



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 05:54 AM GMT

PDB ID : 2V8V
Title : CRYSTAL STRUCTURE OF MUTANT R322A OF BETA-ALANINE SYNTHASE FROM SACCHAROMYCES KLUYVERI
Authors : Lundgren, S.; Andersen, B.; Piskur, J.; Dobritsch, D.
Deposited on : 2007-08-15
Resolution : 2.90 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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

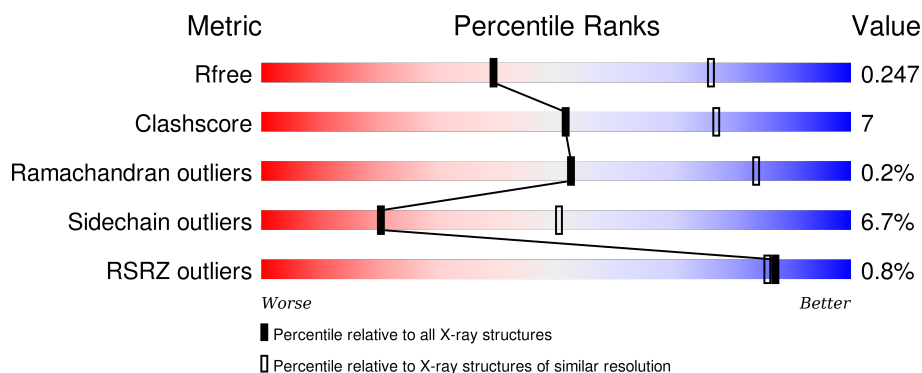
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.90 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	1451 (2.90-2.90)
Clashscore	102246	1668 (2.90-2.90)
Ramachandran outliers	100387	1630 (2.90-2.90)
Sidechain outliers	100360	1632 (2.90-2.90)
RSRZ outliers	91569	1456 (2.90-2.90)

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 ≥ 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	474	 74% 16% • 8%
1	B	474	 74% 15% • 9%
1	C	474	 76% 14% • 9%
1	D	474	 77% 13% • 8%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard

residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	URP	C	1457	-	-	-	X
3	URP	D	1456	-	-	-	X

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 13410 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 BETA-ALANINE SYNTHASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	435	Total	C	N	O	S	0	1	0
			3360	2120	575	649	16			
1	B	431	Total	C	N	O	S	0	0	0
			3324	2097	567	644	16			
1	C	431	Total	C	N	O	S	0	0	0
			3324	2097	567	644	16			
1	D	435	Total	C	N	O	S	0	0	0
			3355	2117	572	650	16			

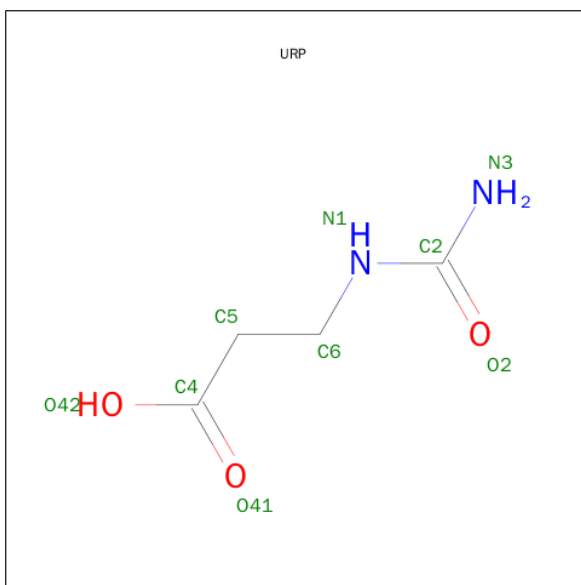
There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	322	ALA	ARG	ENGINEERED MUTATION	UNP Q96W94
B	322	ALA	ARG	ENGINEERED MUTATION	UNP Q96W94
C	322	ALA	ARG	ENGINEERED MUTATION	UNP Q96W94
D	322	ALA	ARG	ENGINEERED MUTATION	UNP Q96W94

