



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 28, 2026 – 10:00 PM UTC

PDB ID : 2FVM / pdb_00002fvm
Title : Crystal structure of dihydropyrimidinase from *Saccharomyces kluyveri* in complex with the reaction product N-carbamyl-beta-alanine
Authors : Dobritsch, D.; Lohkamp, B.
Deposited on : 2006-01-31
Resolution : 2.45 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

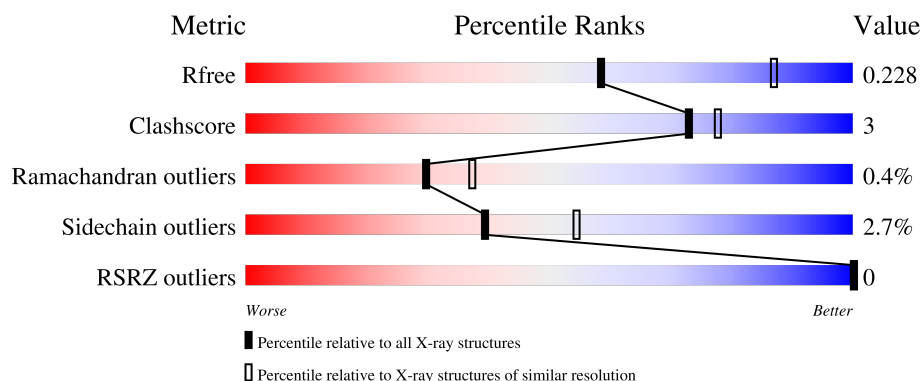
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.45 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1190 (2.46-2.46)
Clashscore	190562	1229 (2.46-2.46)
Ramachandran outliers	187476	1218 (2.46-2.46)
Sidechain outliers	187428	1218 (2.46-2.46)
RSRZ outliers	180081	1190 (2.46-2.46)

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	559	 86% 8% 5%
1	B	559	 85% 10% 5%
1	C	559	 86% 8% 5%
1	D	559	 85% 10% 5%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 17433 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 dihydropyrimidinase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	532	Total	C	N	O	S	0	1	0
			4155	2638	680	810	27			
1	B	532	Total	C	N	O	S	0	1	0
			4155	2638	680	810	27			
1	C	531	Total	C	N	O	S	0	1	0
			4145	2632	677	809	27			
1	D	532	Total	C	N	O	S	0	1	0
			4157	2639	680	811	27			

There are 76 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	167	KCX	LYS	modified residue	UNP Q9P903
A	543	PRO	-	expression tag	UNP Q9P903
A	544	GLY	-	expression tag	UNP Q9P903
A	545	ASP	-	expression tag	UNP Q9P903
A	546	ASP	-	expression tag	UNP Q9P903
A	547	ASP	-	expression tag	UNP Q9P903
A	548	ASP	-	expression tag	UNP Q9P903
A	549	LYS	-	expression tag	UNP Q9P903
A	550	HIS	-	expression tag	UNP Q9P903
A	551	HIS	-	expression tag	UNP Q9P903
A	552	HIS	-	expression tag	UNP Q9P903
A	553	HIS	-	expression tag	UNP Q9P903
A	554	HIS	-	expression tag	UNP Q9P903
A	555	HIS	-	expression tag	UNP Q9P903
A	556	HIS	-	expression tag	UNP Q9P903
A	557	HIS	-	expression tag	UNP Q9P903
A	558	SER	-	expression tag	UNP Q9P903
A	559	GLY	-	expression tag	UNP Q9P903
A	560	ASP	-	expression tag	UNP Q9P903
B	167	KCX	LYS	modified residue	UNP Q9P903
B	543	PRO	-	expression tag	UNP Q9P903

