	0.74	1/14133 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	274	PRO	N-CA-CB	6.97	110.67	103.00

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	2523	0	2345	20	0
1	B	2457	0	2279	18	0
1	C	2650	0	2510	18	0
1	D	2625	0	2489	18	0
2	A	1	0	0	0	0
3	B	12	0	18	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	C	12	0	18	0	0
3	D	12	0	18	0	0
4	A	69	0	0	0	0
4	B	37	0	0	0	0
4	C	68	0	0	0	0
4	D	75	0	0	0	0
All	All	10541	0	9677	67	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 3.

All (67) 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:14:ASP:OD2	1:D:18:ARG:NH2	2.20	0.74
1:B:322:TYR:HH	1:D:322:TYR:HH	1.34	0.73
1:C:279:GLN:HG2	1:D:276:GLY:HA3	1.73	0.69
1:B:93:LEU:HD21	1:B:242:GLU:HG3	1.76	0.67
1:B:344:ILE:HG22	1:B:346:ASP:H	1.61	0.65
1:D:321:LEU:HD21	1:D:370:ARG:HE	1.61	0.64
1:C:365:THR:H	1:C:368:ILE:HD12	1.63	0.63
1:D:233:ASN:O	1:D:237:SER:OG	2.10	0.62
1:A:322:TYR:HH	1:C:322:TYR:HH	1.50	0.60
1:C:362:GLY:O	1:C:369:ARG:NH2	2.36	0.58
1:C:100:ARG:HH22	1:C:237:SER:HB3	1.69	0.58
1:B:102:GLY:O	1:B:107:ARG:NH1	2.36	0.57
1:C:344:ILE:HG22	1:C:346:ASP:H	1.70	0.57
1:A:344:ILE:HB	1:A:347:TYR:CD2	2.42	0.54
1:B:97:GLN:HE21	1:B:238:GLY:HA3	1.72	0.54
1:B:236:MET:HB3	1:B:313:ARG:NH2	2.25	0.52
1:B:292:PHE:CZ	1:B:296:ARG:HD2	2.45	0.51
1:A:344:ILE:HB	1:A:347:TYR:HD2	1.76	0.51
1:D:151:ASN:OD1	1:D:216:ASP:N	2.32	0.50
1:C:233:ASN:O	1:C:237:SER:OG	2.16	0.50
1:C:292:PHE:CZ	1:C:296:ARG:HD2	2.46	0.50
1:C:243:ARG:HD3	1:C:320:ILE:HG21	1.94	0.50
1:D:292:PHE:CZ	1:D:296:ARG:HD2	2.47	0.49
1:B:89:ALA:O	1:B:93:LEU:HB2	2.12	0.49
1:A:204:MET:HG3	1:A:358:LEU:HD23	1.94	0.49
1:C:14:ASP:OD1	1:C:17:ARG:NH2	2.46	0.48
1:D:276:GLY:O	1:D:280:LEU:HD13	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:292:PHE:CZ	1:A:296:ARG:HD2	2.48	0.48
1:C:102:GLY:O	1:C:107:ARG:NH1	2.47	0.47
1:B:196:ALA:HB3	1:B:211:GLU:HB3	1.96	0.47
1:A:265:VAL:HG21	1:A:285:LEU:HD11	1.95	0.47
1:B:314:LYS:HB2	1:B:373:ILE:HG23	1.97	0.46
1:B:358:LEU:HB2	1:C:343:TYR:CZ	2.50	0.46
1:C:97:GLN:HE21	1:C:238:GLY:HA3	1.80	0.46
1:B:93:LEU:HD21	1:B:242:GLU:CG	2.45	0.46
1:A:344:ILE:HG22	1:A:346:ASP:H	1.80	0.46
1:B:243:ARG:HD2	1:B:317:ALA:HA	1.97	0.46
1:A:314:LYS:HB2	1:A:373:ILE:HG23	1.97	0.46
1:B:345:ASN:ND2	1:C:200:ASP:OD1	2.47	0.45
1:D:233:ASN:OD1	1:D:233:ASN:N	2.41	0.45
1:C:262:VAL:HB	1:C:263:PRO:HD3	2.00	0.44
1:D:262:VAL:HB	1:D:263:PRO:HD3	2.00	0.44
1:C:283:CYS:SG	1:D:280:LEU:HD21	2.58	0.44
1:D:240:ASP:O	1:D:244:VAL:HG23	2.17	0.44
1:C:220:PRO:HB2	1:C:222:GLU:HG2	1.99	0.44
1:A:325:GLU:CD	1:A:370:ARG:HH22	2.23	0.44
1:A:38:PRO:HG2	1:A:41:LEU:HD12	2.00	0.43
1:A:88:GLY:O	1:A:92:ASN:HB3	2.18	0.43
1:B:312:THR:HG23	1:B:315:ASP:HB2	2.00	0.42
1:A:240:ASP:O	1:A:244:VAL:HG23	2.18	0.42
1:A:343:TYR:CZ	1:D:358:LEU:HB2	2.54	0.42
1:B:124:ALA:HA	1:B:157:ILE:HD12	2.00	0.42
1:D:181:ILE:O	1:D:231:GLY:N	2.51	0.42
1:A:357:LYS:O	1:A:361:ILE:HG12	2.20	0.42
1:D:154:LYS:HD3	1:D:154:LYS:HA	1.89	0.42
1:A:66:TYR:OH	1:A:100:ARG:HD2	2.19	0.42
1:D:27[B]:LEU:HD13	1:D:38:PRO:HG3	2.02	0.42
1:A:262:VAL:HB	1:A:263:PRO:HD3	2.02	0.42
1:B:262:VAL:HB	1:B:263:PRO:HD3	2.01	0.41
1:C:89:ALA:HA	1:C:93:LEU:HG	2.03	0.41
1:D:123:LEU:HD11	1:D:169:TYR:HE1	1.85	0.41
1:A:155:MET:HE2	1:A:155:MET:HB2	1.95	0.41
1:A:8:GLU:HG2	1:A:64:MET:HE3	2.03	0.41
1:A:56:PRO:HD3	1:A:99:THR:HG23	2.03	0.41
1:A:273:GLN:HE21	1:A:277:GLU:CD	2.29	0.41
1:D:357:LYS:HD2	1:D:357:LYS:HA	1.87	0.40
1:B:51:LEU:HD22	1:B:90:HIS:CD2	2.55	0.40