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

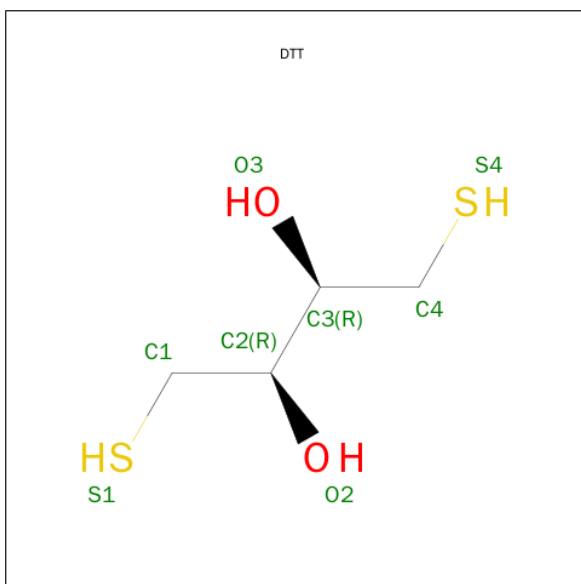
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	2	Total	Zn	0	0
			2	2		
2	A	2	Total	Zn	0	0
			2	2		
2	D	2	Total	Zn	0	0
			2	2		
2	C	2	Total	Zn	0	0
			2	2		

- Molecule 3 is N-(AMINOCARBONYL)-BETA-ALANINE (three-letter code: URP) (formula: C₄H₈N₂O₃).



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

- Molecule 4 is 2,3-DIHYDROXY-1,4-DITHIOBUTANE (three-letter code: DTT) (formula: $C_4H_{10}O_2S_2$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	C	1	Total	C	O	S	0	0
			8	4	2	2		

- Molecule 5 is water.

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

- Molecule 1: BETA-ALANINE SYNTHASE

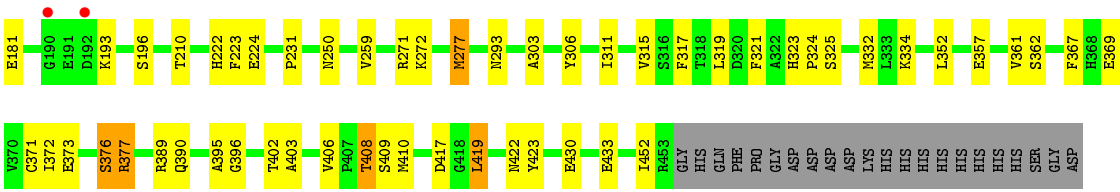
ASP	E135	T318	SER
ASP	R138	L319	LVS
HIS	F157	L329	VAL
HIS	R166	A330	HIS
HIS	S171	T331	SER
HIS	S172	M332	THR
HIS	S188	L333	ILE
HIS	D192	K334	THR
GLY	D198	E339	VAL
ASP	L352	D348	SER
ASP	S356	L352	ALA
	V361	S356	PER
	F367	V361	ASP
	C371	F367	GLY
	R377	C371	THR
	S378	R377	L20
	S393	S378	A25
	D398	S393	L28
	C400	D398	S32
	Q401	C400	Q45
	T402	Q401	
	A403	T402	R51
	V406	A403	M52
	P407	V406	G53
	T408	P407	F59
	S409	T408	K39
	S420	S409	V90
	E425	S420	D91
	E430	E425	N95
	L440	E430	M96
	Q441	L440	G105
	N445	Q441	G106
	C454	N445	K107
HIS	G545	C454	T111
GLN	PHE	G545	G112
PER	PRO	PHE	S113
GLY	ASP	PRO	H114
ASP		GLY	K123
		ASP	I124
			A125
			G126
			I127
			V130
			L131
			L132