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Chain	Residue	Modelled	Actual	Comment	Reference
B	544	GLY	-	expression tag	UNP Q9P903
B	545	ASP	-	expression tag	UNP Q9P903
B	546	ASP	-	expression tag	UNP Q9P903
B	547	ASP	-	expression tag	UNP Q9P903
B	548	ASP	-	expression tag	UNP Q9P903
B	549	LYS	-	expression tag	UNP Q9P903
B	550	HIS	-	expression tag	UNP Q9P903
B	551	HIS	-	expression tag	UNP Q9P903
B	552	HIS	-	expression tag	UNP Q9P903
B	553	HIS	-	expression tag	UNP Q9P903
B	554	HIS	-	expression tag	UNP Q9P903
B	555	HIS	-	expression tag	UNP Q9P903
B	556	HIS	-	expression tag	UNP Q9P903
B	557	HIS	-	expression tag	UNP Q9P903
B	558	SER	-	expression tag	UNP Q9P903
B	559	GLY	-	expression tag	UNP Q9P903
B	560	ASP	-	expression tag	UNP Q9P903
C	167	KCX	LYS	modified residue	UNP Q9P903
C	543	PRO	-	expression tag	UNP Q9P903
C	544	GLY	-	expression tag	UNP Q9P903
C	545	ASP	-	expression tag	UNP Q9P903
C	546	ASP	-	expression tag	UNP Q9P903
C	547	ASP	-	expression tag	UNP Q9P903
C	548	ASP	-	expression tag	UNP Q9P903
C	549	LYS	-	expression tag	UNP Q9P903
C	550	HIS	-	expression tag	UNP Q9P903
C	551	HIS	-	expression tag	UNP Q9P903
C	552	HIS	-	expression tag	UNP Q9P903
C	553	HIS	-	expression tag	UNP Q9P903
C	554	HIS	-	expression tag	UNP Q9P903
C	555	HIS	-	expression tag	UNP Q9P903
C	556	HIS	-	expression tag	UNP Q9P903
C	557	HIS	-	expression tag	UNP Q9P903
C	558	SER	-	expression tag	UNP Q9P903
C	559	GLY	-	expression tag	UNP Q9P903
C	560	ASP	-	expression tag	UNP Q9P903
D	167	KCX	LYS	modified residue	UNP Q9P903
D	543	PRO	-	expression tag	UNP Q9P903
D	544	GLY	-	expression tag	UNP Q9P903
D	545	ASP	-	expression tag	UNP Q9P903
D	546	ASP	-	expression tag	UNP Q9P903
D	547	ASP	-	expression tag	UNP Q9P903

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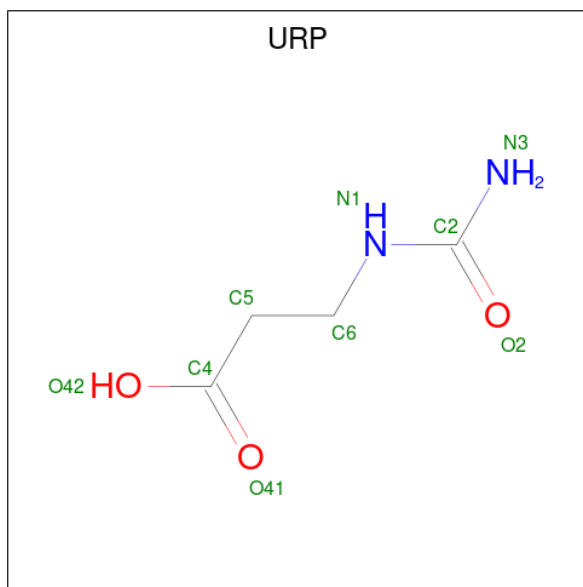
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Chain	Residue	Modelled	Actual	Comment	Reference
D	548	ASP	-	expression tag	UNP Q9P903
D	549	LYS	-	expression tag	UNP Q9P903
D	550	HIS	-	expression tag	UNP Q9P903
D	551	HIS	-	expression tag	UNP Q9P903
D	552	HIS	-	expression tag	UNP Q9P903
D	553	HIS	-	expression tag	UNP Q9P903
D	554	HIS	-	expression tag	UNP Q9P903
D	555	HIS	-	expression tag	UNP Q9P903
D	556	HIS	-	expression tag	UNP Q9P903
D	557	HIS	-	expression tag	UNP Q9P903
D	558	SER	-	expression tag	UNP Q9P903
D	559	GLY	-	expression tag	UNP Q9P903
D	560	ASP	-	expression tag	UNP Q9P903

