



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 11:26 AM GMT

PDB ID : 3P0W  
Title : Crystal structure of D-Glucarate dehydratase from Ralstonia solanacearum complexed with Mg and D-glucarate  
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 : 2010-09-29  
Resolution : 1.71 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

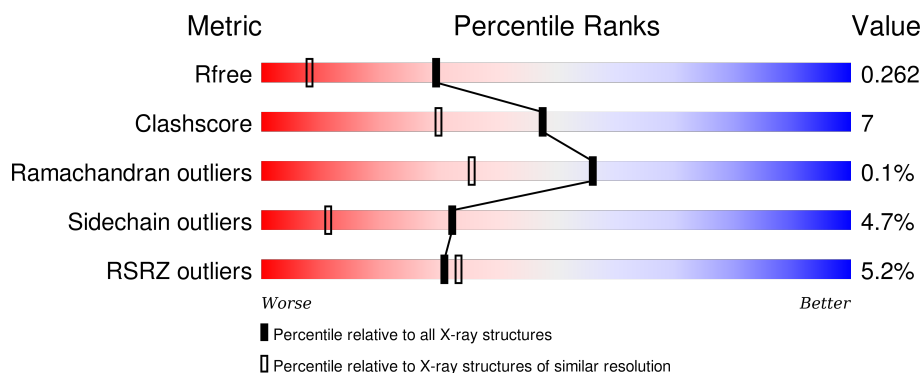
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 1.71 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	3998 (1.74-1.70)
Clashscore	102246	4425 (1.74-1.70)
Ramachandran outliers	100387	4360 (1.74-1.70)
Sidechain outliers	100360	4360 (1.74-1.70)
RSRZ outliers	91569	4010 (1.74-1.70)

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	470	<div> <div>2%</div> <div>78% 11% 10%</div> </div>
1	B	470	<div> <div>7%</div> <div>77% 13% 9%</div> </div>
1	C	470	<div> <div>4%</div> <div>71% 17% 10%</div> </div>
1	D	470	<div> <div>6%</div> <div>72% 17% 10%</div> </div>

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 13261 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 Mandelate racemase/muconate lactonizing protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	424	Total	C	N	O	S	0	0	0
			3237	2040	587	590	20			
1	B	428	Total	C	N	O	S	0	0	0
			3270	2061	592	597	20			
1	C	421	Total	C	N	O	S	0	0	0
			3220	2031	583	586	20			
1	D	425	Total	C	N	O	S	0	0	0
			3244	2044	588	592	20			

There are 44 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	EXPRESSION TAG	UNP B2UIZ1
A	2	SER	-	EXPRESSION TAG	UNP B2UIZ1
A	3	LEU	-	EXPRESSION TAG	UNP B2UIZ1
A	463	GLU	-	EXPRESSION TAG	UNP B2UIZ1
A	464	GLY	-	EXPRESSION TAG	UNP B2UIZ1
A	465	HIS	-	EXPRESSION TAG	UNP B2UIZ1
A	466	HIS	-	EXPRESSION TAG	UNP B2UIZ1
A	467	HIS	-	EXPRESSION TAG	UNP B2UIZ1
A	468	HIS	-	EXPRESSION TAG	UNP B2UIZ1
A	469	HIS	-	EXPRESSION TAG	UNP B2UIZ1
A	470	HIS	-	EXPRESSION TAG	UNP B2UIZ1
B	1	MET	-	EXPRESSION TAG	UNP B2UIZ1
B	2	SER	-	EXPRESSION TAG	UNP B2UIZ1
B	3	LEU	-	EXPRESSION TAG	UNP B2UIZ1
B	463	GLU	-	EXPRESSION TAG	UNP B2UIZ1
B	464	GLY	-	EXPRESSION TAG	UNP B2UIZ1
B	465	HIS	-	EXPRESSION TAG	UNP B2UIZ1
B	466	HIS	-	EXPRESSION TAG	UNP B2UIZ1
B	467	HIS	-	EXPRESSION TAG	UNP B2UIZ1
B	468	HIS	-	EXPRESSION TAG	UNP B2UIZ1
B	469	HIS	-	EXPRESSION TAG	UNP B2UIZ1