• Molecule 1: BETA-ALANINE SYNTHASE

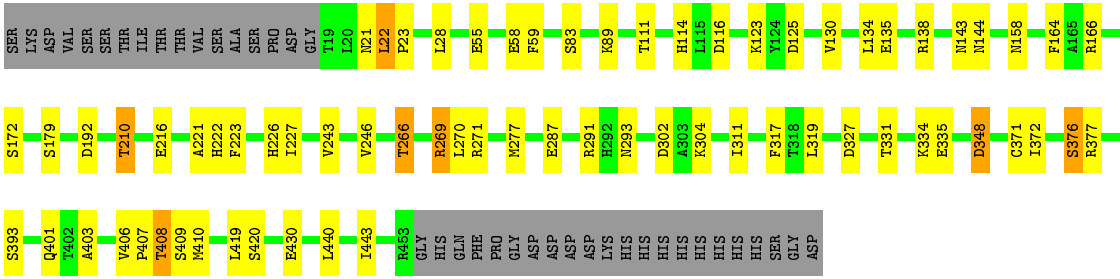
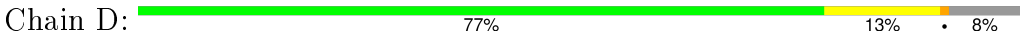
ASP	ASP	I301	V130	SER
LVS	LVS	Y306	L134	LVS
HIS	HIS	N309	L137	VAL
HIS	HIS	P312	R138	SER
HIS	HIS	F317	V153	THR
HIS	HIS	T318	N158	THR
HIS	HIS	L319	R166	VAL
SER	SER	H323	S167	SER
ASP	ASP	P324	S179	SER
		K334	L180	PRO
		E335	E181	GLY
		I362	Y184	THR
		E357	G190	LEU
		C371	D192	ASN
		I372	K193	ASN
		C374	P194	P23
		V375	V197	A24
		S376	L201	A25
		R377		
		Q390	T210	A50
		Q401	D220	R51
		T402	A221	H52
		A403	H222	G53
			F223	Q54
		V406	E228	E55
		P407	Q229	S56
		T408	G230	H57
		S409	P231	E58
		I413		F59
		D417	N250	G60
		G418	Q252	L84
		L419	H262	V90
		Y423		F97
		E430	T265	Y100
		R453	L275	P101
GLY	GLY	HIS	L276	K107
GLN	GLN	GLN	H277	T111
PRO	PRO	PHE	S286	G112
GLY	GLY	ASP	R291	S113
ASP	ASP		G294	Q118
				A121
				G122
				K123
				L128
				G129

- Molecule 1: BETA-ALANINE SYNTHASE

SER	LYS	VAL	SER	THR	ILE	THR	THR	VAL	SER	ALA	SER	PRO	ASP	GLY	THR	LEU	ASN	LEU	P23	A50	W52	G53	Q54	E55	S56	H57	E58	F59	V90	G105	T111	G112	S113	K123	I127	V130	L131	A132	G133	L134	E135	V136	R166
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● Molecule 1: BETA-ALANINE SYNTHASE



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	77.48Å 84.90Å 104.85Å 67.45° 67.81° 62.75°	Depositor
Resolution (Å)	45.00 – 2.90 43.80 – 2.90	Depositor EDS
% Data completeness (in resolution range)	93.5 (45.00-2.90) 76.5 (43.80-2.90)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.25 (at 2.90Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.194 , 0.246 0.198 , 0.247	Depositor DCC
R_{free} test set	2012 reflections (5.32%)	DCC
Wilson B-factor (Å ²)	33.8	Xtriage
Anisotropy	0.390	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 26.9	EDS
Estimated twinning fraction	0.430 for h,h-k,h-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 39859 reflections	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	13410	wwPDB-VP
Average B, all atoms (Å ²)	35.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.54% 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, 0.375 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: ZN, URP, DTT

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	0.59	0/3440	0.69	1/4666 (0.0%)
1	B	0.53	0/3401	0.64	0/4613
1	C	0.54	0/3401	0.66	0/4613
1	D	0.59	0/3432	0.67	1/4657 (0.0%)
All	All	0.56	0/13674	0.67	2/18549 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	125	ASP	CB-CG-OD1	6.58	124.22	118.30
1	D	125	ASP	CB-CG-OD1	5.87	123.58	118.30

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	3360	0	3252	57	0
1	B	3324	0	3209	50	0
1	C	3324	0	3208	38	0
1	D	3355	0	3243	45	0
2	A	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	2	0	0	0	0
2	C	2	0	0	0	0
2	D	2	0	0	0	0
3	B	9	0	7	0	0
3	C	9	0	7	2	0
3	D	9	0	7	0	0
4	C	8	0	9	0	0
5	A	1	0	0	0	0
5	B	1	0	0	0	0
5	C	1	0	0	0	0
5	D	1	0	0	0	0
All	All	13410	0	12942	178	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 7.