- Molecule 2 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

- Molecule 3 is N-(AMINOCARBONYL)-BETA-ALANINE (CCD ID: URP) (formula: C₄H₈N₂O₃).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			9	4	2	3		
3	B	1	Total	C	N	O	0	0
			9	4	2	3		

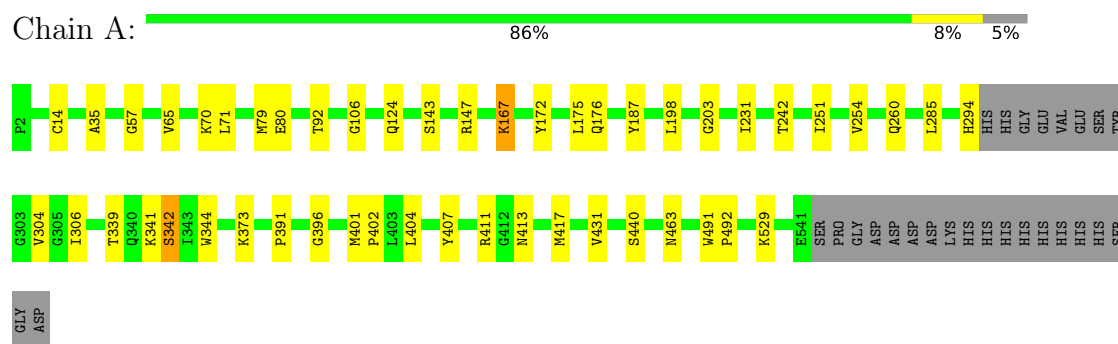
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	218	Total	O	0	0
			218	218		
4	B	191	Total	O	0	0
			191	191		
4	C	200	Total	O	0	0
			200	200		
4	D	186	Total	O	0	0
			186	186		

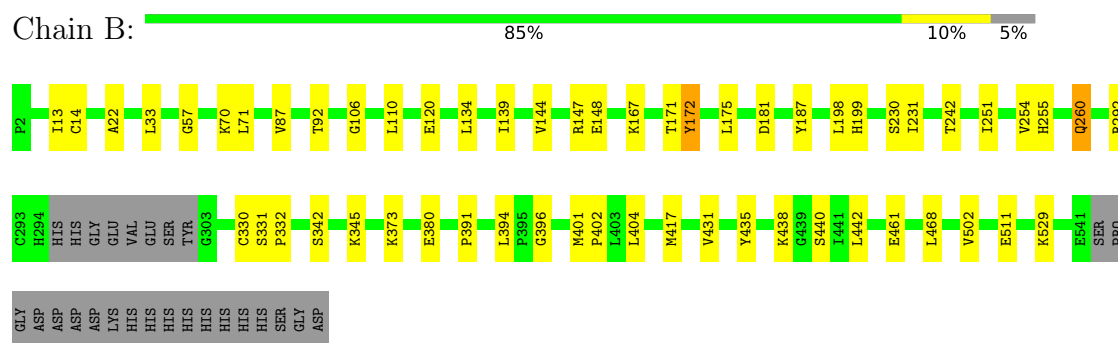
3 Residue-property plots

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.

