



# Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 06:37 PM GMT

PDB ID : 1BQG  
Title : THE STRUCTURE OF THE D-GLUCARATE DEHYDRATASE PROTEIN  
FROM PSEUDOMONAS PUTIDA  
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Deposited on : 1998-08-15  
Resolution : 2.30 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](mailto: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.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
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) : trunk26865

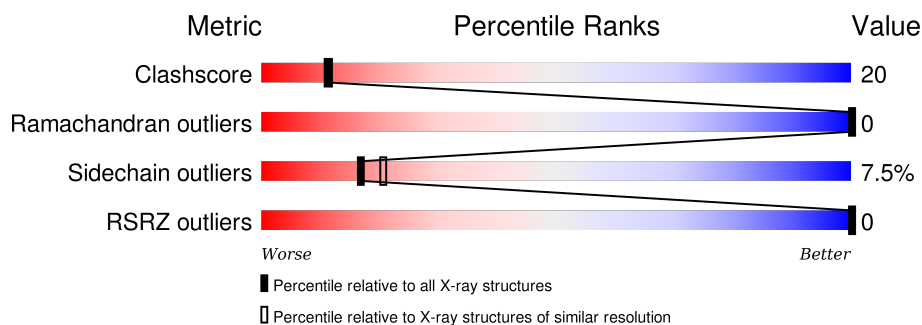
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*


The reported resolution of this entry is 2.30 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))
Clashscore	102246	4452 (2.30-2.30)
Ramachandran outliers	100387	4410 (2.30-2.30)
Sidechain outliers	100360	4409 (2.30-2.30)
RSRZ outliers	91569	3857 (2.30-2.30)

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  $\geq 3$ , 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	451	

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 3178 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 D-GLUCARATE DEHYDRATASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	399	Total	C	N	O	S	0	0	0
			3033	1912	543	565	13			

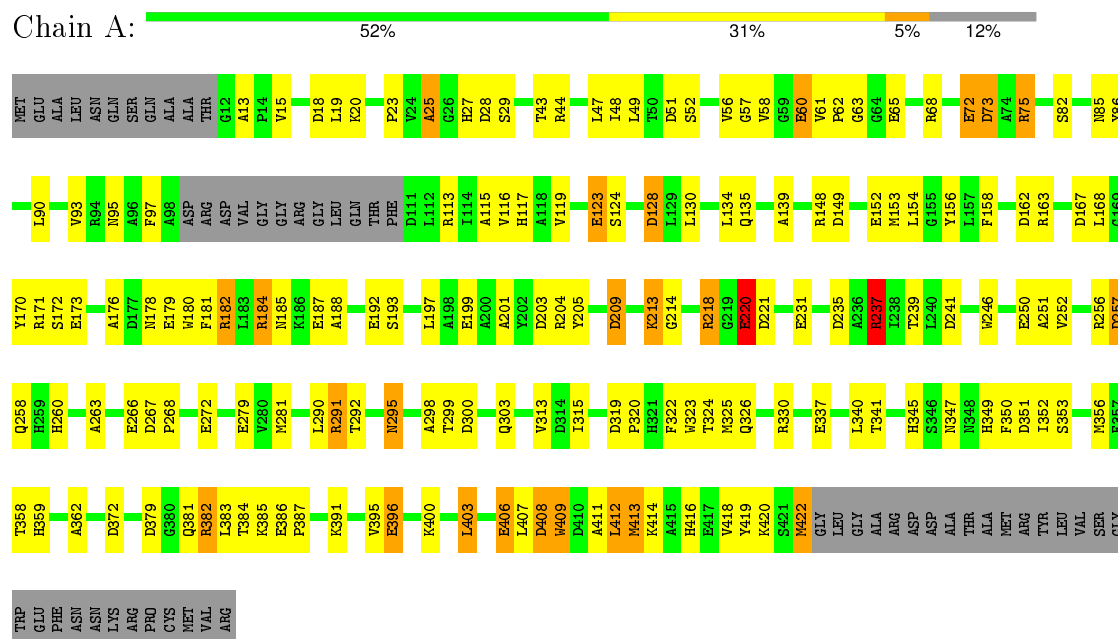
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	145	Total	O	0	0
			145	145		