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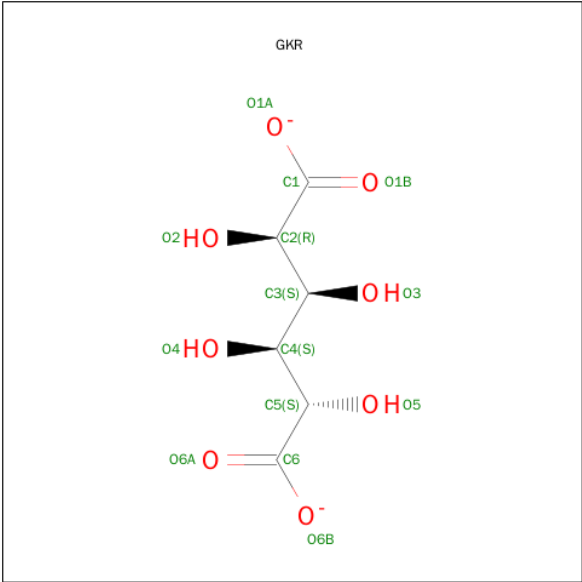
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Chain	Residue	Modelled	Actual	Comment	Reference
B	470	HIS	-	EXPRESSION TAG	UNP B2UIZ1
C	1	MET	-	EXPRESSION TAG	UNP B2UIZ1
C	2	SER	-	EXPRESSION TAG	UNP B2UIZ1
C	3	LEU	-	EXPRESSION TAG	UNP B2UIZ1
C	463	GLU	-	EXPRESSION TAG	UNP B2UIZ1
C	464	GLY	-	EXPRESSION TAG	UNP B2UIZ1
C	465	HIS	-	EXPRESSION TAG	UNP B2UIZ1
C	466	HIS	-	EXPRESSION TAG	UNP B2UIZ1
C	467	HIS	-	EXPRESSION TAG	UNP B2UIZ1
C	468	HIS	-	EXPRESSION TAG	UNP B2UIZ1
C	469	HIS	-	EXPRESSION TAG	UNP B2UIZ1
C	470	HIS	-	EXPRESSION TAG	UNP B2UIZ1
D	1	MET	-	EXPRESSION TAG	UNP B2UIZ1
D	2	SER	-	EXPRESSION TAG	UNP B2UIZ1
D	3	LEU	-	EXPRESSION TAG	UNP B2UIZ1
D	463	GLU	-	EXPRESSION TAG	UNP B2UIZ1
D	464	GLY	-	EXPRESSION TAG	UNP B2UIZ1
D	465	HIS	-	EXPRESSION TAG	UNP B2UIZ1
D	466	HIS	-	EXPRESSION TAG	UNP B2UIZ1
D	467	HIS	-	EXPRESSION TAG	UNP B2UIZ1
D	468	HIS	-	EXPRESSION TAG	UNP B2UIZ1
D	469	HIS	-	EXPRESSION TAG	UNP B2UIZ1
D	470	HIS	-	EXPRESSION TAG	UNP B2UIZ1

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

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

- Molecule 3 is D-GLUCARATE (three-letter code: GKR) (formula: C<sub>6</sub>H<sub>8</sub>O<sub>8</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			14	6	8		
3	B	1	Total	C	O	0	0
			14	6	8		
3	C	1	Total	C	O	0	0
			14	6	8		
3	D	1	Total	C	O	0	0
			14	6	8		

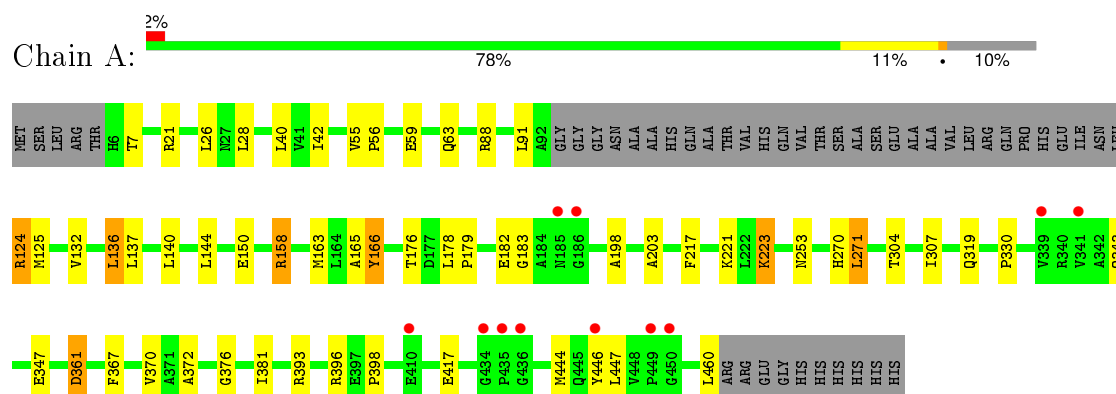
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	51	Total	O	0	0
			51	51		
4	B	99	Total	O	0	0
			99	99		
4	C	42	Total	O	0	0
			42	42		
4	D	38	Total	O	0	0
			38	38		