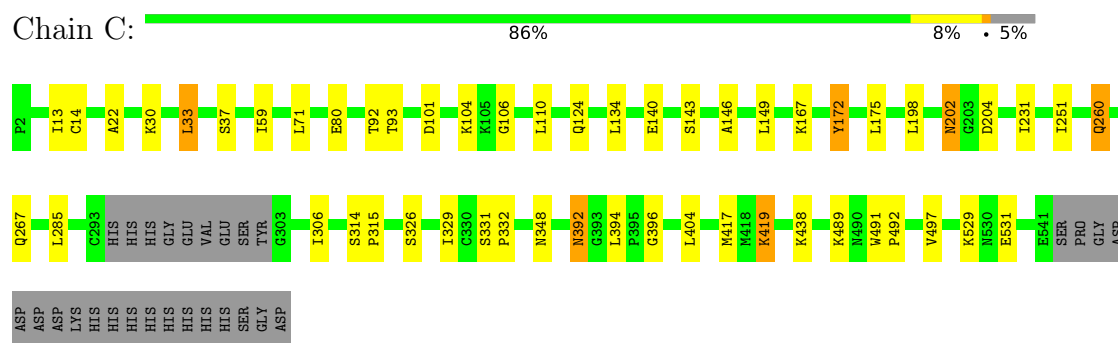
• Molecule 1: dihydropyrimidinase



• Molecule 1: dihydropyrimidinase



• Molecule 1: dihydropyrimidinase



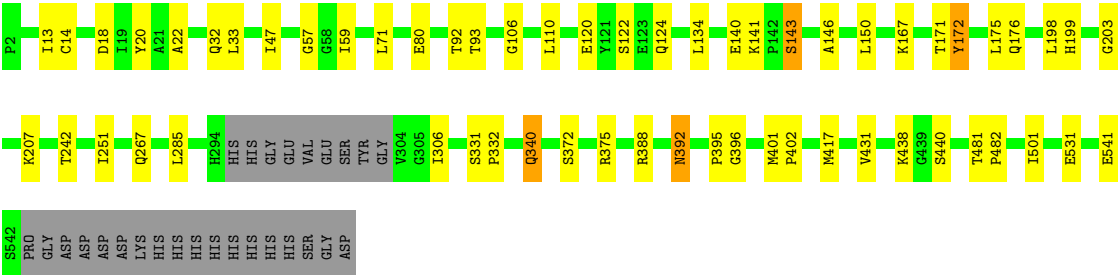
• Molecule 1: dihydropyrimidinase

Chain D:

85%

10%

5%



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	91.14Å 73.03Å 164.10Å 90.00° 91.98° 90.00°	Depositor
Resolution (Å)	44.37 – 2.45 44.37 – 2.45	Depositor EDS
% Data completeness (in resolution range)	97.3 (44.37-2.45) 97.2 (44.37-2.45)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.09	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.89 (at 2.45Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.182 , 0.237 0.189 , 0.228	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	17.7	Xtriage
Anisotropy	0.592	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 0.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	0.177 for h,-k,-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	17433	wwPDB-VP
Average B, all atoms (Å ²)	22.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.99% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, KCX, URP

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	0.58	0/4239	0.82	3/5752 (0.1%)
1	B	0.58	0/4239	0.83	2/5752 (0.0%)
1	C	0.58	0/4228	0.83	2/5737 (0.0%)
1	D	0.57	0/4241	0.81	3/5755 (0.1%)
All	All	0.58	0/16947	0.82	10/22996 (0.0%)

There are no bond length outliers.

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	106	GLY	CA-C-N	6.04	126.48	119.47
1	C	106	GLY	C-N-CA	6.04	126.48	119.47
1	A	106	GLY	CA-C-N	6.01	125.90	119.28
1	A	106	GLY	C-N-CA	6.01	125.90	119.28
1	A	143	SER	N-CA-C	5.93	117.42	111.07
1	B	106	GLY	CA-C-N	5.45	125.28	119.28
1	B	106	GLY	C-N-CA	5.45	125.28	119.28
1	D	143	SER	N-CA-C	5.31	117.07	111.28
1	D	106	GLY	CA-C-N	5.23	125.04	119.28
1	D	106	GLY	C-N-CA	5.23	125.04	119.28

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	4155	0	4084	24	0
1	B	4155	0	4084	29	0
1	C	4145	0	4077	29	0
1	D	4157	0	4086	30	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
2	C	2	0	0	0	0
2	D	2	0	0	0	0
3	A	9	0	7	0	0
3	B	9	0	7	1	0
4	A	218	0	0	1	0
4	B	191	0	0	1	0
4	C	200	0	0	2	0
4	D	186	0	0	2	0
All	All	17433	0	16345	106	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 3.