### 3 Residue-property plots

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: D-GLUCARATE DEHYDRATASE



## 4 Data and refinement statistics

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	69.62Å 108.79Å 122.57Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 2.30 42.37 – 1.96	Depositor EDS
% Data completeness (in resolution range)	96.0 (30.00-2.30) 75.6 (42.37-1.96)	Depositor EDS
$R_{merge}$	0.04	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	0.00 (at 1.95Å)	Xtriage
Refinement program	TNT V. 5-D	Depositor
R, $R_{free}$	0.190 , (Not available) 0.165 , (Not available)	Depositor DCC
$R_{free}$ test set	No test flags present.	DCC
Wilson B-factor (Å <sup>2</sup> )	27.0	Xtriage
Anisotropy	0.151	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 141.8	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.51$ , $\langle L^2 \rangle = 0.34$	Xtriage
Outliers	0 of 29034 reflections	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	3178	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	37.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.32% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

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	1.11	17/3100 (0.5%)	1.45	52/4219 (1.2%)

All (17) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	396	GLU	CD-OE1	7.61	1.34	1.25
1	A	152	GLU	CD-OE1	7.21	1.33	1.25
1	A	220	GLU	CD-OE2	7.19	1.33	1.25
1	A	72	GLU	CD-OE2	7.14	1.33	1.25
1	A	231	GLU	CD-OE2	6.62	1.32	1.25
1	A	179	GLU	CD-OE2	6.61	1.32	1.25
1	A	337	GLU	CD-OE1	6.51	1.32	1.25
1	A	192	GLU	CD-OE2	6.37	1.32	1.25
1	A	65	GLU	CD-OE1	6.01	1.32	1.25
1	A	199	GLU	CD-OE2	5.96	1.32	1.25
1	A	123	GLU	CD-OE2	-5.89	1.19	1.25
1	A	266	GLU	CD-OE2	5.85	1.32	1.25
1	A	187	GLU	CD-OE2	5.80	1.32	1.25
1	A	250	GLU	CD-OE2	5.77	1.31	1.25
1	A	406	GLU	CD-OE2	5.72	1.31	1.25
1	A	279	GLU	CD-OE1	-5.69	1.19	1.25
1	A	60	GLU	CD-OE2	5.04	1.31	1.25

All (52) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	267	ASP	CB-CG-OD2	-9.58	109.68	118.30
1	A	372	ASP	CB-CG-OD1	8.50	125.95	118.30
1	A	323	TRP	C-N-CA	-8.46	100.55	121.70
1	A	203	ASP	CB-CG-OD1	-8.01	111.09	118.30
1	A	379	ASP	CB-CG-OD2	-7.76	111.31	118.30
1	A	203	ASP	CB-CG-OD2	7.63	125.16	118.30
1	A	28	ASP	CB-CG-OD2	-7.50	111.56	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	324	THR	CA-CB-CG2	-7.20	102.32	112.40
1	A	267	ASP	CB-CG-OD1	7.17	124.75	118.30
1	A	291	ARG	NE-CZ-NH2	-7.07	116.76	120.30
1	A	221	ASP	CB-CG-OD2	-7.07	111.94	118.30
1	A	28	ASP	CB-CG-OD1	6.92	124.53	118.30
1	A	379	ASP	CB-CG-OD1	6.87	124.48	118.30
1	A	382	ARG	NE-CZ-NH1	6.79	123.70	120.30
1	A	372	ASP	CB-CG-OD2	-6.64	112.33	118.30
1	A	209	ASP	CB-CG-OD2	-6.63	112.33	118.30
1	A	18	ASP	CB-CG-OD2	-6.62	112.34	118.30
1	A	235	ASP	CB-CG-OD2	-6.55	112.41	118.30
1	A	291	ARG	NE-CZ-NH1	6.51	123.56	120.30
1	A	300	ASP	CB-CA-C	-6.42	97.57	110.40
1	A	209	ASP	CB-CG-OD1	6.32	123.99	118.30
1	A	351	ASP	CB-CG-OD1	-6.25	112.68	118.30
1	A	149	ASP	CB-CG-OD1	-6.10	112.81	118.30
1	A	408	ASP	CB-CG-OD1	-6.09	112.82	118.30
1	A	128	ASP	CB-CG-OD2	-5.95	112.94	118.30
1	A	237	ARG	NE-CZ-NH1	5.94	123.27	120.30
1	A	330	ARG	NE-CZ-NH2	-5.82	117.39	120.30
1	A	257	ASP	CB-CG-OD1	5.75	123.48	118.30
1	A	18	ASP	CB-CG-OD1	5.74	123.47	118.30
1	A	400	LYS	N-CA-C	-5.74	95.50	111.00
1	A	272	GLU	CB-CA-C	-5.68	99.03	110.40
1	A	73	ASP	CB-CG-OD1	-5.67	113.20	118.30
1	A	162	ASP	CB-CG-OD1	5.59	123.33	118.30
1	A	403	LEU	CB-CG-CD1	-5.57	101.53	111.00
1	A	241	ASP	CB-CG-OD2	5.49	123.24	118.30
1	A	149	ASP	CB-CG-OD2	5.48	123.23	118.30
1	A	128	ASP	CB-CG-OD1	5.47	123.22	118.30
1	A	295	ASN	N-CA-CB	5.45	120.41	110.60
1	A	235	ASP	CB-CG-OD1	5.45	123.20	118.30
1	A	408	ASP	CB-CG-OD2	5.43	123.19	118.30
1	A	182	ARG	NE-CZ-NH1	5.42	123.01	120.30
1	A	221	ASP	CB-CG-OD1	5.41	123.17	118.30
1	A	422	MET	N-CA-CB	-5.41	100.87	110.60
1	A	97	PHE	CB-CG-CD1	-5.39	117.03	120.80
1	A	330	ARG	NE-CZ-NH1	5.38	122.99	120.30
1	A	351	ASP	N-CA-CB	-5.29	101.08	110.60
1	A	93	VAL	CA-CB-CG2	-5.24	103.04	110.90
1	A	412	LEU	CA-CB-CG	-5.21	103.33	115.30
1	A	218	ARG	N-CA-CB	-5.19	101.26	110.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	382	ARG	NE-CZ-NH2	-5.10	117.75	120.30
1	A	351	ASP	CB-CG-OD2	5.06	122.85	118.30
1	A	25	ALA	N-CA-CB	5.04	117.15	110.10