All (178) 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:D:403:ALA:HA	1:D:408:THR:CG2	2.04	0.86
1:A:265:THR:HG21	1:B:229:GLN:O	1.77	0.84
1:A:403:ALA:HA	1:A:408:THR:HG23	1.59	0.83
1:C:57:HIS:O	1:C:123:LYS:NZ	2.12	0.82
1:D:22:LEU:HB2	1:D:23:PRO:HD2	1.64	0.77
1:B:57:HIS:O	1:B:123:LYS:NZ	2.17	0.77
1:D:22:LEU:HD23	1:D:22:LEU:H	1.48	0.76
1:C:403:ALA:HA	1:C:408:THR:CG2	2.16	0.75
1:B:403:ALA:HA	1:B:408:THR:HG23	1.69	0.75
1:D:406:VAL:O	1:D:408:THR:HG22	1.87	0.74
1:A:406:VAL:O	1:A:408:THR:HG22	1.87	0.74
1:C:403:ALA:HA	1:C:408:THR:HG23	1.68	0.74
1:D:291:ARG:NH2	1:D:335:GLU:OE1	2.19	0.74
1:A:309:ASN:HD22	1:A:309:ASN:C	1.91	0.74
1:A:266:THR:HG23	1:B:231:PRO:HG3	1.70	0.74
1:A:403:ALA:HA	1:A:408:THR:CG2	2.17	0.73
1:A:59:PHE:O	1:A:123:LYS:HE2	1.89	0.73
1:D:22:LEU:N	1:D:22:LEU:CD2	2.55	0.70
1:D:22:LEU:H	1:D:22:LEU:CD2	2.03	0.70
1:B:403:ALA:HA	1:B:408:THR:CG2	2.22	0.69
1:B:84:LEU:HD21	1:B:138:ARG:HG3	1.73	0.69
1:C:59:PHE:O	1:C:123:LYS:HE2	1.93	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:403:ALA:HA	1:D:408:THR:HG21	1.76	0.68
1:B:309:ASN:HD22	1:B:309:ASN:H	1.42	0.67
1:A:28:LEU:HD12	1:A:440:LEU:HD11	1.76	0.67
1:C:317:PHE:HE1	1:C:319:LEU:HD21	1.59	0.67
1:D:55:GLU:HB2	1:D:58:GLU:HG3	1.77	0.66
1:B:262:HIS:HB3	1:B:265:THR:HG22	1.78	0.66
1:A:277:MET:HG3	1:A:352:LEU:HD22	1.77	0.66
1:C:395:ALA:HA	3:C:1457:URP:H51	1.79	0.64
1:C:231:PRO:HG3	1:D:266:THR:HG23	1.79	0.64
1:B:317:PHE:HE1	1:B:319:LEU:HD21	1.63	0.64
1:D:403:ALA:HA	1:D:408:THR:HG23	1.80	0.64
1:A:222:HIS:HB3	1:A:408:THR:HB	1.82	0.61
1:A:302:ASP:OD2	1:B:306:TYR:OH	2.19	0.60
1:A:135:GLU:OE1	1:A:135:GLU:HA	2.00	0.60
1:C:317:PHE:CE1	1:C:319:LEU:HD21	2.37	0.59
1:D:172:SER:HA	1:D:401:GLN:HE21	1.68	0.59
1:A:229:GLN:O	1:B:265:THR:HG21	2.03	0.59
1:A:171:SER:OG	1:A:398:ASP:OD1	2.19	0.58
1:A:371:CYS:HB2	1:A:409:SER:HB2	1.84	0.58
1:A:25:ALA:HB2	1:A:445:ASN:HD21	1.69	0.57
1:C:306:TYR:OH	1:D:302:ASP:OD2	2.21	0.57
1:C:389:ARG:HG2	1:C:390:GLN:O	2.05	0.57
1:D:28:LEU:HD12	1:D:440:LEU:HD11	1.88	0.56
1:C:406:VAL:O	1:C:408:THR:HG22	2.06	0.56
1:A:246:VAL:HG22	1:A:393:SER:HB3	1.88	0.55
1:B:371:CYS:HB3	1:B:409:SER:HB3	1.88	0.55
1:A:271:ARG:HG2	1:A:311:ILE:HD13	1.89	0.55
1:A:371:CYS:CB	1:A:409:SER:HB2	2.37	0.55
1:C:259:VAL:HG23	1:C:272:LYS:HD2	1.89	0.55
1:A:262:HIS:HB3	1:A:265:THR:HG22	1.89	0.54
1:B:252:GLN:HB2	1:B:319:LEU:HB2	1.89	0.53
1:C:373:GLU:O	1:C:377:ARG:HB2	2.08	0.53
1:B:317:PHE:CE1	1:B:319:LEU:HD21	2.43	0.53
1:C:271:ARG:HG2	1:C:311:ILE:HD13	1.91	0.53
1:D:317:PHE:CE1	1:D:319:LEU:HD21	2.44	0.53
1:D:222:HIS:HB3	1:D:408:THR:HB	1.90	0.53
1:B:371:CYS:O	1:B:375:VAL:HG23	2.09	0.52
1:B:90:VAL:O	1:B:210:THR:HG23	2.10	0.52
1:D:403:ALA:CA	1:D:408:THR:HG21	2.39	0.52
