



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 25, 2026 – 04:31 PM EDT

PDB ID : 4GRS / pdb_00004grs
Title : