



Full wwPDB X-ray Structure Validation Report ⓘ

Jun 16, 2024 – 06:29 PM EDT

PDB ID : 3NXL
Title : Crystal structure of Glucarate dehydratase from Burkholderia cepacia complexed with magnesium
Authors : Fedorov, A.A.; Fedorov, E.V.; Gerlt, J.A.; Burley, S.K.; Almo, S.C.; New York SGX Research Center for Structural Genomics (NYSGXRC)
Deposited on : 2010-07-14
Resolution : 1.89 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	:	4.02b-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

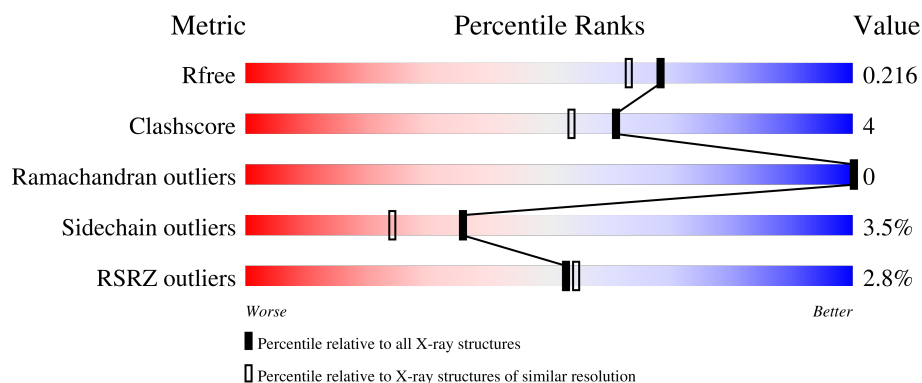
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

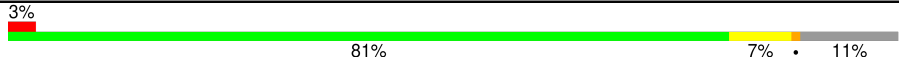
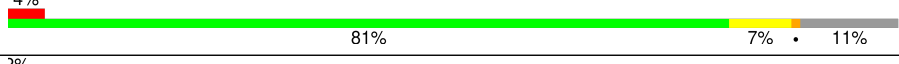

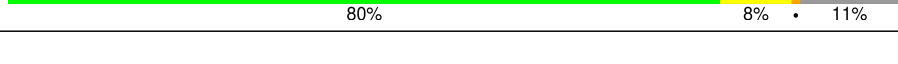
The reported resolution of this entry is 1.89 Å.

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	9470 (1.90-1.86)
Clashscore	141614	10282 (1.90-1.86)
Ramachandran outliers	138981	10152 (1.90-1.86)
Sidechain outliers	138945	10152 (1.90-1.86)
RSRZ outliers	127900	9303 (1.90-1.86)

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	475	
1	B	475	
1	C	475	
1	D	475	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 13917 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 Glucarate dehydratase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	424	Total	C	N	O	S	Se	0	1	0
			3246	2036	591	601	5	13			
1	B	423	Total	C	N	O	S	Se	0	1	0
			3240	2033	590	599	5	13			
1	C	425	Total	C	N	O	S	Se	0	1	0
			3250	2038	592	602	5	13			
1	D	425	Total	C	N	O	S	Se	0	4	0
			3281	2058	598	607	5	13			

There are 44 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MSE	-	expression tag	UNP Q39KL8
A	2	SER	-	expression tag	UNP Q39KL8
A	3	LEU	-	expression tag	UNP Q39KL8
A	468	GLU	-	expression tag	UNP Q39KL8
A	469	GLY	-	expression tag	UNP Q39KL8
A	470	HIS	-	expression tag	UNP Q39KL8
A	471	HIS	-	expression tag	UNP Q39KL8
A	472	HIS	-	expression tag	UNP Q39KL8
A	473	HIS	-	expression tag	UNP Q39KL8
A	474	HIS	-	expression tag	UNP Q39KL8
A	475	HIS	-	expression tag	UNP Q39KL8
B	1	MSE	-	expression tag	UNP Q39KL8
B	2	SER	-	expression tag	UNP Q39KL8
B	3	LEU	-	expression tag	UNP Q39KL8
B	468	GLU	-	expression tag	UNP Q39KL8
B	469	GLY	-	expression tag	UNP Q39KL8
B	470	HIS	-	expression tag	UNP Q39KL8
B	471	HIS	-	expression tag	UNP Q39KL8
B	472	HIS	-	expression tag	UNP Q39KL8
B	473	HIS	-	expression tag	UNP Q39KL8
B	474	HIS	-	expression tag	UNP Q39KL8