1:B:406:VAL:O	1:B:408:THR:HG22	2.10	0.52
1:B:323:HIS:ND1	1:B:324:PRO:HD2	2.24	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:22:LEU:HD23	1:D:22:LEU:N	2.16	0.52
1:B:373:GLU:O	1:B:377:ARG:HB2	2.10	0.52
1:B:222:HIS:HB3	1:B:408:THR:HB	1.92	0.52
1:A:309:ASN:C	1:A:309:ASN:ND2	2.61	0.51
1:D:403:ALA:N	1:D:408:THR:HG21	2.25	0.51
1:A:51[B]:ARG:NH1	1:A:53:GLY:O	2.35	0.51
1:D:372:ILE:O	1:D:376:SER:HB2	2.10	0.51
1:D:158:ASN:HD21	1:D:164:PHE:HB2	1.75	0.51
1:C:181:GLU:H	1:C:181:GLU:CD	2.14	0.51
1:B:402:THR:OG1	1:B:408:THR:HG21	2.12	0.50
1:A:207:ILE:O	1:A:207:ILE:HG22	2.12	0.49
1:B:277:MET:HG3	1:B:352:LEU:HD22	1.93	0.49
1:D:158:ASN:ND2	1:D:164:PHE:HB2	2.27	0.49
1:B:181:GLU:H	1:B:181:GLU:CD	2.15	0.49
1:C:111:THR:HA	1:C:223:PHE:O	2.13	0.49
1:A:378:SER:OG	1:A:441:GLN:HB3	2.12	0.49
1:D:22:LEU:HB2	1:D:23:PRO:CD	2.37	0.49
1:A:90:VAL:O	1:A:210:THR:HG23	2.13	0.49
1:C:422:ASN:OD1	1:C:423:TYR:N	2.46	0.49
1:A:157:PHE:CE1	1:A:201:LEU:HD21	2.48	0.48
1:D:59:PHE:O	1:D:123:LYS:HE2	2.14	0.48
1:A:247:GLN:HE22	1:A:295:LEU:HD12	1.79	0.47
1:A:329:LEU:O	1:A:332:MET:HB2	2.14	0.47
1:A:193:LYS:HE2	1:D:327:ASP:OD2	2.14	0.47
1:C:222:HIS:HB3	1:C:408:THR:HB	1.96	0.47
1:D:371:CYS:HB3	1:D:409:SER:HB3	1.96	0.47
1:D:111:THR:HA	1:D:223:PHE:O	2.14	0.47
1:A:111:THR:HA	1:A:223:PHE:O	2.15	0.47
1:B:262:HIS:HB3	1:B:265:THR:CG2	2.43	0.47
1:C:127:ILE:CG2	1:C:131:LEU:HD12	2.44	0.46
1:D:348:ASP:OD2	1:D:348:ASP:N	2.49	0.46
1:B:107:LYS:HE3	1:B:220:ASP:OD1	2.14	0.46
1:A:224:GLU:OE2	1:A:399:SER:OG	2.30	0.46
1:C:323:HIS:ND1	1:C:324:PRO:HD2	2.30	0.46
1:A:265:THR:HG23	1:B:230:GLY:HA2	1.97	0.46
1:A:263:ALA:O	1:A:271:ARG:NH2	2.48	0.46
1:C:55:GLU:HB2	1:C:58:GLU:HG3	1.96	0.46
1:C:419:LEU:HD11	1:C:422:ASN:HD22	1.81	0.46
1:D:269:ARG:HG2	1:D:270:LEU:HG	1.97	0.46
1:D:226:HIS:HD1	1:D:227:ILE:N	2.13	0.46
1:C:396:GLY:H	3:C:1457:URP:C4	2.29	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:60:GLY:HA3	1:B:423:TYR:CD2	2.51	0.46
1:C:303:ALA:HA	1:C:315:VAL:HG22	1.97	0.46
1:C:371:CYS:HB3	1:C:409:SER:HB3	1.98	0.45
1:D:221:ALA:HB1	1:D:407:PRO:O	2.17	0.45
1:B:60:GLY:HA3	1:B:423:TYR:HD2	1.81	0.45
1:B:111:THR:HA	1:B:223:PHE:O	2.17	0.45
1:A:25:ALA:HB2	1:A:445:ASN:ND2	2.32	0.45
1:B:291:ARG:NH2	1:B:335:GLU:OE1	2.49	0.45
1:A:291:ARG:HG3	1:A:291:ARG:HH11	1.81	0.45
1:D:143:ASN:O	1:D:144:ASN:HB2	2.17	0.45
1:A:91:ASP:OD1	1:A:95:ASN:HB2	2.16	0.45
1:B:100:TYR:HA	1:B:101:PRO:HD3	1.89	0.45
1:C:259:VAL:N	1:C:272:LYS:HB2	2.31	0.44
1:C:367:PHE:HB3	1:C:408:THR:O	2.18	0.44
1:B:401:GLN:NE2	1:B:401:GLN:HA	2.31	0.44
1:D:271:ARG:HG2	1:D:311:ILE:HD13	1.99	0.44
1:D:243:VAL:HB	1:D:410:MET:HB2	2.00	0.44
1:A:90:VAL:HG22	1:A:96:MET:HG2	2.00	0.44
1:B:275:LEU:HB2	1:B:312:PRO:HG2	1.99	0.44