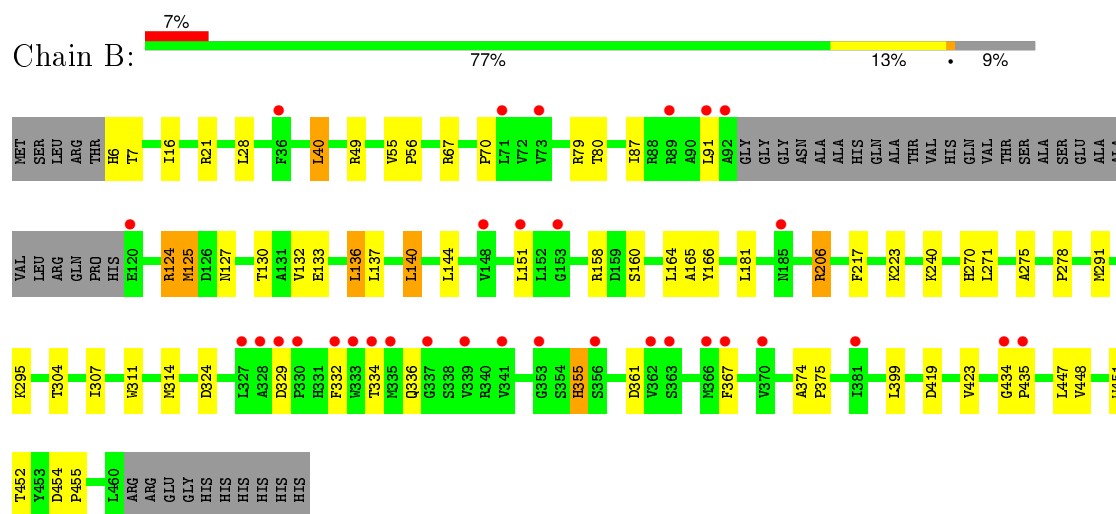
### 3 Residue-property plots

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.

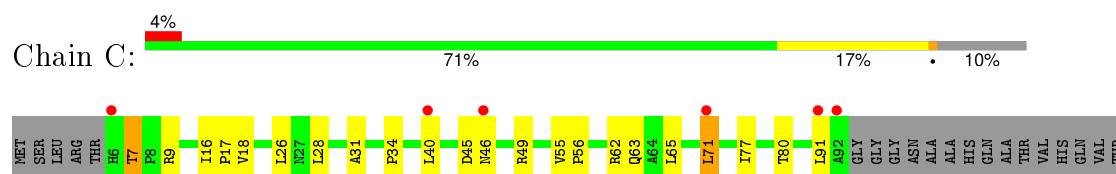
- Molecule 1: Mandelate racemase/muconate lactonizing protein

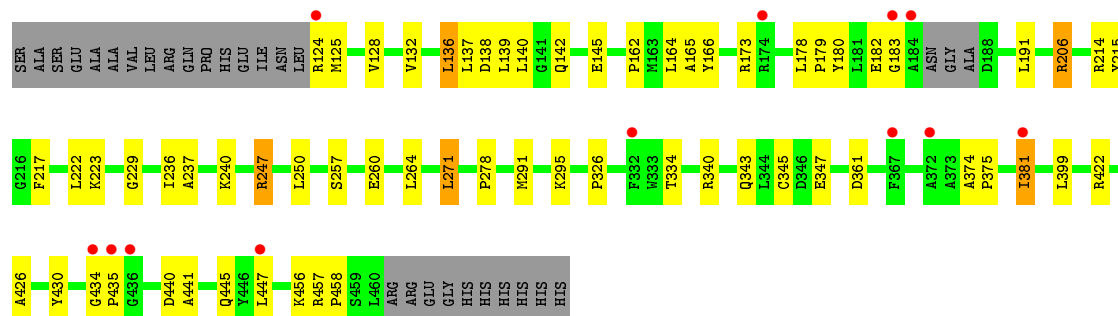


- Molecule 1: Mandelate racemase/muconate lactonizing protein

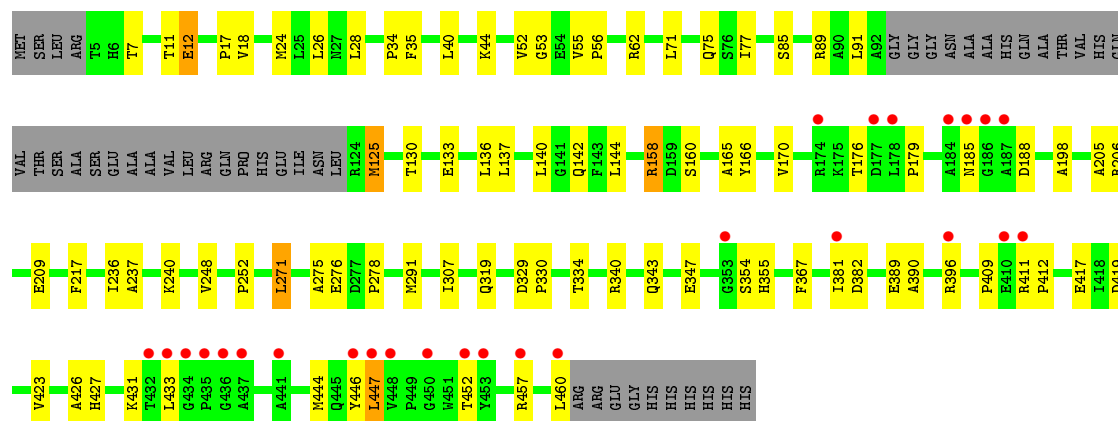


- Molecule 1: Mandelate racemase/muconate lactonizing protein





- Molecule 1: Mandelate racemase/muconate lactonizing protein



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	79.96Å 128.82Å 178.10Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	39.01 – 1.71 39.01 – 1.71	Depositor EDS
% Data completeness (in resolution range)	76.7 (39.01-1.71) 76.8 (39.01-1.71)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	0.83 (at 1.71Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.5_2)	Depositor
R, $R_{free}$	0.227 , 0.265 0.224 , 0.262	Depositor DCC
$R_{free}$ test set	7649 reflections (5.28%)	DCC
Wilson B-factor (Å <sup>2</sup> )	34.7	Xtriage
Anisotropy	0.320	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 35.6	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.30$	Xtriage
Outliers	21 of 152430 reflections (0.014%)	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	13261	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	41.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.67% 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](#)