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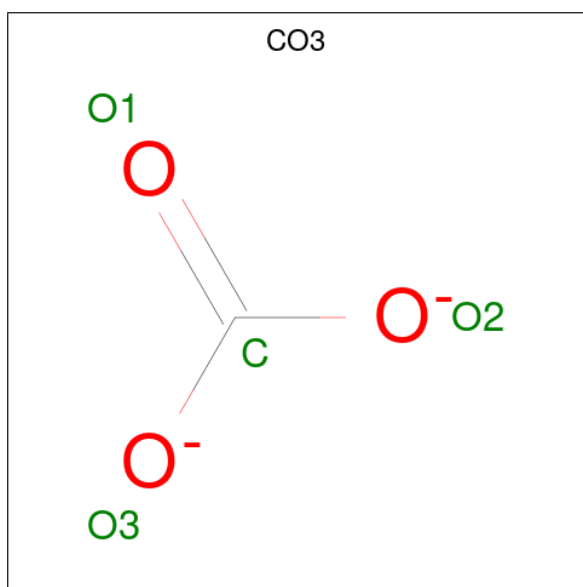
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Chain	Residue	Modelled	Actual	Comment	Reference
B	475	HIS	-	expression tag	UNP Q39KL8
C	1	MSE	-	expression tag	UNP Q39KL8
C	2	SER	-	expression tag	UNP Q39KL8
C	3	LEU	-	expression tag	UNP Q39KL8
C	468	GLU	-	expression tag	UNP Q39KL8
C	469	GLY	-	expression tag	UNP Q39KL8
C	470	HIS	-	expression tag	UNP Q39KL8
C	471	HIS	-	expression tag	UNP Q39KL8
C	472	HIS	-	expression tag	UNP Q39KL8
C	473	HIS	-	expression tag	UNP Q39KL8
C	474	HIS	-	expression tag	UNP Q39KL8
C	475	HIS	-	expression tag	UNP Q39KL8
D	1	MSE	-	expression tag	UNP Q39KL8
D	2	SER	-	expression tag	UNP Q39KL8
D	3	LEU	-	expression tag	UNP Q39KL8
D	468	GLU	-	expression tag	UNP Q39KL8
D	469	GLY	-	expression tag	UNP Q39KL8
D	470	HIS	-	expression tag	UNP Q39KL8
D	471	HIS	-	expression tag	UNP Q39KL8
D	472	HIS	-	expression tag	UNP Q39KL8
D	473	HIS	-	expression tag	UNP Q39KL8
D	474	HIS	-	expression tag	UNP Q39KL8
D	475	HIS	-	expression tag	UNP Q39KL8

- Molecule 2 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

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

- Molecule 3 is CARBONATE ION (three-letter code: CO3) (formula: CO₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			4	1	3		
3	B	1	Total	C	O	0	0
			4	1	3		
3	C	1	Total	C	O	0	0
			4	1	3		
3	D	1	Total	C	O	0	0
			4	1	3		

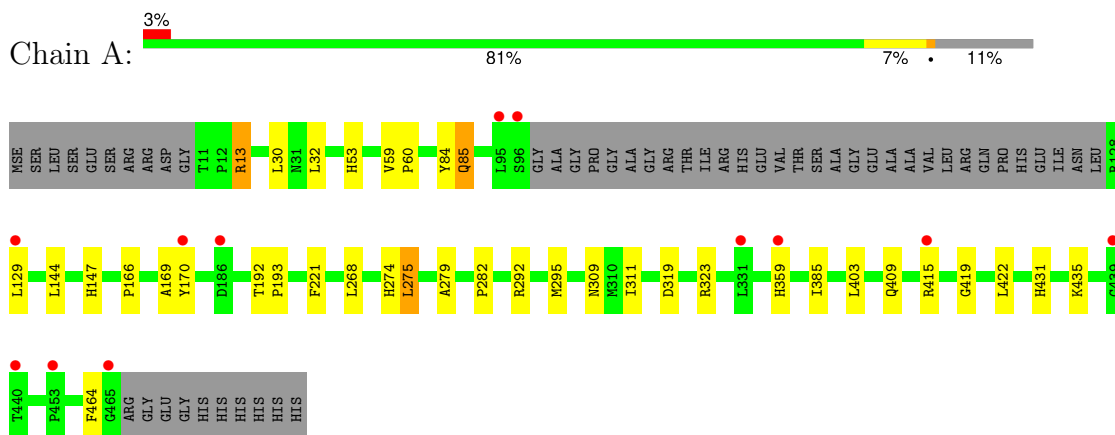
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	254	Total	O	0	0
			254	254		
4	B	190	Total	O	0	0
			190	190		
4	C	207	Total	O	0	0
			207	207		
4	D	229	Total	O	0	0
			229	229		