1:A:352:LEU:HD12	1:A:352:LEU:N	2.33	0.44
1:D:114:HIS:HB2	1:D:116:ASP:OD1	2.18	0.44
1:C:127:ILE:HG23	1:C:131:LEU:HD12	2.00	0.44
1:D:277:MET:HB3	1:D:277:MET:HE2	1.67	0.44
1:D:419:LEU:HG	1:D:420:SER:N	2.33	0.44
1:C:361:VAL:HG12	1:C:362:SER:N	2.32	0.43
1:B:301:ILE:HG13	1:B:317:PHE:HB3	2.00	0.43
1:B:55:GLU:HB2	1:B:58:GLU:HG3	2.00	0.43
1:A:339:GLU:HA	1:A:339:GLU:OE1	2.17	0.43
1:B:97:PHE:N	1:B:97:PHE:CD1	2.86	0.43
1:C:323:HIS:CG	1:C:324:PRO:HD2	2.53	0.43
1:B:197:VAL:O	1:B:201:LEU:HG	2.19	0.43
1:D:246:VAL:HG22	1:D:393:SER:HB3	2.01	0.43
1:A:262:HIS:HB3	1:A:265:THR:CG2	2.48	0.42
1:A:277:MET:HE2	1:A:277:MET:HB3	1.66	0.42
1:A:198:TYR:CE2	1:D:293:ASN:HB2	2.53	0.42
1:B:134:LEU:HD22	1:B:138:ARG:HD3	2.01	0.42
1:C:259:VAL:H	1:C:272:LYS:HB2	1.84	0.42
1:D:89:LYS:HB3	1:D:210:THR:HG21	2.00	0.42
1:C:403:ALA:N	1:C:408:THR:HG21	2.35	0.42
1:A:51[B]:ARG:HB3	1:A:51[B]:ARG:HH11	1.84	0.42
1:B:193:LYS:HG2	1:B:193:LYS:O	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:317:PHE:CE1	1:A:319:LEU:HD21	2.54	0.42
1:A:334:LYS:HE2	1:A:334:LYS:HB3	1.79	0.42
1:A:265:THR:CG2	1:B:229:GLN:O	2.60	0.42
1:A:402:THR:OG1	1:A:408:THR:HG21	2.20	0.42
1:A:127:ILE:O	1:A:131:LEU:HB2	2.20	0.41
1:B:371:CYS:HB3	1:B:409:SER:CB	2.49	0.41
1:A:89:LYS:HB3	1:A:210:THR:HG21	2.02	0.41
1:B:193:LYS:O	1:B:193:LYS:CG	2.68	0.41
1:B:180:LEU:HD11	1:B:184:TYR:CE1	2.56	0.41
1:A:367:PHE:HB3	1:A:408:THR:O	2.20	0.41
1:D:172:SER:HA	1:D:401:GLN:NE2	2.33	0.41
1:C:133:GLY:O	1:C:136:VAL:HB	2.21	0.41
1:C:321:PHE:HD2	1:C:332:MET:HE3	1.86	0.41
1:B:128:LEU:HD22	1:B:413:ILE:HD11	2.02	0.41
1:A:420:SER:HA	1:A:425:GLU:HG3	2.02	0.41
1:A:265:THR:HG23	1:B:230:GLY:CA	2.51	0.41
1:D:22:LEU:N	1:D:22:LEU:HD22	2.32	0.41
1:A:131:LEU:HA	1:A:131:LEU:HD23	1.88	0.41
1:A:134:LEU:HD22	1:A:138:ARG:HG3	2.03	0.41
1:D:135:GLU:HA	1:D:138:ARG:HB2	2.03	0.41
1:B:118:GLN:HB2	1:B:121:ALA:HB2	2.03	0.41
1:B:137:LEU:HD11	1:B:153:VAL:HG23	2.03	0.41
1:C:224:GLU:HB3	1:C:410:MET:HG2	2.02	0.40
1:B:192:ASP:O	1:B:194:PRO:HD3	2.20	0.40
1:A:114:HIS:CE1	1:A:126:GLY:HA3	2.56	0.40
1:D:111:THR:HB	1:D:443:ILE:HD11	2.03	0.40
1:A:172:SER:HA	1:A:401:GLN:HE21	1.86	0.40
1:C:372:ILE:O	1:C:376:SER:HB3	2.21	0.40
1:C:402:THR:OG1	1:C:408:THR:HG21	2.21	0.40
1:B:294:GLY:CA	1:B:323:HIS:HD2	2.34	0.40
1:C:277:MET:HG3	1:C:352:LEU:HD22	2.04	0.40
1:B:306:TYR:HE2	1:D:21:ASN:HD21	1.69	0.40
1:A:157:PHE:CD1	1:A:201:LEU:HD21	2.56	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	434/474 (92%)	423 (98%)	11 (2%)	0	100	100
1	B	429/474 (90%)	412 (96%)	15 (4%)	2 (0%)	34	71
1	C	429/474 (90%)	412 (96%)	16 (4%)	1 (0%)	52	84
1	D	433/474 (91%)	420 (97%)	13 (3%)	0	100	100
All	All	1725/1896 (91%)	1667 (97%)	55 (3%)	3 (0%)	52	84