There are no chirality outliers.

There are no planarity outliers.

## 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	3033	0	2925	122	0
2	A	145	0	0	13	0
All	All	3178	0	2925	122	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 20.

All (122) 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:124:SER:HA	1:A:325:MET:HE1	1.41	1.01
1:A:353:SER:HA	1:A:356:MET:HE3	1.54	0.88
1:A:419:TYR:HA	1:A:422:MET:CE	2.03	0.88
1:A:43:THR:HG22	1:A:63:GLY:HA3	1.59	0.84
1:A:153:MET:HE2	2:A:648:HOH:O	1.76	0.83
1:A:61:VAL:HB	1:A:62:PRO:HD2	1.59	0.81
1:A:13:ALA:HB3	1:A:82:SER:OG	1.81	0.78
1:A:60:GLU:HB3	1:A:356:MET:HE1	1.64	0.78
1:A:123:GLU:OE2	1:A:326:GLN:HG3	1.83	0.78
1:A:353:SER:CA	1:A:356:MET:HE3	2.14	0.78
1:A:350:PHE:CD1	1:A:383:LEU:HD11	2.21	0.75
1:A:358:THR:HA	2:A:648:HOH:O	1.86	0.75
1:A:419:TYR:HA	1:A:422:MET:HE2	1.70	0.74
1:A:60:GLU:HB3	1:A:356:MET:CE	2.18	0.73
1:A:57:GLY:HA2	1:A:128:ASP:OD2	1.88	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:385:LYS:HD2	1:A:406:GLU:HG2	1.71	0.73
1:A:124:SER:HA	1:A:325:MET:CE	2.19	0.71
1:A:352:ILE:HG22	1:A:356:MET:HE2	1.72	0.71
1:A:382:ARG:C	1:A:383:LEU:HD12	2.11	0.71
1:A:292:THR:HG22	1:A:313:VAL:HG12	1.73	0.69
1:A:134:LEU:O	1:A:135:GLN:HB2	1.93	0.69
1:A:353:SER:HA	1:A:356:MET:CE	2.23	0.69
1:A:383:LEU:N	1:A:383:LEU:HD12	2.08	0.69
1:A:113:ARG:O	1:A:116:VAL:HG12	1.94	0.68
1:A:15:VAL:HG23	1:A:52:SER:HB3	1.74	0.68
1:A:173:GLU:N	2:A:616:HOH:O	2.18	0.67
1:A:326:GLN:NE2	2:A:605:HOH:O	2.27	0.67
1:A:19:LEU:HB3	1:A:75:ARG:HD3	1.75	0.67
1:A:51:ASP:OD2	2:A:502:HOH:O	2.13	0.67
1:A:260:HIS:H	1:A:260:HIS:CD2	2.14	0.66
1:A:340:LEU:HD12	1:A:340:LEU:N	2.12	0.65
1:A:353:SER:N	1:A:356:MET:HE3	2.12	0.65
1:A:299:THR:H	1:A:303:GLN:NE2	1.94	0.65
1:A:19:LEU:HD23	1:A:20:LYS:N	2.11	0.64
1:A:382:ARG:O	1:A:411:ALA:HB1	1.98	0.63
1:A:352:ILE:HG22	1:A:356:MET:CE	2.29	0.62
1:A:407:LEU:C	1:A:407:LEU:HD12	2.20	0.61
1:A:414:LYS:O	1:A:418:VAL:HG23	2.01	0.61
1:A:359:HIS:ND1	1:A:403:LEU:HD23	2.16	0.61
1:A:68:ARG:NH1	1:A:72:GLU:OE1	2.34	0.60
1:A:47:LEU:C	1:A:48:ILE:HD12	2.21	0.59
1:A:181:PHE:HA	1:A:184:ARG:HD2	1.85	0.58
1:A:116:VAL:HG21	1:A:322:PHE:O	2.05	0.56
1:A:359:HIS:HD1	1:A:403:LEU:HD23	1.70	0.56
1:A:347:ASN:O	1:A:349:HIS:HD2	1.88	0.56
1:A:359:HIS:HE1	1:A:403:LEU:O	1.88	0.56
1:A:61:VAL:HB	1:A:62:PRO:CD	2.34	0.54
1:A:411:ALA:HA	2:A:552:HOH:O	2.08	0.53
1:A:25:ALA:HB2	1:A:422:MET:HE1	1.91	0.53
1:A:384:THR:HA	1:A:407:LEU:HA	1.90	0.53
1:A:171:ARG:NE	1:A:185:ASN:OD1	2.41	0.53
1:A:298:ALA:HA	1:A:303:GLN:HB3	1.90	0.53
1:A:408:ASP:HB3	1:A:411:ALA:HB3	1.91	0.53
1:A:23:PRO:HG3	1:A:68:ARG:CD	2.39	0.53
1:A:15:VAL:O	1:A:51:ASP:HB2	2.09	0.52
1:A:220:GLU:CD	1:A:220:GLU:H	2.13	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:385:LYS:HE3	1:A:407:LEU:O	2.10	0.52