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	338/390 (87%)	331 (98%)	7 (2%)	0	100	100
1	B	332/390 (85%)	324 (98%)	8 (2%)	0	100	100
1	C	354/390 (91%)	345 (98%)	9 (2%)	0	100	100
1	D	349/390 (90%)	339 (97%)	10 (3%)	0	100	100
All	All	1373/1560 (88%)	1339 (98%)	34 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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	233/305 (76%)	231 (99%)	2 (1%)	70	84
1	B	226/305 (74%)	225 (100%)	1 (0%)	84	92
1	C	254/305 (83%)	251 (99%)	3 (1%)	63	78
1	D	252/305 (83%)	249 (99%)	3 (1%)	63	78
All	All	965/1220 (79%)	956 (99%)	9 (1%)	70	84

All (9) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	33	ARG
1	A	172	THR

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Mol	Chain	Res	Type
1	B	105	GLU
1	C	155	MET
1	C	279	GLN
1	C	371	MET
1	D	172	THR
1	D	233	ASN
1	D	234	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	-1	HIS
1	A	101	ASN
1	A	119	HIS
1	B	101	ASN
1	B	119	HIS
1	B	223	ASN
1	B	329	GLN
1	C	-1	HIS
1	C	101	ASN
1	C	329	GLN
1	D	-3	HIS
1	D	-1	HIS
1	D	119	HIS
1	D	223	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 oligosaccharides in this entry.

5.6 Ligand geometry

Of 4 ligands modelled in this entry, 1 is monoatomic - leaving 3 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
3	PG5	D	401	-	11,11,11	0.69	0	10,10,10	0.24	0
3	PG5	C	401	-	11,11,11	0.69	0	10,10,10	0.21	0
3	PG5	B	401	-	11,11,11	0.70	0	10,10,10	0.25	0

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
3	PG5	D	401	-	-	1/9/9/9	-
3	PG5	C	401	-	-	4/9/9/9	-
3	PG5	B	401	-	-	6/9/9/9	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (11) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	401	PG5	O2-C4-C5-O3
3	B	401	PG5	O3-C6-C7-O4
3	C	401	PG5	O3-C6-C7-O4
3	D	401	PG5	C7-C6-O3-C5
3	B	401	PG5	C7-C6-O3-C5
3	C	401	PG5	C2-C3-O2-C4
3	B	401	PG5	C4-C5-O3-C6
3	C	401	PG5	C6-C7-O4-C8
3	B	401	PG5	C3-C2-O1-C1

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Mol	Chain	Res	Type	Atoms
3	C	401	PG5	O1-C2-C3-O2
3	B	401	PG5	O1-C2-C3-O2