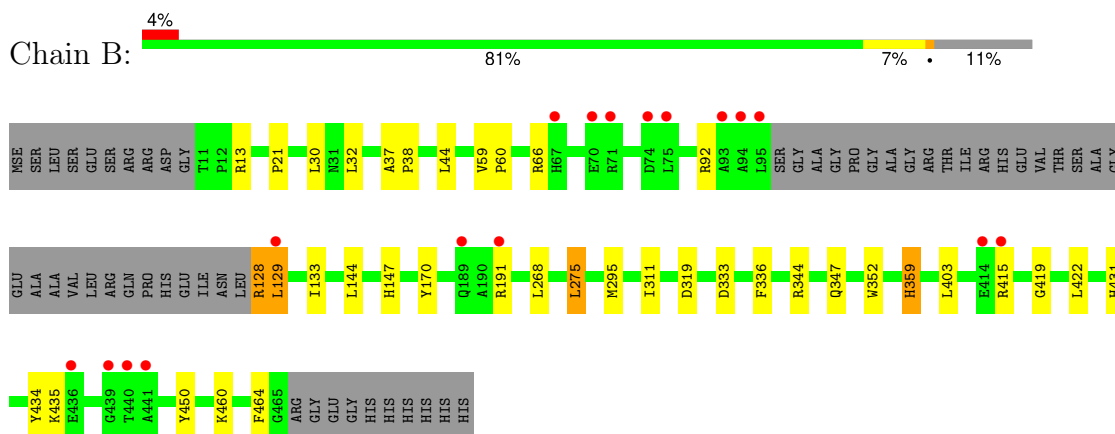
3 Residue-property plots [i](#)

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.

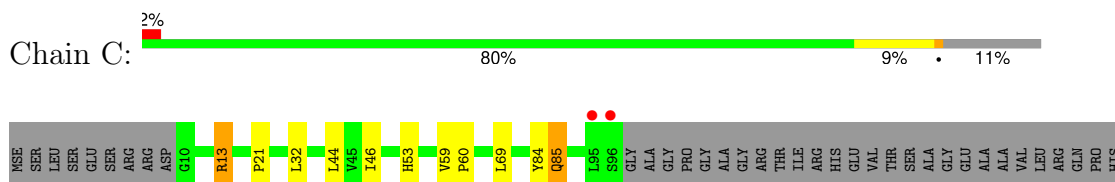
- Molecule 1: Glucarate dehydratase

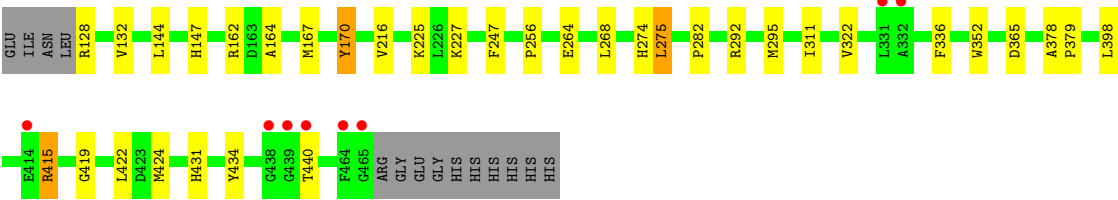


- Molecule 1: Glucarate dehydratase

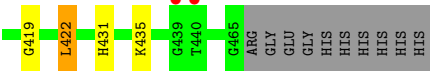
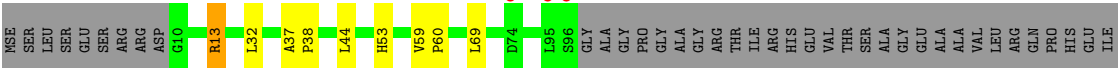
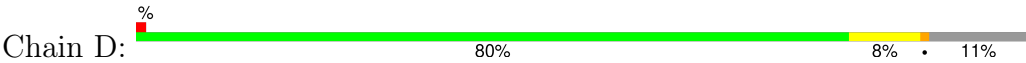