All (106) 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:198:LEU:HD12	1:A:251:ILE:HD11	1.29	1.08
1:C:198:LEU:HD12	1:C:251:ILE:HD11	1.32	1.07
1:D:198:LEU:HD12	1:D:251:ILE:HD11	1.35	1.04
1:B:198:LEU:HD12	1:B:251:ILE:HD11	1.46	0.96
1:C:260:GLN:HE21	1:C:260:GLN:H	1.33	0.76
1:D:285:LEU:HB3	1:D:306:ILE:HD12	1.67	0.76
1:B:71:LEU:HD11	1:B:175:LEU:HD21	1.71	0.72
1:B:14[B]:CYS:SG	1:B:417:MET:HB3	2.31	0.70
1:A:304:VAL:HG11	1:A:341:LYS:HE3	1.76	0.68
1:B:230:SER:HB3	1:B:260:GLN:HE22	1.58	0.68
1:C:140:GLU:O	1:C:146:ALA:HB2	1.93	0.68
1:A:440:SER:HB3	4:A:642:HOH:O	1.97	0.64
1:D:198:LEU:HD12	1:D:251:ILE:CD1	2.19	0.63
1:D:198:LEU:CD1	1:D:251:ILE:HD11	2.21	0.63
1:D:340:GLN:CD	1:D:340:GLN:H	2.07	0.63
1:C:71:LEU:HD11	1:C:175:LEU:HD21	1.81	0.62
1:D:140:GLU:O	1:D:146:ALA:HB2	2.01	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:57:GLY:HA3	1:B:92:THR:OG1	2.00	0.61
1:C:202:ASN:C	1:C:202:ASN:HD22	2.10	0.60
1:B:147:ARG:HD2	1:B:187:TYR:CE2	2.36	0.60
1:D:13:ILE:HD12	1:D:22:ALA:HB3	1.83	0.60
1:C:140:GLU:O	1:C:146:ALA:CB	2.54	0.55
1:A:198:LEU:HD12	1:A:251:ILE:CD1	2.20	0.55
1:B:87:VAL:HG11	1:B:502:VAL:HG12	1.90	0.54
1:C:13:ILE:HD12	1:C:22:ALA:HB3	1.90	0.53
1:A:147:ARG:HD2	1:A:187:TYR:CE2	2.43	0.53
1:A:14[B]:CYS:SG	1:A:417:MET:HB3	2.49	0.53
1:D:110:LEU:HB3	1:D:134:LEU:HD21	1.91	0.52
1:C:198:LEU:HD12	1:C:251:ILE:CD1	2.23	0.52
1:B:330:CYS:HB3	1:B:394:LEU:HD13	1.91	0.51
1:D:140:GLU:O	1:D:146:ALA:CB	2.59	0.50
1:D:141:LYS:HG3	4:D:2781:HOH:O	2.11	0.50
1:A:35:ALA:HB2	1:C:33:LEU:HD12	1.94	0.50
1:A:71:LEU:HD11	1:A:175:LEU:HD21	1.94	0.50
1:C:110:LEU:HB3	1:C:134:LEU:HD21	1.93	0.50
1:C:231:ILE:HG12	1:D:242:THR:HG23	1.94	0.50
1:D:47:ILE:HD11	1:D:501:ILE:HD11	1.93	0.50
1:D:372:SER:O	1:D:375:ARG:HB3	2.12	0.50
1:A:57:GLY:HA3	1:A:92:THR:OG1	2.11	0.49
4:B:618:HOH:O	1:D:440:SER:HB3	2.13	0.49
1:D:71:LEU:HD11	1:D:175:LEU:HD21	1.94	0.49
1:A:491:TRP:CD1	1:A:492:PRO:HD2	2.47	0.49
1:A:167:KCX:HE2	1:A:254:VAL:HG21	1.94	0.49
1:A:339:THR:O	1:A:342:SER:HB2	2.14	0.48
1:B:331:SER:H	3:B:604:URP:HN31	1.60	0.48
1:C:30:LYS:HE2	4:C:1801:HOH:O	2.13	0.48
1:C:143:SER:HA	1:C:146:ALA:HB3	1.96	0.48
1:C:202:ASN:HD21	1:C:204:ASP:HB2	1.79	0.47
1:C:59:ILE:HG12	1:C:93:THR:HB	1.96	0.47
1:D:57:GLY:HA3	1:D:92:THR:OG1	2.15	0.47
1:A:242:THR:HG23	1:B:231:ILE:HG12	1.96	0.46
1:B:199:HIS:C	1:B:199:HIS:CD2	2.93	0.46
1:A:147:ARG:HD2	1:A:187:TYR:CD2	2.50	0.46
1:C:331:SER:HA	1:C:332:PRO:C	2.40	0.46
1:C:14[B]:CYS:SG	1:C:417:MET:HB3	2.55	0.46
1:C:92:THR:HG22	1:C:497:VAL:HG22	1.97	0.46