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	350/390 (89%)	0.39	27 (7%)	19	17	30, 53, 99, 127	0
1	B	342/390 (87%)	0.65	27 (7%)	18	16	35, 66, 106, 133	0
1	C	362/390 (92%)	0.40	30 (8%)	17	15	33, 53, 101, 134	0
1	D	358/390 (91%)	0.31	22 (6%)	27	24	27, 50, 104, 144	1 (0%)
All	All	1412/1560 (90%)	0.43	106 (7%)	20	17	27, 55, 104, 144	1 (0%)

All (106) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	368	ILE	5.8
1	C	126	SER	4.8
1	B	146	ASP	4.6
1	B	311	THR	4.6
1	A	276	GLY	4.6
1	C	276	GLY	4.5
1	D	235	LEU	4.3
1	C	239	LEU	4.2
1	C	125	MET	4.1
1	C	363	ALA	4.0
1	D	346	ASP	3.9
1	D	172	THR	3.9
1	A	274	PRO	3.8
1	B	278	PHE	3.8
1	B	239	LEU	3.7
1	C	268	ARG	3.7
1	C	137	MET	3.6
1	A	172	THR	3.6
1	D	342	GLY	3.5
1	A	364	GLY	3.5
1	A	346	ASP	3.5

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Mol	Chain	Res	Type	RSRZ
1	B	312	THR	3.4
1	A	378	PHE	3.3
1	D	137	MET	3.3
1	B	172	THR	3.3
1	D	237	SER	3.3
1	A	372	LEU	3.1
1	A	146	ASP	3.1
1	C	146	ASP	3.1
1	B	124	ALA	3.1
1	A	202	LEU	3.1
1	B	236	MET	3.0
1	C	371	MET	3.0
1	C	238	GLY	3.0
1	B	367	GLU	3.0
1	D	234	VAL	3.0
1	C	-2	HIS	3.0
1	D	370	ARG	2.9
1	A	347	TYR	2.9
1	A	200	ASP	2.9
1	D	146	ASP	2.9
1	B	58	ASP	2.9
1	B	-1	HIS	2.9
1	C	235	LEU	2.9
1	A	379	GLN	2.8
1	D	239	LEU	2.8
1	B	237	SER	2.8
1	D	372	LEU	2.8
1	C	231	GLY	2.8
1	C	362	GLY	2.8
1	C	172	THR	2.7
1	B	241	TYR	2.7
1	C	366	SER	2.7
1	C	227	THR	2.7
1	B	216	ASP	2.6
1	A	363	ALA	2.6
1	D	126	SER	2.6
1	A	369	ARG	2.6
1	D	216	ASP	2.6
1	D	238	GLY	2.6
1	C	241	TYR	2.6
1	C	345	ASN	2.5
1	B	182	SER	2.5

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Mol	Chain	Res	Type	RSRZ
1	B	190	PHE	2.5
1	A	370	ARG	2.5
1	B	147	ARG	2.5
1	A	374	GLY	2.5
1	B	150	LEU	2.4
1	A	371	MET	2.4
1	D	232	VAL	2.4
1	A	125	MET	2.4
1	A	239	LEU	2.4
1	B	-2	HIS	2.4
1	A	312	THR	2.4
1	C	233	ASN	2.3
1	D	125	MET	2.3
1	B	313	ARG	2.3
1	C	-3	HIS	2.3
1	C	244	VAL	2.3
1	C	278	PHE	2.2
1	A	226	GLY	2.2
1	C	311	THR	2.2
1	A	138	LYS	2.2
1	C	378	PHE	2.2
1	A	203	GLY	2.2
1	A	279	GLN	2.2
1	C	312	THR	2.2
1	A	156	TRP	2.2
1	D	-3	HIS	2.2
1	D	281	MET	2.1
1	C	277	GLU	2.1
1	B	279	GLN	2.1
1	C	237	SER	2.1
1	C	236	MET	2.1
1	D	228	GLU	2.1
1	D	240	ASP	2.1
1	B	149	VAL	2.1
1	B	231	GLY	2.1
1	C	364	GLY	2.1
1	B	243	ARG	2.1
1	B	15	THR	2.0
1	A	58	ASP	2.0
1	B	223	ASN	2.0
1	D	229	GLY	2.0
1	B	361	ILE	2.0

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Mol	Chain	Res	Type	RSRZ
1	D	275	ILE	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 oligosaccharides 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	PG5	D	401	12/12	0.84	0.16	50,62,71,74	0
3	PG5	B	401	12/12	0.88	0.14	49,57,75,75	0
3	PG5	C	401	12/12	0.89	0.15	46,53,65,65	0
2	CA	A	401	1/1	0.91	0.16	91,91,91,91	0

6.5 Other polymers [i](#)

There are no such residues in this entry.