1:A:176:ALA:HB3	1:A:182:ARG:HG3	1.92	0.52
1:A:90:LEU:HD21	1:A:123:GLU:CA	2.41	0.51
1:A:13:ALA:HB3	1:A:82:SER:HG	1.76	0.51
1:A:180:TRP:CZ3	1:A:197:LEU:HD23	2.46	0.51
1:A:19:LEU:HD23	1:A:19:LEU:C	2.31	0.50
1:A:322:PHE:CD1	1:A:322:PHE:N	2.78	0.50
1:A:383:LEU:N	1:A:383:LEU:CD1	2.74	0.50
1:A:23:PRO:HG3	1:A:68:ARG:HD3	1.94	0.50
1:A:185:ASN:HB3	2:A:532:HOH:O	2.11	0.50
1:A:419:TYR:HA	1:A:422:MET:HE3	1.92	0.49
1:A:358:THR:CA	2:A:648:HOH:O	2.52	0.49
1:A:19:LEU:HB3	1:A:75:ARG:CD	2.42	0.49
1:A:90:LEU:HD21	1:A:123:GLU:HA	1.96	0.48
1:A:47:LEU:HG	1:A:48:ILE:N	2.27	0.48
1:A:139:ALA:H	1:A:359:HIS:HD2	1.61	0.48
1:A:204:ARG:HB2	2:A:612:HOH:O	2.13	0.47
1:A:319:ASP:HB3	2:A:541:HOH:O	2.13	0.47
1:A:181:PHE:N	1:A:181:PHE:CD1	2.83	0.47
1:A:148:ARG:HG2	1:A:362:ALA:HA	1.96	0.47
1:A:48:ILE:O	1:A:49:LEU:HD23	2.15	0.47
1:A:48:ILE:N	1:A:48:ILE:HD12	2.30	0.46
1:A:124:SER:CA	1:A:325:MET:CE	2.91	0.46
1:A:113:ARG:O	1:A:116:VAL:CG1	2.64	0.45
1:A:181:PHE:N	1:A:181:PHE:HD1	2.14	0.45
1:A:407:LEU:HD11	1:A:409:TRP:CZ3	2.52	0.45
1:A:47:LEU:O	1:A:58:VAL:HA	2.16	0.45
1:A:188:ALA:HA	1:A:193:SER:OG	2.17	0.45
1:A:48:ILE:N	1:A:48:ILE:CD1	2.79	0.45
1:A:352:ILE:C	1:A:356:MET:HE3	2.37	0.45
1:A:209:ASP:OD1	1:A:237:ARG:HD2	2.17	0.45
1:A:139:ALA:H	1:A:359:HIS:CD2	2.35	0.44
1:A:27:HIS:H	1:A:381:GLN:HE22	1.66	0.44
1:A:163:ARG:HB2	1:A:170:TYR:HB2	1.99	0.44
1:A:134:LEU:O	1:A:135:GLN:CB	2.57	0.44
1:A:15:VAL:CG2	1:A:52:SER:HB3	2.44	0.44
1:A:154:LEU:C	1:A:154:LEU:HD12	2.39	0.43
1:A:412:LEU:HD12	1:A:412:LEU:HA	1.72	0.43
1:A:86:TYR:O	1:A:90:LEU:HD12	2.18	0.43
1:A:252:VAL:O	1:A:256:ARG:HB2	2.19	0.43
1:A:130:LEU:HA	1:A:130:LEU:HD12	1.61	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:20:LYS:HB2	1:A:48:ILE:HB	2.00	0.43
1:A:23:PRO:O	1:A:416:HIS:HD2	2.02	0.42
1:A:115:ALA:O	1:A:119:VAL:HG23	2.19	0.42
1:A:43:THR:C	1:A:44:ARG:HG2	2.38	0.42
1:A:315:ILE:HA	1:A:341:THR:O	2.19	0.42
1:A:239:THR:HG22	1:A:263:ALA:HB3	2.00	0.42
1:A:246:TRP:CE3	1:A:251:ALA:HA	2.55	0.42
1:A:319:ASP:HA	1:A:320:PRO:HD2	1.94	0.41
1:A:168:LEU:HA	1:A:168:LEU:HD23	1.85	0.41
1:A:409:TRP:O	1:A:413:MET:N	2.32	0.41
1:A:56:VAL:HG12	2:A:548:HOH:O	2.19	0.41
1:A:158:PHE:CE2	1:A:213:LYS:HG2	2.56	0.41
1:A:213:LYS:HD3	1:A:214:GLY:N	2.36	0.41
1:A:48:ILE:O	1:A:48:ILE:HG22	2.17	0.41
1:A:345:HIS:HD2	2:A:526:HOH:O	2.02	0.41
1:A:268:PRO:HD2	1:A:281:MET:SD	2.61	0.41
1:A:290:LEU:HD23	2:A:561:HOH:O	2.20	0.41
1:A:153:MET:HE1	1:A:395:VAL:HG21	2.03	0.41
1:A:116:VAL:HG13	1:A:117:HIS:N	2.36	0.41
1:A:201:ALA:O	1:A:205:TYR:N	2.45	0.40
1:A:43:THR:HG22	1:A:63:GLY:CA	2.41	0.40
1:A:60:GLU:H	1:A:356:MET:CE	2.35	0.40
1:A:409:TRP:O	1:A:413:MET:HB2	2.20	0.40
1:A:180:TRP:HZ3	1:A:197:LEU:HD23	1.85	0.40
1:A:386:GLU:HA	1:A:387:PRO:HD2	1.88	0.40