1:B:110:LEU:HB3	1:B:134:LEU:HD21	1.98	0.45
1:B:230:SER:HB3	1:B:260:GLN:NE2	2.30	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:407:TYR:HA	1:A:411:ARG:HD2	1.97	0.45
1:D:146:ALA:O	1:D:150:LEU:HB2	2.16	0.45
1:B:442:LEU:HD22	1:D:20:TYR:CE2	2.50	0.45
1:C:392:ASN:N	1:C:392:ASN:HD22	2.14	0.45
1:B:13:ILE:HD12	1:B:22:ALA:HB3	1.99	0.45
1:B:435:TYR:OH	1:D:18:ASP:OD1	2.32	0.45
1:B:139:ILE:HG13	1:B:181:ASP:HB3	1.98	0.45
1:B:342:SER:HA	1:B:345:LYS:HG2	1.98	0.44
1:C:285:LEU:HB3	1:C:306:ILE:HD12	2.00	0.44
1:B:373:LYS:HD3	1:B:391:PRO:HG2	2.00	0.44
1:D:331:SER:HA	1:D:332:PRO:C	2.42	0.44
1:A:401:MET:HB2	1:A:402:PRO:HD3	2.00	0.43
1:B:230:SER:CB	1:B:260:GLN:HE22	2.28	0.43
1:B:440:SER:HB3	4:D:2683:HOH:O	2.18	0.43
1:A:167:KCX:HZ	1:A:167:KCX:HG3	1.64	0.43
1:C:314:SER:HB2	1:C:315:PRO:HD2	1.99	0.43
1:D:14[B]:CYS:SG	1:D:417:MET:HB3	2.58	0.43
1:D:80:GLU:HB2	1:D:124:GLN:HB3	1.99	0.43
1:B:171:THR:O	1:B:172:TYR:HB2	2.19	0.43
1:C:202:ASN:C	1:C:202:ASN:ND2	2.76	0.43
1:D:395:PRO:HD2	1:D:482:PRO:HD3	2.00	0.43
1:A:373:LYS:HD3	1:A:391:PRO:HG2	2.01	0.42
1:A:80:GLU:HB2	1:A:124:GLN:HB3	2.01	0.42
1:A:285:LEU:HB3	1:A:306:ILE:HG13	2.01	0.42
1:C:348:ASN:HA	1:C:419:LYS:HD3	2.01	0.42
1:C:491:TRP:CD1	1:C:492:PRO:HD2	2.55	0.42
1:B:331:SER:HA	1:B:332:PRO:C	2.44	0.42
1:C:326:SER:HA	1:C:329:ILE:HG12	2.02	0.42
1:A:65:VAL:HG21	1:A:79:MET:HE2	2.02	0.41
1:A:344:TRP:CD2	1:A:413:ASN:HB3	2.55	0.41
1:B:401:MET:HB2	1:B:402:PRO:HD3	2.02	0.41
1:D:176:GLN:OE1	1:D:203:GLY:HA3	2.21	0.41
1:C:267:GLN:HB3	4:C:1799:HOH:O	2.18	0.41
1:D:392:ASN:HD22	1:D:392:ASN:N	2.19	0.41
1:D:401:MET:HB2	1:D:402:PRO:HD3	2.02	0.41
1:C:172:TYR:OH	1:C:331:SER:HB2	2.20	0.41
1:D:59:ILE:HG12	1:D:93:THR:HB	2.03	0.41
1:D:143:SER:HA	1:D:146:ALA:HB3	2.02	0.41
1:B:144:VAL:HA	1:B:147:ARG:HG3	2.03	0.41
1:A:231:ILE:HG12	1:B:242:THR:HG23	2.02	0.41
1:C:101:ASP:OD2	1:C:104:LYS:HE2	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:199:HIS:CD2	1:D:199:HIS:C	2.98	0.41
1:A:176:GLN:OE1	1:A:203:GLY:HA3	2.21	0.41
1:B:254:VAL:HG23	1:B:255:HIS:CE1	2.56	0.41
1:D:171:THR:O	1:D:172:TYR:HB2	2.20	0.41
1:B:198:LEU:HD12	1:B:251:ILE:CD1	2.34	0.40
1:B:260:GLN:NE2	1:B:260:GLN:H	2.19	0.40
1:C:80:GLU:HB2	1:C:124:GLN:HB3	2.03	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	528/559 (94%)	508 (96%)	18 (3%)	2 (0%)	30	37
1	B	528/559 (94%)	512 (97%)	14 (3%)	2 (0%)	30	37
1	C	527/559 (94%)	513 (97%)	12 (2%)	2 (0%)	30	37
1	D	528/559 (94%)	516 (98%)	10 (2%)	2 (0%)	30	37
All	All	2111/2236 (94%)	2049 (97%)	54 (3%)	8 (0%)	30	37

