



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 04:51 PM GMT

PDB ID : 4GE9  
Title : Kynurenine Aminotransferase II Inhibitors  
Authors : Pandit, J.  
Deposited on : 2012-08-01  
Resolution : 2.43 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

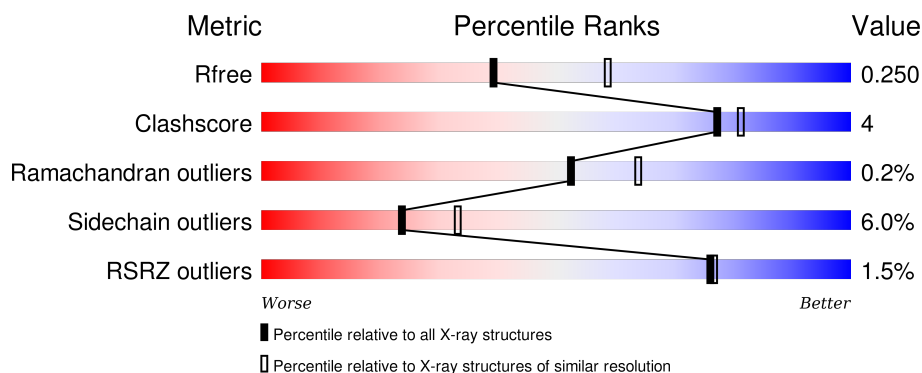
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.43 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	1003 (2.46-2.42)
Clashscore	102246	1071 (2.46-2.42)
Ramachandran outliers	100387	1065 (2.46-2.42)
Sidechain outliers	100360	1065 (2.46-2.42)
RSRZ outliers	91569	1005 (2.46-2.42)

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	439	<div> <div></div> <div>83%13% ..</div> </div>
1	B	439	<div> <div>%</div> <div>85%11% ..</div> </div>
1	C	439	<div> <div>3%</div> <div>86%10% ..</div> </div>
1	D	439	<div> <div>%</div> <div>84%12% ..</div> </div>

## 2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 14269 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 Kynurenine/alpha-aminoadipate aminotransferase, mitochondrial.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	428	Total	C	N	O	S	0	0	0
			3344	2145	561	620	18			
1	B	428	Total	C	N	O	S	0	0	0
			3344	2145	561	620	18			
1	C	428	Total	C	N	O	S	0	0	0
			3344	2145	561	620	18			
1	D	428	Total	C	N	O	S	0	0	0
			3344	2145	561	620	18			

There are 64 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	240	SER	LYS	ENGINEERED MUTATION	UNP Q8N5Z0
A	241	GLY	PHE	ENGINEERED MUTATION	UNP Q8N5Z0
A	426	LEU	-	EXPRESSION TAG	UNP Q8N5Z0
A	427	VAL	-	EXPRESSION TAG	UNP Q8N5Z0
A	428	PRO	-	EXPRESSION TAG	UNP Q8N5Z0
A	429	ARG	-	EXPRESSION TAG	UNP Q8N5Z0
A	430	GLY	-	EXPRESSION TAG	UNP Q8N5Z0
A	431	SER	-	EXPRESSION TAG	UNP Q8N5Z0
A	432	LEU	-	EXPRESSION TAG	UNP Q8N5Z0
A	433	GLU	-	EXPRESSION TAG	UNP Q8N5Z0
A	434	HIS	-	EXPRESSION TAG	UNP Q8N5Z0
A	435	HIS	-	EXPRESSION TAG	UNP Q8N5Z0
A	436	HIS	-	EXPRESSION TAG	UNP Q8N5Z0
A	437	HIS	-	EXPRESSION TAG	UNP Q8N5Z0
A	438	HIS	-	EXPRESSION TAG	UNP Q8N5Z0
A	439	HIS	-	EXPRESSION TAG	UNP Q8N5Z0
B	240	SER	LYS	ENGINEERED MUTATION	UNP Q8N5Z0
B	241	GLY	PHE	ENGINEERED MUTATION	UNP Q8N5Z0
B	426	LEU	-	EXPRESSION TAG	UNP Q8N5Z0
B	427	VAL	-	EXPRESSION TAG	UNP Q8N5Z0