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	395/451 (88%)	377 (95%)	18 (5%)	0	100	100

There are no Ramachandran outliers to report.

### 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	306/360 (85%)	283 (92%)	23 (8%)	17	21

All (23) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	29	SER
1	A	73	ASP
1	A	75	ARG
1	A	85	ASN
1	A	95	ASN
1	A	156	TYR
1	A	167	ASP
1	A	172	SER
1	A	178	ASN
1	A	184	ARG
1	A	213	LYS
1	A	218	ARG
1	A	220	GLU
1	A	237	ARG
1	A	257	ASP
1	A	258	GLN
1	A	291	ARG
1	A	295	ASN
1	A	391	LYS
1	A	396	GLU
1	A	409	TRP
1	A	413	MET
1	A	420	LYS

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

Mol	Chain	Res	Type
1	A	45	ASN
1	A	76	HIS
1	A	80	ASN
1	A	85	ASN
1	A	95	ASN
1	A	146	GLN
1	A	147	GLN
1	A	260	HIS
1	A	295	ASN
1	A	303	GLN
1	A	347	ASN
1	A	359	HIS
1	A	381	GLN
1	A	416	HIS

### 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 carbohydrates in this entry.

### 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

### 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	399/451 (88%)	-0.77	0 100 100	14, 33, 71, 100	0

There are no RSRZ outliers to report.

### 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 carbohydrates in this entry.

### 6.4 Ligands [i](#)

There are no ligands in this entry.

### 6.5 Other polymers [i](#)

There are no such residues in this entry.