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

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	0.40	0/3312	0.58	0/4504
1	B	0.42	0/3345	0.60	0/4549
1	C	0.39	0/3294	0.55	0/4478
1	D	0.40	0/3319	0.55	0/4514
All	All	0.41	0/13270	0.57	0/18045

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	3237	0	3196	35	1
1	B	3270	0	3230	49	0
1	C	3220	0	3181	53	0
1	D	3244	0	3203	63	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	14	0	8	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	14	0	8	3	0
3	C	14	0	8	0	0
3	D	14	0	8	0	0
4	A	51	0	0	3	0
4	B	99	0	0	2	0
4	C	42	0	0	5	0
4	D	38	0	0	1	1
All	All	13261	0	12842	192	1

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 7.

All (192) 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:C:206:ARG:HH11	1:C:206:ARG:HG3	1.07	1.10
1:B:206:ARG:HH11	1:B:206:ARG:HG3	1.02	1.08
1:C:9:ARG:H	1:C:46:ASN:HB2	1.31	0.94
1:D:158:ARG:HH11	1:D:158:ARG:HG2	1.33	0.91
1:B:206:ARG:HG3	1:B:206:ARG:NH1	1.83	0.88
1:C:206:ARG:HG3	1:C:206:ARG:NH1	1.87	0.87
1:A:343:GLN:O	1:A:347:GLU:HG2	1.76	0.85
1:C:236:ILE:HG22	1:C:271:LEU:HD12	1.62	0.82
1:B:91:LEU:HD13	1:B:125:MET:HB2	1.61	0.81
1:C:16:ILE:HB	1:C:40:LEU:HD11	1.66	0.78
1:B:206:ARG:CG	1:B:206:ARG:HH11	1.93	0.77
1:B:355:HIS:CD2	3:B:472:GKR:H51	2.21	0.76
1:D:158:ARG:HH11	1:D:158:ARG:CG	2.00	0.75
1:B:16:ILE:HB	1:B:40:LEU:CD1	2.17	0.74
1:A:166:TYR:CZ	1:A:221:LYS:HE2	2.23	0.73
1:A:166:TYR:CE1	1:A:221:LYS:HE2	2.24	0.72
1:D:319:GLN:NE2	4:D:503:HOH:O	2.23	0.71
1:C:206:ARG:HH11	1:C:206:ARG:CG	1.96	0.70
1:B:16:ILE:HB	1:B:40:LEU:HD11	1.72	0.70
1:D:55:VAL:HB	1:D:56:PRO:HD2	1.73	0.69
1:B:124:ARG:HH11	1:B:124:ARG:HG2	1.56	0.69
1:B:275:ALA:HB1	1:B:278:PRO:HG3	1.75	0.68
1:B:158:ARG:NH1	1:B:374:ALA:O	2.25	0.68
1:D:206:ARG:HH11	1:D:206:ARG:HG3	1.57	0.68
1:D:343:GLN:O	1:D:347:GLU:HG2	1.94	0.66
1:D:165:ALA:HB2	1:D:217:PHE:CD2	2.31	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:16:ILE:HB	1:C:40:LEU:CD1	2.27	0.65
1:D:409:PRO:HB3	1:D:411:ARG:NH2	2.13	0.64
1:C:340:ARG:HG3	1:D:340:ARG:HD2	1.79	0.63
1:D:133:GLU:O	1:D:137:LEU:HD23	1.99	0.63
1:D:91:LEU:HD12	1:D:125:MET:HE1	1.81	0.61
1:B:124:ARG:NH1	1:B:124:ARG:HG2	2.13	0.60
1:C:278:PRO:HD2	1:C:291:MET:SD	2.42	0.60
1:A:21:ARG:HD2	4:A:520:HOH:O	2.02	0.60
1:A:132:VAL:HG12	1:A:136:LEU:HD22	1.84	0.60
1:D:133:GLU:HG2	1:D:137:LEU:HD23	1.84	0.59
1:B:355:HIS:NE2	3:B:472:GKR:H51	2.16	0.59
1:D:206:ARG:NH1	1:D:206:ARG:HG3	2.18	0.58
1:B:164:LEU:HD12	1:B:164:LEU:C	2.24	0.58
1:A:91:LEU:HB2	1:A:125:MET:HE2	1.85	0.57
1:D:236:ILE:HG22	1:D:271:LEU:CD1	2.35	0.57
1:D:278:PRO:HD2	1:D:291:MET:SD	2.44	0.57
1:C:17:PRO:HB2	1:C:430:TYR:CD2	2.40	0.57
1:B:132:VAL:HG12	1:B:136:LEU:HD22	1.87	0.57
1:C:457:ARG:HG2	1:C:458:PRO:O	2.05	0.56
1:A:150:GLU:HG3	1:B:79:ARG:NH1	2.20	0.56
1:D:158:ARG:NH1	1:D:158:ARG:CG	2.66	0.56
1:C:326:PRO:HG2	1:C:345:CYS:SG	2.46	0.56
1:B:448:VAL:O	1:B:451:TRP:HB2	2.06	0.56
1:D:236:ILE:HG22	1:D:271:LEU:HD12	1.87	0.55
1:B:367:PHE:HZ	4:B:557:HOH:O	1.90	0.55
1:A:163:MET:HE2	1:A:381:ILE:HD11	1.88	0.55
1:C:173:ARG:HH22	1:C:182:GLU:CD	2.09	0.55