- Molecule 1: Glucarate dehydratase





● Molecule 1: Glucarate dehydratase



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	165.29Å 121.45Å 108.65Å 90.00° 92.60° 90.00°	Depositor
Resolution (Å)	34.23 – 1.89 34.23 – 1.89	Depositor EDS
% Data completeness (in resolution range)	97.5 (34.23-1.89) 97.5 (34.23-1.89)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.01 (at 1.88Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.5_2)	Depositor
R, R_{free}	0.190 , 0.221 0.186 , 0.216	Depositor DCC
R_{free} test set	8434 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	26.4	Xtriage
Anisotropy	0.345	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 42.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.017 for -h,-k,l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	13917	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 3.20% 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: MG, CO3

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	0/3306	0.55	0/4477
1	B	0.36	0/3300	0.51	0/4469
1	C	0.36	0/3310	0.51	0/4482
1	D	0.37	0/3342	0.53	0/4524
All	All	0.37	0/13258	0.52	0/17952

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	3246	0	3174	27	0
1	B	3240	0	3169	25	0
1	C	3250	0	3177	32	0
1	D	3281	0	3202	36	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
3	A	4	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	4	0	0	0	0
3	C	4	0	0	0	0
3	D	4	0	0	0	0
4	A	254	0	0	7	0
4	B	190	0	0	1	0
4	C	207	0	0	4	0
4	D	229	0	0	8	0
All	All	13917	0	12722	115	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 4.