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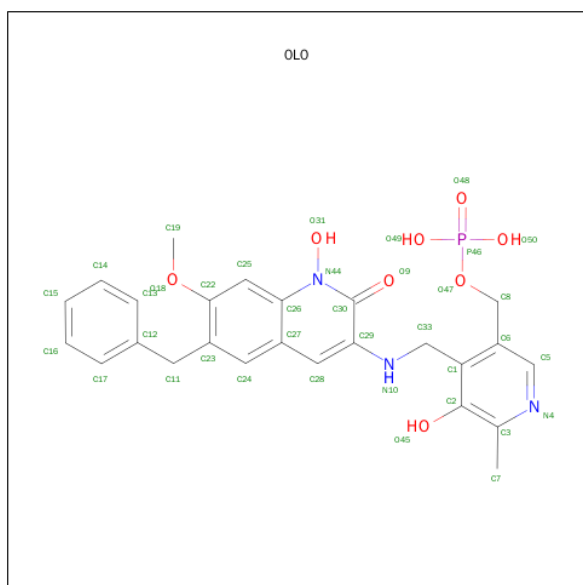
Chain	Residue	Modelled	Actual	Comment	Reference
B	428	PRO	-	EXPRESSION TAG	UNP Q8N5Z0
B	429	ARG	-	EXPRESSION TAG	UNP Q8N5Z0
B	430	GLY	-	EXPRESSION TAG	UNP Q8N5Z0
B	431	SER	-	EXPRESSION TAG	UNP Q8N5Z0
B	432	LEU	-	EXPRESSION TAG	UNP Q8N5Z0
B	433	GLU	-	EXPRESSION TAG	UNP Q8N5Z0
B	434	HIS	-	EXPRESSION TAG	UNP Q8N5Z0
B	435	HIS	-	EXPRESSION TAG	UNP Q8N5Z0
B	436	HIS	-	EXPRESSION TAG	UNP Q8N5Z0
B	437	HIS	-	EXPRESSION TAG	UNP Q8N5Z0
B	438	HIS	-	EXPRESSION TAG	UNP Q8N5Z0
B	439	HIS	-	EXPRESSION TAG	UNP Q8N5Z0
C	240	SER	LYS	ENGINEERED MUTATION	UNP Q8N5Z0
C	241	GLY	PHE	ENGINEERED MUTATION	UNP Q8N5Z0
C	426	LEU	-	EXPRESSION TAG	UNP Q8N5Z0
C	427	VAL	-	EXPRESSION TAG	UNP Q8N5Z0
C	428	PRO	-	EXPRESSION TAG	UNP Q8N5Z0
C	429	ARG	-	EXPRESSION TAG	UNP Q8N5Z0
C	430	GLY	-	EXPRESSION TAG	UNP Q8N5Z0
C	431	SER	-	EXPRESSION TAG	UNP Q8N5Z0
C	432	LEU	-	EXPRESSION TAG	UNP Q8N5Z0
C	433	GLU	-	EXPRESSION TAG	UNP Q8N5Z0
C	434	HIS	-	EXPRESSION TAG	UNP Q8N5Z0
C	435	HIS	-	EXPRESSION TAG	UNP Q8N5Z0
C	436	HIS	-	EXPRESSION TAG	UNP Q8N5Z0
C	437	HIS	-	EXPRESSION TAG	UNP Q8N5Z0
C	438	HIS	-	EXPRESSION TAG	UNP Q8N5Z0
C	439	HIS	-	EXPRESSION TAG	UNP Q8N5Z0
D	240	SER	LYS	ENGINEERED MUTATION	UNP Q8N5Z0
D	241	GLY	PHE	ENGINEERED MUTATION	UNP Q8N5Z0
D	426	LEU	-	EXPRESSION TAG	UNP Q8N5Z0
D	427	VAL	-	EXPRESSION TAG	UNP Q8N5Z0
D	428	PRO	-	EXPRESSION TAG	UNP Q8N5Z0
D	429	ARG	-	EXPRESSION TAG	UNP Q8N5Z0
D	430	GLY	-	EXPRESSION TAG	UNP Q8N5Z0
D	431	SER	-	EXPRESSION TAG	UNP Q8N5Z0
D	432	LEU	-	EXPRESSION TAG	UNP Q8N5Z0
D	433	GLU	-	EXPRESSION TAG	UNP Q8N5Z0
D	434	HIS	-	EXPRESSION TAG	UNP Q8N5Z0
D	435	HIS	-	EXPRESSION TAG	UNP Q8N5Z0
D	436	HIS	-	EXPRESSION TAG	UNP Q8N5Z0
D	437	HIS	-	EXPRESSION TAG	UNP Q8N5Z0