1:D:24:MET:HE1	1:D:447:LEU:HD11	1.89	0.55
1:C:237:ALA:HA	1:C:271:LEU:HD11	1.90	0.54
1:A:270:HIS:CD2	1:A:271:LEU:HD13	2.42	0.54
1:B:16:ILE:HB	1:B:40:LEU:HD12	1.88	0.54
1:A:144:LEU:HA	1:B:7:THR:HG21	1.90	0.54
1:A:223:LYS:HE3	1:A:253:ASN:OD1	2.08	0.54
1:B:295:LYS:HZ2	1:B:324:ASP:CG	2.11	0.53
1:A:40:LEU:HD12	1:A:40:LEU:C	2.29	0.53
1:C:229:GLY:HA3	1:C:264:LEU:HD11	1.91	0.53
1:A:223:LYS:HD2	4:A:513:HOH:O	2.08	0.53
1:D:176:THR:HG22	1:D:446:TYR:CB	2.39	0.53
1:D:427:HIS:O	1:D:431:LYS:HG2	2.09	0.53
1:D:12:GLU:HG3	1:D:44:LYS:HB2	1.91	0.53
1:D:55:VAL:HB	1:D:56:PRO:CD	2.38	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:130:THR:OG1	1:D:334:THR:HA	2.09	0.52
1:C:178:LEU:HD12	1:C:180:TYR:HE1	1.74	0.52
1:C:257:SER:OG	1:C:260:GLU:HG3	2.09	0.52
1:B:223:LYS:HA	1:B:223:LYS:HE3	1.90	0.52
1:C:91:LEU:HD11	1:C:128:VAL:HG11	1.90	0.52
1:C:49:ARG:HD2	4:C:501:HOH:O	2.09	0.51
1:A:330:PRO:HD2	1:A:367:PHE:HE1	1.75	0.51
1:A:55:VAL:HB	1:A:56:PRO:HD2	1.92	0.51
1:C:138:ASP:O	1:C:142:GLN:HG3	2.10	0.51
1:C:240:LYS:HG3	1:C:271:LEU:HD13	1.93	0.51
1:D:236:ILE:HD12	1:D:248:VAL:HG12	1.92	0.51
1:C:456:LYS:HD3	4:C:506:HOH:O	2.11	0.51
1:B:133:GLU:OE2	1:B:336:GLN:HG2	2.10	0.51
1:B:87:ILE:O	1:B:91:LEU:HG	2.11	0.50
1:B:361:ASP:OD1	1:B:361:ASP:N	2.44	0.50
1:C:162:PRO:O	1:C:381:ILE:HG23	2.11	0.50
1:A:7:THR:HG21	1:B:144:LEU:HA	1.93	0.50
1:D:444:MET:CE	1:D:460:LEU:HD21	2.42	0.50
1:B:124:ARG:HH11	1:B:124:ARG:CG	2.23	0.49
1:D:11:THR:C	1:D:12:GLU:HG2	2.32	0.49
1:D:133:GLU:O	1:D:137:LEU:CD2	2.60	0.48
1:D:17:PRO:HG3	1:D:62:ARG:HD3	1.95	0.48
1:A:198:ALA:HB1	1:A:203:ALA:HB1	1.95	0.48
1:C:206:ARG:HD2	4:C:510:HOH:O	2.13	0.48
1:D:355:HIS:HA	1:D:382:ASP:HB2	1.96	0.48
1:C:222:LEU:O	1:C:250:LEU:HD12	2.13	0.48
1:D:176:THR:HG22	1:D:446:TYR:HB3	1.96	0.48
1:D:396:ARG:HD3	1:D:417:GLU:OE2	2.14	0.48
1:C:45:ASP:HB3	1:C:139:LEU:HD13	1.95	0.48
1:D:419:ASP:O	1:D:423:VAL:HG23	2.13	0.48
1:D:35:PHE:CB	1:D:433:LEU:HD11	2.42	0.48
1:D:35:PHE:CD2	1:D:433:LEU:HD21	2.49	0.48
1:B:329:ASP:HB3	1:B:332:PHE:CE1	2.49	0.48
1:A:176:THR:HA	1:A:446:TYR:CD1	2.49	0.48
1:A:304:THR:HG21	1:A:307:ILE:HG12	1.97	0.47
1:D:24:MET:HE1	1:D:447:LEU:CD1	2.45	0.47
1:C:223:LYS:HD2	4:C:507:HOH:O	2.14	0.47
1:A:178:LEU:HA	1:A:179:PRO:HD3	1.74	0.47
1:C:361:ASP:N	1:C:361:ASP:OD1	2.36	0.47
1:C:55:VAL:HB	1:C:56:PRO:HD2	1.97	0.47
1:D:176:THR:HG22	1:D:446:TYR:CG	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:291:MET:HG3	1:D:307:ILE:HD13	1.97	0.46
1:A:40:LEU:HD13	1:A:42:ILE:HG13	1.96	0.46
1:B:80:THR:HG23	1:B:136:LEU:HD23	1.96	0.46
1:D:330:PRO:HD2	1:D:367:PHE:HE1	1.79	0.46
1:B:49:ARG:HD2	4:B:559:HOH:O	2.14	0.46
1:D:34:PRO:HG2	1:D:179:PRO:HD2	1.96	0.46
1:A:330:PRO:HG3	1:A:370:VAL:HG11	1.96	0.46
1:C:247:ARG:NH1	4:C:499:HOH:O	2.48	0.46
1:B:278:PRO:HD2	1:B:291:MET:SD	2.56	0.46
1:D:133:GLU:HG2	1:D:137:LEU:CD2	2.45	0.46
1:A:88:ARG:CZ	4:A:519:HOH:O	2.64	0.45
1:D:18:VAL:HB	1:D:426:ALA:HB1	1.98	0.45
1:C:62:ARG:NH2	1:C:63:GLN:HG2	2.32	0.45
1:A:124:ARG:HD3	1:A:124:ARG:HA	1.83	0.45
1:D:205:ALA:O	1:D:209:GLU:HG3	2.15	0.45
1:C:18:VAL:HB	1:C:426:ALA:HB1	1.99	0.45