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	172	TYR
1	B	172	TYR
1	C	172	TYR
1	D	172	TYR
1	A	396	GLY
1	B	396	GLY
1	C	396	GLY
1	D	396	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	456/479 (95%)	448 (98%)	8 (2%)	51	65
1	B	456/479 (95%)	442 (97%)	14 (3%)	35	50
1	C	455/479 (95%)	442 (97%)	13 (3%)	37	52
1	D	457/479 (95%)	443 (97%)	14 (3%)	35	50
All	All	1824/1916 (95%)	1775 (97%)	49 (3%)	39	54

All (49) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	70	LYS
1	A	260	GLN
1	A	294	HIS
1	A	342	SER
1	A	404	LEU
1	A	431	VAL
1	A	463	ASN
1	A	529	LYS
1	B	33	LEU
1	B	70	LYS
1	B	120	GLU
1	B	148	GLU
1	B	260	GLN
1	B	292	ARG
1	B	380	GLU
1	B	404	LEU
1	B	431	VAL
1	B	438	LYS
1	B	461	GLU
1	B	468	LEU
1	B	511	GLU
1	B	529	LYS
1	C	33	LEU
1	C	37	SER

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Mol	Chain	Res	Type
1	C	149	LEU
1	C	202	ASN
1	C	260	GLN
1	C	392	ASN
1	C	394	LEU
1	C	404	LEU
1	C	419	LYS
1	C	438	LYS
1	C	489	LYS
1	C	529	LYS
1	C	531	GLU
1	D	32	GLN
1	D	33	LEU
1	D	120	GLU
1	D	122	SER
1	D	207	LYS
1	D	267	GLN
1	D	340	GLN
1	D	388	ARG
1	D	392	ASN
1	D	431	VAL
1	D	438	LYS
1	D	481	THR
1	D	531	GLU
1	D	541	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (19) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	32	GLN
1	A	260	GLN
1	A	267	GLN
1	A	392	ASN
1	A	424	GLN
1	B	260	GLN
1	B	392	ASN
1	B	424	GLN
1	C	27	ASN
1	C	202	ASN
1	C	224	HIS
1	C	260	GLN
1	C	374	HIS

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Mol	Chain	Res	Type
1	C	392	ASN
1	C	424	GLN
1	C	530	ASN
1	D	267	GLN
1	D	318	ASN
1	D	392	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