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Chain	Residue	Modelled	Actual	Comment	Reference
D	438	HIS	-	EXPRESSION TAG	UNP Q8N5Z0
D	439	HIS	-	EXPRESSION TAG	UNP Q8N5Z0

- Molecule 2 is (4-{[(6-BENZYL-1-HYDROXY-7-METHOXY-2-OXO-1,2-DIHYDROQUINOLIN-3-YL)AMINO]METHYL}-5-HYDROXY-6-METHYLPYRIDIN-3-YL)METHYL DIHYDROGEN PHOSPHATE (three-letter code: 0L0) (formula: C<sub>25</sub>H<sub>26</sub>N<sub>3</sub>O<sub>8</sub>P).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			37	25	3	8	1		
2	B	1	Total	C	N	O	P	0	0
			37	25	3	8	1		
2	C	1	Total	C	N	O	P	0	0
			37	25	3	8	1		
2	D	1	Total	C	N	O	P	0	0
			37	25	3	8	1		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	290	Total	O	0	0
			290	290		
3	B	241	Total	O	0	0
			241	241		
3	C	102	Total	O	0	0
			102	102		

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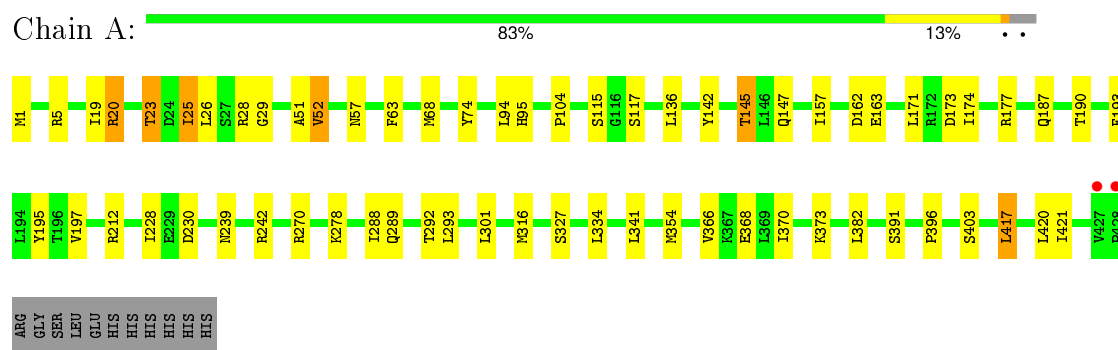
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	D	112	Total	O	0	0
			112	112		

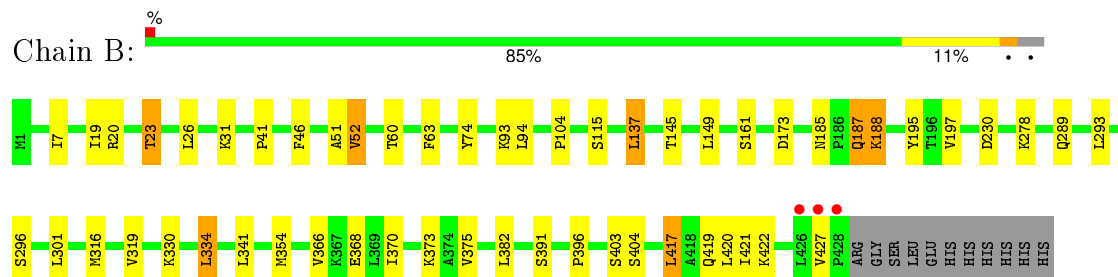
### 3 Residue-property plots

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.