All (115) 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:A:282:PRO:HD2	1:A:295:MSE:SE	2.28	0.83
1:A:13:ARG:CG	1:A:13:ARG:HH11	1.95	0.80
1:D:13:ARG:HG2	1:D:13:ARG:HH11	1.48	0.79
1:C:13:ARG:HG2	1:C:13:ARG:HH11	1.54	0.72
1:A:85:GLN:NE2	4:A:909:HOH:O	2.24	0.71
1:D:336[A]:PHE:CE2	4:D:917:HOH:O	2.44	0.69
1:A:323:ARG:NH2	1:C:322:VAL:O	2.26	0.69
1:D:129:LEU:HD12	1:D:129:LEU:N	2.09	0.66
1:D:170:TYR:CZ	1:D:225:LYS:HE2	2.31	0.65
1:C:85:GLN:NE2	4:C:866:HOH:O	2.29	0.65
1:D:431:HIS:NE2	1:D:435:LYS:HE3	2.12	0.64
1:C:85:GLN:HG3	4:C:528:HOH:O	1.97	0.64
1:D:336[A]:PHE:HE1	4:D:924:HOH:O	1.80	0.64
1:D:299[A]:ARG:NH1	4:D:887:HOH:O	2.31	0.62
1:C:295:MSE:HG3	1:C:311:ILE:HD13	1.79	0.62
1:D:170:TYR:CE1	1:D:225:LYS:HE2	2.35	0.61
1:A:13:ARG:HH11	1:A:13:ARG:HG2	1.66	0.61
1:A:13:ARG:HH11	1:A:13:ARG:HG3	1.65	0.61
1:A:359:HIS:CD2	4:A:902:HOH:O	2.54	0.60
1:A:279:ALA:HB1	1:A:282:PRO:HG3	1.82	0.60
1:B:128:ARG:HD3	1:B:336:PHE:HE2	1.66	0.60
1:D:158:GLU:OE2	1:D:350:ARG:NH2	2.35	0.60
1:A:85:GLN:HG3	4:A:878:HOH:O	2.02	0.60
1:D:129:LEU:N	1:D:129:LEU:CD1	2.66	0.59
1:A:295:MSE:HG3	1:A:311:ILE:HD13	1.85	0.58
1:C:46:ILE:HD13	1:C:424:MSE:HE1	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:332:ALA:HB2	1:D:345:LEU:HD23	1.85	0.57
1:C:256:PRO:HG2	1:C:282:PRO:HA	1.88	0.56
1:D:13:ARG:HH11	1:D:13:ARG:CG	2.18	0.56
1:D:282:PRO:HD2	1:D:295:MSE:SE	2.56	0.56
1:C:147:HIS:HE1	4:C:703:HOH:O	1.89	0.55
1:B:37:ALA:HB1	1:B:38:PRO:HD2	1.87	0.55
1:C:69:LEU:HD23	1:C:132:VAL:HG13	1.87	0.55
1:D:299[A]:ARG:NH2	4:D:627:HOH:O	2.30	0.55
1:A:193:PRO:HG3	1:B:450:TYR:O	2.07	0.54
1:B:333:ASP:HB2	1:B:359:HIS:CD2	2.43	0.54
1:B:128:ARG:HD3	1:B:336:PHE:CE2	2.43	0.54
1:A:431:HIS:NE2	1:A:435:LYS:HE3	2.23	0.53
1:A:147:HIS:HE1	4:A:485:HOH:O	1.91	0.53
1:D:385:ILE:HA	4:D:527:HOH:O	2.07	0.53
1:C:53:HIS:HD2	4:C:546:HOH:O	1.92	0.52
1:D:59:VAL:HB	1:D:60:PRO:HD2	1.92	0.52
1:B:344[B]:ARG:HA	1:B:347:GLN:HE21	1.75	0.51
1:D:53:HIS:HD2	4:D:521:HOH:O	1.93	0.51
1:B:59:VAL:HB	1:B:60:PRO:HD2	1.91	0.51
1:B:319:ASP:HB2	1:D:352:TRP:CD1	2.46	0.51
1:C:282:PRO:HD2	1:C:295:MSE:SE	2.60	0.51
1:D:37:ALA:HB1	1:D:38:PRO:HD2	1.92	0.51
1:C:84:TYR:CZ	1:C:85:GLN:HG2	2.47	0.50
1:A:169:ALA:HB2	1:A:221:PHE:CD2	2.47	0.49
1:C:84:TYR:CE2	1:C:85:GLN:HG2	2.46	0.49
1:B:295:MSE:HG3	1:B:311:ILE:HD13	1.93	0.49
1:B:92:ARG:HE	1:B:133:ILE:CD1	2.26	0.48
1:D:318:MSE:HE1	1:D:330:PRO:HB3	1.94	0.48
1:D:209:ALA:O	1:D:213:GLU:HG3	2.13	0.48
1:B:128:ARG:CD	1:B:336:PHE:HE2	2.27	0.48
1:B:129:LEU:HD23	1:B:133:ILE:HD11	1.95	0.48
1:B:352:TRP:CD1	1:D:319:ASP:HB2	2.49	0.47
1:A:59:VAL:HB	1:A:60:PRO:HD2	1.96	0.47
1:B:344[A]:ARG:HA	1:B:347:GLN:HE21	1.80	0.47
1:C:21:PRO:HD2	1:C:431:HIS:CE1	2.49	0.47
1:D:13:ARG:HG2	1:D:13:ARG:NH1	2.25	0.47
1:D:69:LEU:HD23	1:D:132:VAL:HG13	1.96	0.47
1:A:53:HIS:HD2	4:A:493:HOH:O	1.96	0.47