4 non-standard protein/DNA/RNA residues 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	$\# Z > 2$
1	KCX	D	167	1,2	10,11,12	0.91	0	6,12,14	1.35	1 (16%)
1	KCX	B	167	1,2	10,11,12	0.95	0	6,12,14	1.68	1 (16%)
1	KCX	A	167	1,2	10,11,12	0.89	0	6,12,14	1.42	1 (16%)
1	KCX	C	167	1,2	10,11,12	0.78	0	6,12,14	1.34	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
1	KCX	D	167	1,2	-	0/9/10/12	-
1	KCX	B	167	1,2	-	2/9/10/12	-
1	KCX	A	167	1,2	-	1/9/10/12	-
1	KCX	C	167	1,2	-	2/9/10/12	-

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	B	167	KCX	OQ1-CX-NZ	-3.50	119.60	124.92
1	D	167	KCX	OQ1-CX-NZ	-3.12	120.18	124.92
1	C	167	KCX	OQ1-CX-NZ	-3.09	120.22	124.92
1	A	167	KCX	OQ1-CX-NZ	-3.05	120.29	124.92

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	C	167	KCX	C-CA-CB-CG
1	A	167	KCX	CG-CD-CE-NZ
1	B	167	KCX	CG-CD-CE-NZ
1	B	167	KCX	C-CA-CB-CG
1	C	167	KCX	CA-CB-CG-CD

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	167	KCX	2	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 10 ligands modelled in this entry, 8 are monoatomic - leaving 2 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	URP	A	604	2	8,8,8	0.99	0	9,9,9	2.33	2 (22%)
3	URP	B	604	2	8,8,8	0.94	0	9,9,9	2.56	2 (22%)

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	URP	A	604	2	-	5/6/6/6	-
3	URP	B	604	2	-	5/6/6/6	-

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	604	URP	C6-N1-C2	5.35	129.61	122.64
3	A	604	URP	C6-N1-C2	4.48	128.49	122.64
3	B	604	URP	C5-C6-N1	-4.47	102.49	112.00
3	A	604	URP	C5-C6-N1	-4.41	102.62	112.00

There are no chirality outliers.

All (10) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	604	URP	O41-C4-C5-C6
3	A	604	URP	C4-C5-C6-N1
3	B	604	URP	O42-C4-C5-C6
3	A	604	URP	O42-C4-C5-C6
3	A	604	URP	O41-C4-C5-C6
3	B	604	URP	C4-C5-C6-N1
3	A	604	URP	O2-C2-N1-C6
3	A	604	URP	N3-C2-N1-C6
3	B	604	URP	O2-C2-N1-C6
3	B	604	URP	N3-C2-N1-C6

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	604	URP	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 [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, 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	531/559 (94%)	-1.76	0 100 100	15, 23, 25, 32	2 (0%)
1	B	531/559 (94%)	-1.75	0 100 100	15, 23, 25, 33	2 (0%)
1	C	530/559 (94%)	-1.73	0 100 100	15, 23, 25, 33	1 (0%)
1	D	531/559 (94%)	-1.74	0 100 100	15, 23, 25, 31	1 (0%)
All	All	2123/2236 (94%)	-1.74	0 100 100	15, 23, 25, 33	6 (0%)

There are no RSRZ outliers to report.

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

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
1	KCX	C	167	12/13	0.99	0.04	22,23,30,31	3
1	KCX	D	167	12/13	0.99	0.04	22,24,30,30	3
1	KCX	A	167	12/13	1.00	0.02	22,24,30,31	3
1	KCX	B	167	12/13	1.00	0.03	22,23,30,31	3

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	URP	A	604	9/9	0.99	0.04	44,46,49,49	0
3	URP	B	604	9/9	0.99	0.06	42,44,47,47	0
2	ZN	B	601	1/1	1.00	0.04	32,32,32,32	0
2	ZN	B	602	1/1	1.00	0.05	50,50,50,50	0
2	ZN	C	601	1/1	1.00	0.03	39,39,39,39	0
2	ZN	C	602	1/1	1.00	0.04	45,45,45,45	0
2	ZN	D	601	1/1	1.00	0.03	36,36,36,36	0
2	ZN	D	602	1/1	1.00	0.05	46,46,46,46	0
2	ZN	A	601	1/1	1.00	0.03	34,34,34,34	0
2	ZN	A	602	1/1	1.00	0.04	48,48,48,48	0

6.5 Other polymers [i](#)

There are no such residues in this entry.