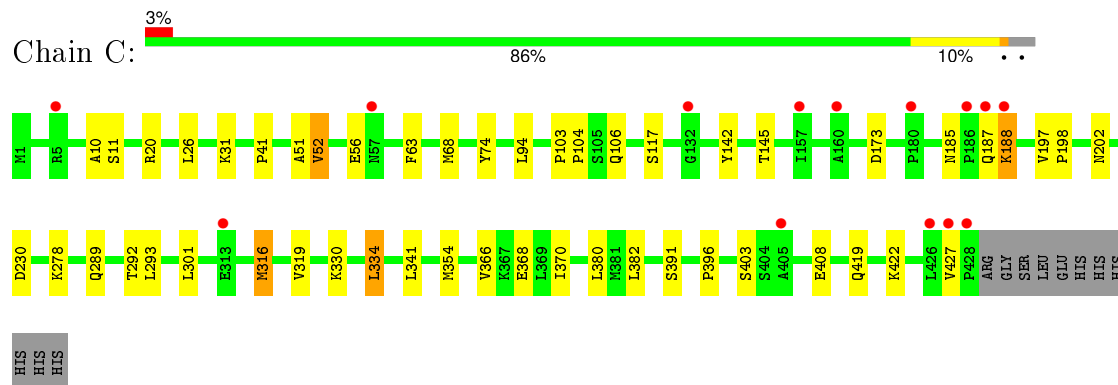
- Molecule 1: Kynurenine/alpha-aminoadipate aminotransferase, mitochondrial



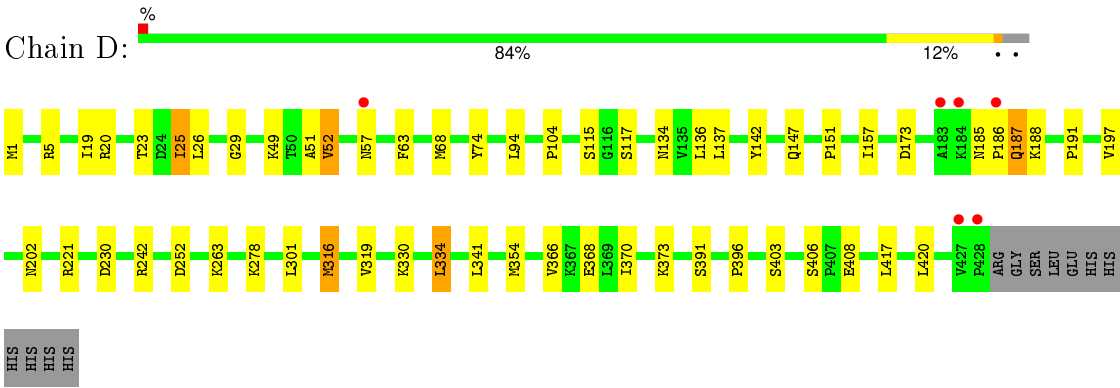
- Molecule 1: Kynurenine/alpha-aminoadipate aminotransferase, mitochondrial



- Molecule 1: Kynurenine/alpha-aminoadipate aminotransferase, mitochondrial



- Molecule 1: Kynurenine/alpha-aminoadipate aminotransferase, mitochondrial





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	69.16Å 107.05Å 116.60Å 90.00° 94.52° 90.00°	Depositor
Resolution (Å)	35.58 – 2.43 35.00 – 2.43	Depositor EDS
% Data completeness (in resolution range)	98.1 (35.58-2.43) 98.1 (35.00-2.43)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.11	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.32 (at 2.42Å)	Xtriage
Refinement program	BUSTER 2.9.3	Depositor
R, $R_{free}$	0.175 , 0.230 0.191 , 0.250	Depositor DCC
$R_{free}$ test set	3193 reflections (5.37%)	DCC
Wilson B-factor (Å <sup>2</sup> )	26.6	Xtriage
Anisotropy	1.032	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.30 , 42.6	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	2 of 62628 reflections (0.003%)	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	14269	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	52.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 44.09 % of the origin peak, indicating pseudo translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 1.6039e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<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: 0L0

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	0.57	0/3426	0.78	0/4653
1	B	0.55	0/3426	0.76	0/4653
1	C	0.44	0/3426	0.69	0/4653
1	D	0.45	0/3426	0.72	0/4653
All	All	0.51	0/13704	0.74	0/18612