1:C:264:GLU:O	1:C:268:LEU:HD23	2.15	0.47
1:D:415:ARG:HB2	1:D:419:GLY:HA2	1.97	0.46
1:B:415:ARG:HB2	1:B:419:GLY:HA2	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:30:LEU:HD13	1:A:464:PHE:HE2	1.80	0.46
1:A:319:ASP:HB2	1:C:352:TRP:CD1	2.50	0.46
1:C:13:ARG:HH11	1:C:13:ARG:CG	2.26	0.46
1:C:274:HIS:CD2	1:C:275:LEU:HD13	2.50	0.46
1:C:128:ARG:HD3	1:C:336:PHE:HD2	1.81	0.46
1:C:227:LYS:HA	1:C:227:LYS:HE3	1.98	0.46
1:D:336[A]:PHE:CE1	4:D:924:HOH:O	2.57	0.45
1:B:147:HIS:HE1	4:D:712:HOH:O	2.00	0.45
1:B:21:PRO:HG2	1:B:66:ARG:CZ	2.47	0.44
1:B:431:HIS:NE2	1:B:435:LYS:HE3	2.32	0.44
1:C:59:VAL:HB	1:C:60:PRO:HD2	1.98	0.44
1:D:13:ARG:CG	1:D:13:ARG:NH1	2.77	0.44
1:B:460:LYS:NZ	4:B:484:HOH:O	2.51	0.44
1:A:292:ARG:HA	1:A:311:ILE:HD12	2.00	0.43
1:D:168:LEU:HD12	1:D:168:LEU:O	2.19	0.43
1:D:422:LEU:HD12	1:D:422:LEU:HA	1.91	0.43
1:B:275:LEU:HD12	1:B:275:LEU:HA	1.92	0.43
1:C:162:ARG:HD3	1:C:164:ALA:O	2.19	0.43
1:D:129:LEU:CD1	1:D:129:LEU:H	2.32	0.43
1:D:291:GLY:HA3	1:D:311:ILE:HG21	2.01	0.43
1:D:168:LEU:HD12	1:D:168:LEU:C	2.39	0.43
1:C:44:LEU:HD21	1:C:398:LEU:HD13	2.01	0.43
1:D:59:VAL:HB	1:D:60:PRO:CD	2.49	0.42
1:A:166:PRO:HA	1:A:409:GLN:HG2	2.01	0.42
1:A:192:THR:HG23	4:A:865:HOH:O	2.20	0.42
1:B:30:LEU:HD13	1:B:464:PHE:HE2	1.83	0.42
1:B:129:LEU:HD23	1:B:133:ILE:CD1	2.49	0.42
1:A:84:TYR:CE2	1:A:85:GLN:HG2	2.55	0.42
1:A:415:ARG:HB2	1:A:419:GLY:HA2	2.01	0.42
1:C:365:ASP:OD1	1:C:365:ASP:N	2.47	0.42
1:D:158:GLU:CD	1:D:350:ARG:HH22	2.22	0.42
1:D:431:HIS:CD2	1:D:435:LYS:HE3	2.54	0.42
1:A:274:HIS:CD2	1:A:275:LEU:HD13	2.55	0.42
1:B:431:HIS:CD2	1:B:435:LYS:HE3	2.55	0.42
1:C:21:PRO:HB2	1:C:434:TYR:CD2	2.55	0.41
1:A:385:ILE:HA	4:A:610:HOH:O	2.20	0.41
1:B:21:PRO:HB2	1:B:434:TYR:CD2	2.56	0.41
1:C:292:ARG:HA	1:C:311:ILE:HD12	2.01	0.41
1:D:329:ILE:HA	1:D:355:THR:O	2.20	0.41
1:C:415:ARG:HD3	1:C:419:GLY:O	2.20	0.41
1:A:84:TYR:CZ	1:A:85:GLN:HG2	2.55	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:216:VAL:HG21	1:C:247:PHE:CZ	2.56	0.40
1:C:415:ARG:H	1:C:415:ARG:HG3	1.47	0.40
1:C:13:ARG:HG2	1:C:13:ARG:NH1	2.27	0.40
1:C:378:ALA:HA	1:C:379:PRO:HD3	1.90	0.40
1:B:128:ARG:NE	1:B:336:PHE:HE2	2.20	0.40
1:C:170:TYR:CZ	1:C:225:LYS:HE3	2.57	0.40
1:A:13:ARG:CG	1:A:13:ARG:NH1	2.65	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	421/475 (89%)	417 (99%)	4 (1%)	0	100	100
1	B	420/475 (88%)	417 (99%)	3 (1%)	0	100	100
1	C	422/475 (89%)	417 (99%)	5 (1%)	0	100	100
1	D	425/475 (90%)	419 (99%)	6 (1%)	0	100	100
All	All	1688/1900 (89%)	1670 (99%)	18 (1%)	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	323/346 (93%)	312 (97%)	11 (3%)	37	25
1	B	322/346 (93%)	309 (96%)	13 (4%)	31	19
1	C	323/346 (93%)	313 (97%)	10 (3%)	40	29
1	D	326/346 (94%)	315 (97%)	11 (3%)	37	25
All	All	1294/1384 (94%)	1249 (96%)	45 (4%)	36	24