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	25	ALA
1	C	25	ALA
1	B	158	ASN

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	358/392 (91%)	331 (92%)	27 (8%)	17	44
1	B	354/392 (90%)	330 (93%)	24 (7%)	20	49
1	C	354/392 (90%)	329 (93%)	25 (7%)	18	47
1	D	358/392 (91%)	338 (94%)	20 (6%)	26	60
All	All	1424/1568 (91%)	1328 (93%)	96 (7%)	20	50

All (96) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	32	SER
1	A	45	GLN
1	A	51[A]	ARG
1	A	51[B]	ARG
1	A	107	LYS
1	A	113	SER
1	A	130	VAL
1	A	134	LEU
1	A	166	ARG
1	A	188	SER
1	A	192	ASP
1	A	207	ILE
1	A	210	THR
1	A	265	THR
1	A	266	THR
1	A	287	GLU
1	A	304	LYS
1	A	307	SER
1	A	309	ASN
1	A	331	THR
1	A	334	LYS
1	A	348	ASP
1	A	356	SER
1	A	361	VAL
1	A	377	ARG
1	A	408	THR
1	A	430	GLU
1	B	54	GLN
1	B	113	SER
1	B	130	VAL
1	B	134	LEU
1	B	166	ARG
1	B	167	SER
1	B	179	SER
1	B	181	GLU
1	B	193	LYS
1	B	210	THR
1	B	228	GLU
1	B	250	ASN
1	B	265	THR
1	B	286	SER
1	B	309	ASN
1	B	334	LYS

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Mol	Chain	Res	Type
1	B	357	GLU
1	B	376	SER
1	B	377	ARG
1	B	390	GLN
1	B	408	THR
1	B	417	ASP
1	B	419	LEU
1	B	430	GLU
1	C	29	SER
1	C	54	GLN
1	C	90	VAL
1	C	113	SER
1	C	130	VAL
1	C	134	LEU
1	C	166	ARG
1	C	193	LYS
1	C	196	SER
1	C	210	THR
1	C	250	ASN
1	C	277	MET
1	C	293	ASN
1	C	325	SER
1	C	334	LYS
1	C	357	GLU
1	C	369	GLU
1	C	376	SER
1	C	377	ARG
1	C	408	THR
1	C	417	ASP
1	C	419	LEU
1	C	430	GLU
1	C	433	GLU
1	C	452	ILE
1	D	22	LEU
1	D	83	SER
1	D	130	VAL
1	D	134	LEU
1	D	166	ARG
1	D	179	SER
1	D	192	ASP
1	D	210	THR
1	D	216	GLU