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	3344	0	3366	32	0
1	B	3344	0	3366	31	0
1	C	3344	0	3366	25	0
1	D	3344	0	3366	30	0
2	A	37	0	24	2	0
2	B	37	0	24	2	0
2	C	37	0	24	2	0
2	D	37	0	24	1	0
3	A	290	0	0	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	241	0	0	1	0
3	C	102	0	0	0	0
3	D	112	0	0	1	0
All	All	14269	0	13560	100	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 (100) 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:380:LEU:HD21	1:D:25:ILE:HD11	1.76	0.66
1:A:366:VAL:HG12	1:A:370:ILE:HG12	1.78	0.66
1:B:366:VAL:HG12	1:B:370:ILE:HG12	1.77	0.65
1:D:366:VAL:HG12	1:D:370:ILE:HG12	1.78	0.64
1:B:185:ASN:HD22	1:B:188:LYS:HG2	1.63	0.63
1:C:366:VAL:HG12	1:C:370:ILE:HG12	1.81	0.63
2:C:4000:OL0:H10	1:D:23:THR:HG21	1.80	0.63
1:C:185:ASN:HD22	1:C:188:LYS:HG2	1.67	0.59
1:A:19:ILE:HG23	1:B:382:LEU:HD11	1.84	0.59
1:D:221:ARG:HG2	1:D:252:ASP:OD2	2.03	0.59
1:A:23:THR:HG21	2:B:4000:OL0:H10	1.84	0.59
1:A:163:GLU:HG2	3:A:4129:HOH:O	2.02	0.58
2:A:4000:OL0:H10	1:B:23:THR:HG21	1.85	0.58
1:B:41:PRO:HG2	1:B:46:PHE:HZ	1.69	0.58
1:A:25:ILE:CD1	1:B:375:VAL:HG13	2.34	0.58
1:D:185:ASN:HD21	1:D:187:GLN:HG2	1.68	0.58
1:B:145:THR:HG21	1:B:195:TYR:CZ	2.40	0.57
1:B:417:LEU:O	1:B:421:ILE:HG13	2.06	0.56
2:C:4000:OL0:H16	1:D:74:TYR:CG	2.40	0.56
1:C:52:VAL:HG13	1:D:52:VAL:HG13	1.86	0.56
1:D:185:ASN:ND2	1:D:187:GLN:HG2	2.20	0.56
1:B:187:GLN:NE2	1:D:57:ASN:HB3	2.20	0.56
1:A:142:TYR:HD1	1:A:145:THR:HG23	1.71	0.55
1:A:95:HIS:HE1	3:A:4107:HOH:O	1.88	0.55
1:B:145:THR:O	1:B:149:LEU:HG	2.08	0.54
1:B:373:LYS:HB3	1:B:420:LEU:HD22	1.91	0.53
1:A:382:LEU:HD13	1:B:19:ILE:HD12	1.91	0.53
1:B:316:MET:HA	1:B:319:VAL:HG22	1.91	0.52
1:A:373:LYS:HB3	1:A:420:LEU:HD22	1.92	0.51
1:A:74:TYR:CG	2:B:4000:OL0:H16	2.44	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:382:LEU:HD11	1:D:19:ILE:HG23	1.93	0.50
1:A:354:MET:SD	1:A:403:SER:HB3	2.52	0.50
1:B:185:ASN:HD22	1:B:188:LYS:CG	2.25	0.49
1:A:104:PRO:HB3	1:A:278:LYS:HD3	1.94	0.49
1:A:157:ILE:HG21	1:A:174:ILE:HG21	1.95	0.49
1:A:382:LEU:HD11	1:B:19:ILE:HG23	1.95	0.49
1:C:330:LYS:HG2	1:C:334:LEU:HD22	1.95	0.49
1:D:185:ASN:HD22	1:D:188:LYS:HG2	1.77	0.49
1:D:104:PRO:HB3	1:D:278:LYS:HD3	1.93	0.49
1:C:316:MET:HA	1:C:319:VAL:HG22	1.95	0.49
1:C:354:MET:SD	1:C:403:SER:HB3	2.53	0.49
1:B:104:PRO:HB3	1:B:278:LYS:HD3	1.94	0.49
1:C:104:PRO:HB3	1:C:278:LYS:HD3	1.94	0.48
1:C:382:LEU:HD13	1:D:19:ILE:HD12	1.95	0.48
1:D:316:MET:HA	1:D:319:VAL:HG22	1.94	0.48
1:A:136:LEU:HD13	1:A:171:LEU:HD11	1.95	0.48
1:B:354:MET:SD	1:B:403:SER:HB3	2.54	0.48
1:A:292:THR:HG22	1:B:115:SER:HB2	1.95	0.47