All (45) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	13	ARG
1	A	32	LEU
1	A	85	GLN
1	A	129	LEU
1	A	144	LEU
1	A	170	TYR
1	A	268	LEU
1	A	275	LEU
1	A	309	ASN
1	A	403	LEU
1	A	422	LEU
1	B	13	ARG
1	B	32	LEU
1	B	44	LEU
1	B	128	ARG
1	B	129	LEU
1	B	144	LEU
1	B	170	TYR
1	B	191	ARG
1	B	268	LEU
1	B	275	LEU
1	B	359	HIS
1	B	403	LEU
1	B	422	LEU
1	C	13	ARG
1	C	32	LEU
1	C	85	GLN
1	C	144	LEU
1	C	167	MSE
1	C	170	TYR
1	C	275	LEU
1	C	415	ARG
1	C	422	LEU

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Mol	Chain	Res	Type
1	C	440	THR
1	D	13	ARG
1	D	32	LEU
1	D	44	LEU
1	D	144	LEU
1	D	167	MSE
1	D	170	TYR
1	D	268	LEU
1	D	275	LEU
1	D	309	ASN
1	D	350	ARG
1	D	422	LEU

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	53	HIS
1	A	147	HIS
1	B	53	HIS
1	B	347	GLN
1	C	53	HIS
1	C	147	HIS
1	C	361	ASN
1	D	53	HIS
1	D	131	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 monosaccharides in this entry.

5.6 Ligand geometry

Of 8 ligands modelled in this entry, 4 are monoatomic - leaving 4 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	CO3	C	477	-	3,3,3	1.02	0	2,3,3	0.28	0
3	CO3	B	477	-	3,3,3	0.79	0	2,3,3	0.15	0
3	CO3	A	477	-	3,3,3	1.00	0	2,3,3	0.21	0
3	CO3	D	477	-	3,3,3	0.98	0	2,3,3	0.20	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

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	411/475 (86%)	-0.11	12 (2%) 51 53	19, 26, 38, 60	0
1	B	410/475 (86%)	0.00	17 (4%) 37 39	20, 29, 49, 62	0
1	C	412/475 (86%)	-0.04	10 (2%) 59 60	19, 28, 42, 62	0
1	D	412/475 (86%)	-0.08	7 (1%) 70 72	20, 28, 43, 64	0
All	All	1645/1900 (86%)	-0.05	46 (2%) 53 54	19, 28, 44, 64	0

All (46) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	439	GLY	4.5
1	C	414	GLU	4.1
1	B	191	ARG	3.6
1	B	95	LEU	3.6
1	B	439	GLY	3.5
1	A	465	GLY	3.3
1	C	96	SER	3.3
1	B	440	THR	3.2
1	C	465	GLY	3.0
1	D	440	THR	3.0
1	A	331	LEU	2.9
1	C	464	PHE	2.9
1	D	96	SER	2.9
1	A	170	TYR	2.9
1	D	74	ASP	2.9
1	C	440	THR	2.8
1	A	95	LEU	2.8
1	B	75	LEU	2.7
1	B	129	LEU	2.7
1	B	414	GLU	2.7
1	D	415	ARG	2.7

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Mol	Chain	Res	Type	RSRZ
1	A	96	SER	2.6
1	B	71	ARG	2.6
1	A	439	GLY	2.6
1	B	415	ARG	2.5
1	D	439	GLY	2.5
1	B	94	ALA	2.5
1	B	189	GLN	2.5
1	B	441	ALA	2.5
1	B	70	GLU	2.5
1	B	93	ALA	2.4
1	A	415	ARG	2.4
1	A	359	HIS	2.3
1	A	129	LEU	2.3
1	A	440	THR	2.3
1	B	67	HIS	2.3
1	C	95	LEU	2.2
1	C	438	GLY	2.2
1	C	331	LEU	2.2
1	B	74	ASP	2.1
1	C	332	ALA	2.1
1	A	186	ASP	2.1
1	D	414	GLU	2.1
1	A	453	PRO	2.1
1	D	95	LEU	2.1
1	B	436	GLU	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 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	MG	B	476	1/1	0.83	0.10	42,42,42,42	0
2	MG	A	476	1/1	0.91	0.10	43,43,43,43	0
3	CO3	C	477	4/4	0.91	0.18	30,35,42,44	0
2	MG	C	476	1/1	0.93	0.13	39,39,39,39	0
3	CO3	A	477	4/4	0.95	0.14	27,28,35,42	0
3	CO3	B	477	4/4	0.95	0.10	28,28,33,43	0
2	MG	D	476	1/1	0.95	0.06	36,36,36,36	0
3	CO3	D	477	4/4	0.96	0.10	28,31,35,43	0

6.5 Other polymers [i](#)

There are no such residues in this entry.