1:C:65:LEU:HD23	1:C:128:VAL:HG13	1.98	0.45
1:B:434:GLY:HA3	1:B:435:PRO:HD3	1.66	0.45
1:D:275:ALA:HB1	1:D:278:PRO:HG3	1.99	0.45
1:A:150:GLU:HG3	1:B:79:ARG:HH11	1.80	0.45
1:C:215:TYR:HB2	1:C:217:PHE:CE2	2.51	0.45
1:D:237:ALA:HA	1:D:271:LEU:HD11	1.98	0.45
1:D:158:ARG:HD3	1:D:160:SER:O	2.17	0.45
1:D:165:ALA:HB2	1:D:217:PHE:CG	2.51	0.45
1:C:34:PRO:HG2	1:C:179:PRO:HD2	1.99	0.45
1:A:361:ASP:N	1:A:361:ASP:OD1	2.40	0.45
1:C:132:VAL:HG12	1:C:136:LEU:HD22	1.99	0.44
1:B:419:ASP:O	1:B:423:VAL:HG23	2.17	0.44
1:B:355:HIS:HE2	3:B:472:GKR:H51	1.79	0.44
1:A:59:GLU:HG3	1:A:63:GLN:NE2	2.32	0.44
1:A:158:ARG:NH2	1:A:376:GLY:O	2.50	0.44
1:A:396:ARG:HD3	1:A:417:GLU:OE1	2.17	0.44
1:D:170:VAL:H	1:D:198:ALA:HB3	1.83	0.44
1:B:67:ARG:O	1:B:70:PRO:HD2	2.17	0.43
1:B:130:THR:OG1	1:B:334:THR:HA	2.17	0.43
1:D:71:LEU:O	1:D:75:GLN:HG3	2.18	0.43
1:D:252:PRO:HG2	1:D:278:PRO:HA	2.01	0.43
1:D:142:GLN:HA	1:D:412:PRO:HB2	1.99	0.43
1:C:178:LEU:HD12	1:C:180:TYR:CE1	2.53	0.43
1:B:55:VAL:HB	1:B:56:PRO:HD2	2.00	0.43
1:C:295:LYS:HB3	1:C:295:LYS:HE2	1.52	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:182:GLU:HG3	1:C:183:GLY:N	2.33	0.43
1:B:295:LYS:HE2	1:B:295:LYS:HB3	1.76	0.43
1:A:444:MET:HE1	1:A:460:LEU:HD21	2.00	0.43
1:C:145:GLU:OE1	1:D:7:THR:HG23	2.19	0.43
1:D:330:PRO:HD2	1:D:367:PHE:CE1	2.53	0.43
1:A:158:ARG:HG2	1:A:372:ALA:HA	2.00	0.43
1:A:393:ARG:HG3	1:A:398:PRO:HG3	2.01	0.43
1:D:444:MET:HE1	1:D:460:LEU:HD21	2.00	0.42
1:A:165:ALA:HB2	1:A:217:PHE:CD2	2.54	0.42
1:C:441:ALA:O	1:C:445:GLN:HG2	2.19	0.42
1:B:374:ALA:HA	1:B:375:PRO:HD3	1.68	0.42
1:D:411:ARG:HA	1:D:412:PRO:HD3	1.86	0.42
1:B:165:ALA:HB2	1:B:217:PHE:CD2	2.54	0.42
1:C:434:GLY:HA3	1:C:435:PRO:HD3	1.71	0.42
1:D:354:SER:HB3	1:D:381:ILE:HB	2.00	0.42
1:D:52:VAL:HG12	1:D:53:GLY:N	2.34	0.42
1:C:165:ALA:HB2	1:C:217:PHE:CD2	2.55	0.42
1:B:55:VAL:HG11	1:B:127:ASN:O	2.20	0.42
1:C:71:LEU:O	1:C:71:LEU:HD23	2.20	0.42
1:C:80:THR:HG23	1:C:136:LEU:HD23	2.01	0.42
1:B:304:THR:HG21	1:B:307:ILE:HG13	2.01	0.41
1:A:182:GLU:HG3	1:A:183:GLY:N	2.35	0.41
1:D:329:ASP:HB2	1:D:355:HIS:CE1	2.55	0.41
1:C:31:ALA:N	1:C:440:ASP:HB3	2.35	0.41
1:D:35:PHE:HB2	1:D:433:LEU:HD11	2.01	0.41
1:B:314:MET:HE2	1:B:314:MET:HB2	1.88	0.41
1:C:343:GLN:O	1:C:347:GLU:HG2	2.21	0.41
1:C:191:LEU:HD11	1:C:214:ARG:CZ	2.51	0.41
1:D:252:PRO:HD2	1:D:276:GLU:O	2.21	0.41
1:C:422:ARG:HB3	1:C:422:ARG:HE	1.56	0.41
1:D:85:SER:O	1:D:89:ARG:HG3	2.21	0.41
1:D:389:GLU:O	1:D:390:ALA:HB3	2.19	0.41
1:C:236:ILE:CG2	1:C:271:LEU:HD12	2.44	0.41
1:A:347:GLU:HB3	1:B:311:TRP:HB3	2.02	0.40
1:D:188:ASP:C	1:D:188:ASP:OD1	2.60	0.40
1:B:140:LEU:HD13	1:B:151:LEU:HD13	2.03	0.40
1:B:454:ASP:HA	1:B:455:PRO:HD3	1.83	0.40
1:B:21:ARG:HD3	1:B:181:LEU:HD11	2.03	0.40
1:B:240:LYS:HE2	1:B:270:HIS:O	2.21	0.40
1:C:374:ALA:HA	1:C:375:PRO:HD3	1.88	0.40
1:B:158:ARG:HD3	1:B:160:SER:O	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:191:LEU:HD23	1:C:191:LEU:HA	1.87	0.40
1:C:7:THR:HG21	1:D:144:LEU:HA	2.04	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:319:GLN:NE2	4:D:503:HOH:O[2_564]	2.18	0.02