1:C:74:TYR:CG	2:D:4000:OL0:H16	2.49	0.47
1:C:419:GLN:HA	1:C:422:LYS:HE3	1.96	0.47
1:A:145:THR:HG21	1:A:195:TYR:CZ	2.50	0.47
1:D:366:VAL:HG23	1:D:396:PRO:HA	1.96	0.47
1:C:142:TYR:CD1	1:C:145:THR:HG23	2.49	0.47
1:B:137:LEU:HD23	1:B:137:LEU:C	2.35	0.46
1:D:406:SER:HB2	3:D:4191:HOH:O	2.15	0.46
1:D:373:LYS:HB3	1:D:420:LEU:HD22	1.96	0.46
1:B:366:VAL:HG23	1:B:396:PRO:HA	1.97	0.46
2:A:4000:OL0:H16	1:B:74:TYR:CG	2.51	0.46
1:A:25:ILE:HD13	1:B:375:VAL:HG13	1.96	0.46
1:B:419:GLN:HA	1:B:422:LYS:HE3	1.98	0.46
1:D:354:MET:SD	1:D:403:SER:HB3	2.56	0.46
1:C:142:TYR:HD1	1:C:145:THR:HG23	1.81	0.45
1:A:162:ASP:OD1	1:A:212:ARG:NH1	2.49	0.45
1:A:20:ARG:NH2	3:A:4194:HOH:O	2.49	0.45
1:A:288:ILE:HG21	3:A:4342:HOH:O	2.17	0.44
1:A:366:VAL:HG23	1:A:396:PRO:HA	1.97	0.44
1:A:142:TYR:CD1	1:A:145:THR:HG23	2.51	0.43
1:A:25:ILE:HD11	1:B:375:VAL:HG13	1.99	0.43
1:C:366:VAL:HG23	1:C:396:PRO:HA	1.99	0.43
1:D:185:ASN:HD22	1:D:188:LYS:CG	2.32	0.43
1:A:417:LEU:O	1:A:421:ILE:HG13	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:52:VAL:HG13	1:B:52:VAL:HG13	2.01	0.43
1:B:289:GLN:O	1:B:293:LEU:HD23	2.19	0.43
1:C:51:ALA:HB3	1:C:63:PHE:HB2	2.01	0.42
1:C:41:PRO:HB3	1:D:263:LYS:HG3	2.01	0.42
1:B:330:LYS:HG2	1:B:334:LEU:HD22	2.01	0.42
1:C:185:ASN:HD22	1:C:188:LYS:CG	2.32	0.42
1:A:19:ILE:HD12	1:B:382:LEU:HD13	2.01	0.42
1:D:51:ALA:HB3	1:D:63:PHE:HB2	2.01	0.42
1:A:197:VAL:HA	1:A:230:ASP:O	2.20	0.42
1:C:197:VAL:HA	1:C:230:ASP:O	2.20	0.42
1:A:115:SER:HA	1:A:270:ARG:O	2.20	0.42
1:D:185:ASN:HA	1:D:186:PRO:HD3	1.96	0.41
1:D:142:TYR:HB2	1:D:202:ASN:HB3	2.03	0.41
1:D:134:ASN:O	1:D:191:PRO:HA	2.20	0.41
1:A:289:GLN:O	1:A:293:LEU:HD23	2.21	0.41
1:C:292:THR:HG22	1:D:115:SER:HB2	2.01	0.41
1:A:193:PHE:CD2	1:A:228:ILE:HD12	2.55	0.41
1:C:56:GLU:CD	1:D:49:LYS:HE3	2.41	0.41
1:C:10:ALA:O	1:D:151:PRO:HB3	2.21	0.41
1:B:197:VAL:HA	1:B:230:ASP:O	2.20	0.41
1:D:330:LYS:HG2	1:D:334:LEU:HD22	2.01	0.41
1:C:142:TYR:HB2	1:C:202:ASN:HB3	2.03	0.41
1:D:136:LEU:HD23	1:D:157:ILE:HB	2.03	0.41
1:B:51:ALA:HB3	1:B:63:PHE:HB2	2.02	0.41
1:D:197:VAL:HA	1:D:230:ASP:O	2.21	0.41
1:C:289:GLN:O	1:C:293:LEU:HD23	2.21	0.40
1:C:103:PRO:HD2	1:C:106:GLN:HB2	2.03	0.40
1:A:51:ALA:HB3	1:A:63:PHE:HB2	2.04	0.40
1:B:296:SER:HB3	3:B:4336:HOH:O	2.22	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	426/439 (97%)	410 (96%)	14 (3%)	2 (0%)	34	41
1	B	426/439 (97%)	415 (97%)	11 (3%)	0	100	100
1	C	426/439 (97%)	414 (97%)	12 (3%)	0	100	100
1	D	426/439 (97%)	408 (96%)	16 (4%)	2 (0%)	34	41
All	All	1704/1756 (97%)	1647 (97%)	53 (3%)	4 (0%)	52	64