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Mol	Chain	Res	Type
1	D	266	THR
1	D	269	ARG
1	D	287	GLU
1	D	304	LYS
1	D	331	THR
1	D	334	LYS
1	D	348	ASP
1	D	376	SER
1	D	377	ARG
1	D	408	THR
1	D	430	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (29) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	21	ASN
1	A	54	GLN
1	A	57	HIS
1	A	143	ASN
1	A	158	ASN
1	A	247	GLN
1	A	309	ASN
1	A	390	GLN
1	A	401	GLN
1	A	445	ASN
1	B	54	GLN
1	B	203	ASN
1	B	250	ASN
1	B	309	ASN
1	B	401	GLN
1	C	54	GLN
1	C	203	ASN
1	C	250	ASN
1	C	366	ASN
1	C	405	HIS
1	C	445	ASN
1	D	57	HIS
1	D	158	ASN
1	D	217	ASN
1	D	250	ASN
1	D	397	HIS
1	D	401	GLN

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Mol	Chain	Res	Type
1	D	405	HIS
1	D	445	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 12 ligands modelled in this entry, 8 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	URP	B	1456	-	5,8,8	0.53	0	6,9,9	0.77	0
4	DTT	C	1456	1	7,7,7	0.45	0	4,8,8	1.74	1 (25%)
3	URP	C	1457	-	5,8,8	0.62	0	6,9,9	1.33	1 (16%)
3	URP	D	1456	-	5,8,8	0.58	0	6,9,9	1.42	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	URP	B	1456	-	-	0/4/6/6	0/0/0/0
4	DTT	C	1456	1	-	0/8/8/8	0/0/0/0
3	URP	C	1457	-	-	0/4/6/6	0/0/0/0
3	URP	D	1456	-	-	0/4/6/6	0/0/0/0

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	C	1456	DTT	C2-C1-S1	-2.90	109.09	113.91
3	C	1457	URP	N3-C2-N1	2.15	118.79	116.17
3	D	1456	URP	N3-C2-N1	2.32	119.01	116.17

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	1457	URP	2	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, 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	435/474 (91%)	-0.33	1 (0%) 95 95	30, 36, 39, 42	0
1	B	431/474 (90%)	-0.09	4 (0%) 85 84	30, 36, 38, 42	0
1	C	431/474 (90%)	-0.08	9 (2%) 67 62	30, 36, 39, 41	0
1	D	435/474 (91%)	-0.31	0 100 100	30, 36, 39, 43	0
All	All	1732/1896 (91%)	-0.20	14 (0%) 87 86	30, 36, 39, 43	0

All (14) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	105	GLY	4.4
1	B	190	GLY	3.9
1	C	192	ASP	3.1
1	A	105	GLY	2.8
1	B	50	ALA	2.5
1	B	52	TRP	2.4
1	C	50	ALA	2.4
1	C	190	GLY	2.4
1	B	56	SER	2.4
1	C	24	ALA	2.3
1	C	54	GLN	2.3
1	C	52	TRP	2.2
1	C	56	SER	2.2
1	C	23	PRO	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 [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, 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	LLDF	B-factors(\AA^2)	Q<0.9
3	URP	C	1457	9/9	0.90	0.31	4.43	52,56,63,64	0
3	URP	D	1456	9/9	0.93	0.27	2.52	75,76,77,78	0
3	URP	B	1456	9/9	0.94	0.21	0.87	46,49,50,51	0
4	DTT	C	1456	8/8	0.91	0.17	0.04	54,62,64,67	0
2	ZN	D	1454	1/1	1.00	0.05	-2.33	29,29,29,29	0
2	ZN	A	1455	1/1	0.99	0.04	-2.63	29,29,29,29	0
2	ZN	B	1454	1/1	0.99	0.03	-2.73	36,36,36,36	0
2	ZN	A	1456	1/1	0.98	0.03	-2.87	35,35,35,35	0
2	ZN	B	1455	1/1	0.99	0.03	-2.91	38,38,38,38	0
2	ZN	D	1455	1/1	0.99	0.02	-4.13	33,33,33,33	0
2	ZN	C	1454	1/1	0.99	0.02	-4.61	34,34,34,34	0
2	ZN	C	1455	1/1	0.94	0.04	-4.73	36,36,36,36	0

6.5 Other polymers [i](#)

There are no such residues in this entry.