## 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	420/470 (89%)	410 (98%)	10 (2%)	0	100	100
1	B	424/470 (90%)	413 (97%)	11 (3%)	0	100	100
1	C	415/470 (88%)	404 (97%)	10 (2%)	1 (0%)	52	32
1	D	421/470 (90%)	407 (97%)	14 (3%)	0	100	100
All	All	1680/1880 (89%)	1634 (97%)	45 (3%)	1 (0%)	56	36

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	334	THR

### 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	325/361 (90%)	313 (96%)	12 (4%)	41	17
1	B	329/361 (91%)	314 (95%)	15 (5%)	33	12
1	C	324/361 (90%)	306 (94%)	18 (6%)	26	8
1	D	326/361 (90%)	310 (95%)	16 (5%)	31	10
All	All	1304/1444 (90%)	1243 (95%)	61 (5%)	32	11

All (61) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	26	LEU
1	A	28	LEU
1	A	124	ARG
1	A	136	LEU
1	A	137	LEU
1	A	140	LEU
1	A	158	ARG
1	A	166	TYR
1	A	223	LYS
1	A	271	LEU
1	A	361	ASP
1	A	447	LEU
1	B	6	HIS
1	B	28	LEU
1	B	40	LEU
1	B	124	ARG
1	B	125	MET
1	B	136	LEU
1	B	137	LEU
1	B	140	LEU
1	B	166	TYR
1	B	206	ARG
1	B	271	LEU
1	B	355	HIS
1	B	399	LEU
1	B	447	LEU
1	B	452	THR
1	C	7	THR
1	C	26	LEU
1	C	28	LEU

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Mol	Chain	Res	Type
1	C	71	LEU
1	C	77	ILE
1	C	124	ARG
1	C	125	MET
1	C	136	LEU
1	C	137	LEU
1	C	140	LEU
1	C	164	LEU
1	C	166	TYR
1	C	206	ARG
1	C	247	ARG
1	C	271	LEU
1	C	381	ILE
1	C	399	LEU
1	C	447	LEU
1	D	12	GLU
1	D	26	LEU
1	D	28	LEU
1	D	40	LEU
1	D	77	ILE
1	D	125	MET
1	D	136	LEU
1	D	140	LEU
1	D	158	ARG
1	D	166	TYR
1	D	185	ASN
1	D	240	LYS
1	D	271	LEU
1	D	447	LEU
1	D	452	THR
1	D	457	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 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 [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

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	GKR	A	472	2	5,13,13	2.41	2 (40%)	6,18,18	1.09	0
3	GKR	B	472	2	5,13,13	2.53	1 (20%)	6,18,18	1.65	1 (16%)
3	GKR	C	472	2	5,13,13	2.50	2 (40%)	6,18,18	0.95	0
3	GKR	D	472	2	5,13,13	2.48	2 (40%)	6,18,18	1.36	1 (16%)

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	GKR	A	472	2	-	0/12/20/20	0/0/0/0
3	GKR	B	472	2	-	0/12/20/20	0/0/0/0
3	GKR	C	472	2	-	0/12/20/20	0/0/0/0
3	GKR	D	472	2	-	0/12/20/20	0/0/0/0