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	242	ARG
1	A	242	ARG
1	A	29	GLY
1	D	29	GLY

### 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	372/382 (97%)	345 (93%)	27 (7%)	17	23
1	B	372/382 (97%)	350 (94%)	22 (6%)	24	34
1	C	372/382 (97%)	352 (95%)	20 (5%)	27	39
1	D	372/382 (97%)	351 (94%)	21 (6%)	26	36
All	All	1488/1528 (97%)	1398 (94%)	90 (6%)	24	33

All (90) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	MET
1	A	5	ARG
1	A	20	ARG
1	A	23	THR
1	A	25	ILE
1	A	26	LEU
1	A	28	ARG

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Mol	Chain	Res	Type
1	A	52	VAL
1	A	57	ASN
1	A	68	MET
1	A	94	LEU
1	A	117	SER
1	A	145	THR
1	A	147	GLN
1	A	173	ASP
1	A	177	ARG
1	A	187	GLN
1	A	190	THR
1	A	239	ASN
1	A	301	LEU
1	A	316	MET
1	A	327	SER
1	A	334	LEU
1	A	341	LEU
1	A	368	GLU
1	A	391	SER
1	A	417	LEU
1	B	7	ILE
1	B	20	ARG
1	B	23	THR
1	B	26	LEU
1	B	31	LYS
1	B	52	VAL
1	B	60	THR
1	B	93	LYS
1	B	94	LEU
1	B	137	LEU
1	B	161	SER
1	B	173	ASP
1	B	187	GLN
1	B	188	LYS
1	B	301	LEU
1	B	334	LEU
1	B	341	LEU
1	B	368	GLU
1	B	391	SER
1	B	404	SER
1	B	417	LEU
1	B	427	VAL

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Mol	Chain	Res	Type
1	C	11	SER
1	C	20	ARG
1	C	26	LEU
1	C	31	LYS
1	C	52	VAL
1	C	68	MET
1	C	94	LEU
1	C	117	SER
1	C	173	ASP
1	C	187	GLN
1	C	188	LYS
1	C	198	PRO
1	C	301	LEU
1	C	316	MET
1	C	334	LEU
1	C	341	LEU
1	C	368	GLU
1	C	391	SER
1	C	408	GLU
1	C	427	VAL
1	D	1	MET
1	D	5	ARG
1	D	20	ARG
1	D	25	ILE
1	D	26	LEU
1	D	52	VAL
1	D	68	MET
1	D	94	LEU
1	D	117	SER
1	D	137	LEU
1	D	147	GLN
1	D	173	ASP
1	D	187	GLN
1	D	301	LEU
1	D	316	MET
1	D	334	LEU
1	D	341	LEU
1	D	368	GLU
1	D	391	SER
1	D	408	GLU
1	D	417	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (21) such



sidechains are listed below:

Mol	Chain	Res	Type
1	A	62	GLN
1	A	95	HIS
1	A	147	GLN
1	A	187	GLN
1	A	237	GLN
1	A	305	GLN
1	A	328	ASN
1	B	2	ASN
1	B	62	GLN
1	B	95	HIS
1	B	185	ASN
1	B	187	GLN
1	B	328	ASN
1	C	185	ASN
1	C	187	GLN
1	C	237	GLN
1	D	62	GLN
1	D	95	HIS
1	D	147	GLN
1	D	185	ASN
1	D	187	GLN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

4 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and

the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	OL0	A	4000	-	38,40,40	1.05	3 (7%)	45,58,58	1.27	4 (8%)
2	OL0	B	4000	-	38,40,40	1.05	3 (7%)	45,58,58	1.39	4 (8%)
2	OL0	C	4000	-	38,40,40	0.86	3 (7%)	45,58,58	1.15	2 (4%)
2	OL0	D	4000	-	38,40,40	0.86	2 (5%)	45,58,58	1.26	4 (8%)

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
2	OL0	A	4000	-	-	0/17/17/17	0/4/4/4
2	OL0	B	4000	-	-	0/17/17/17	0/4/4/4
2	OL0	C	4000	-	-	0/17/17/17	0/4/4/4
2	OL0	D	4000	-	-	0/17/17/17	0/4/4/4

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	4000	OL0	C30-N44	-3.30	1.34	1.40
2	A	4000	OL0	C30-N44	-2.93	1.35	1.40
2	D	4000	OL0	C30-N44	-2.79	1.35	1.40
2	C	4000	OL0	C30-N44	-2.65	1.36	1.40
2	C	4000	OL0	C25-C22	2.13	1.40	1.36
2	B	4000	OL0	C25-C22	2.14	1.40	1.36
2	A	4000	OL0	C2-C3	2.15	1.42	1.40
2	C	4000	OL0	C28-C27	2.24	1.47	1.42
2	D	4000	OL0	C28-C27	2.33	1.47	1.42
2	B	4000	OL0	C28-C27	2.37	1.47	1.42
2	A	4000	OL0	C28-C27	2.65	1.48	1.42

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	4000	OL0	O18-C22-C25	-4.81	118.80	125.25

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	4000	OL0	O18-C22-C25	-4.33	119.44	125.25
2	D	4000	OL0	O18-C22-C25	-3.87	120.07	125.25
2	C	4000	OL0	O18-C22-C25	-3.78	120.18	125.25
2	B	4000	OL0	C11-C23-C24	-3.44	117.90	122.13
2	D	4000	OL0	C11-C23-C24	-3.15	118.25	122.13
2	A	4000	OL0	C11-C23-C24	-3.05	118.37	122.13
2	D	4000	OL0	C22-C25-C26	2.19	121.04	117.09
2	A	4000	OL0	O45-C2-C3	2.22	121.52	117.66
2	B	4000	OL0	C22-C25-C26	2.23	121.11	117.09
2	C	4000	OL0	O18-C22-C23	3.29	120.05	115.83
2	D	4000	OL0	O18-C22-C23	3.41	120.21	115.83
2	A	4000	OL0	O18-C22-C23	3.48	120.29	115.83
2	B	4000	OL0	O18-C22-C23	4.71	121.87	115.83

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	4000	OL0	2	0
2	B	4000	OL0	2	0
2	C	4000	OL0	2	0
2	D	4000	OL0	1	0

## 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, 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	428/439 (97%)	-0.80	2 (0%) 91 92	6, 30, 63, 114	0
1	B	428/439 (97%)	-0.75	3 (0%) 89 90	15, 35, 71, 125	0
1	C	428/439 (97%)	0.05	14 (3%) 50 48	43, 70, 109, 146	0
1	D	428/439 (97%)	-0.19	6 (1%) 78 79	39, 63, 97, 149	0
All	All	1712/1756 (97%)	-0.42	25 (1%) 76 77	6, 53, 95, 149	0

All (25) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	428	PRO	8.3
1	C	428	PRO	6.7
1	D	428	PRO	5.6
1	B	426	LEU	5.1
1	C	426	LEU	3.6
1	B	428	PRO	3.5
1	C	187	GLN	3.4
1	B	427	VAL	3.2
1	D	186	PRO	3.1
1	C	405	ALA	3.1
1	C	427	VAL	3.0
1	D	183	ALA	2.9
1	D	184	LYS	2.9
1	D	427	VAL	2.8
1	C	160	ALA	2.8
1	C	157	ILE	2.8
1	C	57	ASN	2.5
1	C	313	GLU	2.4
1	C	188	LYS	2.3
1	C	132	GLY	2.3
1	A	427	VAL	2.3

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Mol	Chain	Res	Type	RSRZ
1	C	180	PRO	2.1
1	C	186	PRO	2.0
1	C	5	ARG	2.0
1	D	57	ASN	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 carbohydrates 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. 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
2	0L0	D	4000	37/37	0.96	0.15	0.59	41,51,61,65	0
2	0L0	C	4000	37/37	0.96	0.12	-0.31	47,56,59,63	0
2	0L0	A	4000	37/37	0.98	0.09	-0.45	9,20,30,33	0
2	0L0	B	4000	37/37	0.99	0.08	-0.96	12,21,31,33	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.