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	472	GKR	C4-C3	2.07	1.57	1.53
3	A	472	GKR	C4-C3	2.18	1.57	1.53
3	D	472	GKR	C4-C3	2.26	1.57	1.53
3	D	472	GKR	O2-C2	4.65	1.52	1.42
3	A	472	GKR	O2-C2	4.74	1.52	1.42
3	C	472	GKR	O2-C2	4.92	1.52	1.42
3	B	472	GKR	O2-C2	5.18	1.53	1.42

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	472	GKR	O4-C4-C3	2.07	114.41	109.45
3	B	472	GKR	O4-C4-C3	3.15	117.00	109.45

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	472	GKR	3	0

## 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, 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	424/470 (90%)	0.10	11 (2%) 59 64	31, 39, 51, 68	0
1	B	428/470 (91%)	0.27	32 (7%) 17 19	28, 37, 50, 69	0
1	C	421/470 (89%)	0.27	18 (4%) 39 43	30, 41, 55, 73	0
1	D	425/470 (90%)	0.33	27 (6%) 23 25	31, 41, 58, 70	0
All	All	1698/1880 (90%)	0.24	88 (5%) 31 33	28, 39, 55, 73	0

All (88) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	92	ALA	6.6
1	B	434	GLY	6.4
1	D	435	PRO	6.3
1	D	434	GLY	5.2
1	C	435	PRO	5.2
1	C	434	GLY	4.9
1	D	186	GLY	4.9
1	D	433	LEU	4.7
1	B	435	PRO	4.4
1	D	436	GLY	4.3
1	D	185	ASN	4.0
1	D	411	ARG	4.0
1	B	92	ALA	3.7
1	C	447	LEU	3.6
1	D	184	ALA	3.6
1	C	184	ALA	3.5
1	B	367	PHE	3.5
1	C	436	GLY	3.4
1	B	366	MET	3.4
1	B	148	VAL	3.4
1	D	410	GLU	3.2

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Mol	Chain	Res	Type	RSRZ
1	C	6	HIS	3.2
1	D	381	ILE	3.2
1	B	91	LEU	3.1
1	B	370	VAL	3.1
1	D	187	ALA	3.0
1	D	446	TYR	3.0
1	B	332	PHE	3.0
1	C	367	PHE	3.0
1	C	91	LEU	3.0
1	B	334	THR	2.9
1	B	341	VAL	2.9
1	B	337	GLY	2.9
1	D	447	LEU	2.8
1	A	435	PRO	2.8
1	B	335	MET	2.8
1	B	381	ILE	2.8
1	C	332	PHE	2.7
1	B	363	SER	2.7
1	D	452	THR	2.7
1	A	339	VAL	2.7
1	D	457	ARG	2.7
1	B	356	SER	2.6
1	C	174	ARG	2.6
1	B	333	TRP	2.6
1	A	450	GLY	2.5
1	B	328	ALA	2.5
1	B	339	VAL	2.5
1	A	186	GLY	2.5
1	B	71	LEU	2.4
1	B	120	GLU	2.4
1	D	178	LEU	2.4
1	D	353	GLY	2.4
1	D	177	ASP	2.4
1	B	353	GLY	2.4
1	C	124	ARG	2.3
1	A	449	PRO	2.3
1	B	330	PRO	2.3
1	D	432	THR	2.3
1	A	185	ASN	2.3
1	B	151	LEU	2.2
1	B	327	LEU	2.2
1	A	434	GLY	2.2

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Mol	Chain	Res	Type	RSRZ
1	C	183	GLY	2.2
1	D	450	GLY	2.2
1	A	410	GLU	2.2
1	B	185	ASN	2.2
1	D	453	TYR	2.2
1	D	396	ARG	2.2
1	C	372	ALA	2.2
1	A	341	VAL	2.2
1	B	36	PHE	2.1
1	B	89	ARG	2.1
1	D	437	ALA	2.1
1	C	381	ILE	2.1
1	B	153	GLY	2.1
1	C	46	ASN	2.1
1	B	73	VAL	2.1
1	C	71	LEU	2.1
1	D	460	LEU	2.1
1	A	446	TYR	2.0
1	A	436	GLY	2.0
1	C	40	LEU	2.0
1	B	362	VAL	2.0
1	D	448	VAL	2.0
1	D	441	ALA	2.0
1	D	174	ARG	2.0
1	B	329	ASP	2.0

## 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 ⓘ

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, 95<sup>th</sup> 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( $\text{\AA}^2$ )	Q<0.9
3	GKR	D	472	14/14	0.80	0.14	1.51	43,50,53,60	0
2	MG	B	471	1/1	0.94	0.15	1.12	38,38,38,38	0
2	MG	A	471	1/1	0.93	0.12	0.97	40,40,40,40	0
3	GKR	A	472	14/14	0.85	0.12	0.86	41,46,50,50	0
3	GKR	C	472	14/14	0.81	0.14	0.81	43,47,52,52	0
3	GKR	B	472	14/14	0.88	0.11	-0.06	35,41,42,44	0
2	MG	D	471	1/1	0.90	0.09	-0.46	45,45,45,45	0
2	MG	C	471	1/1	0.94	0.06	-1.61	43,43,43,43	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.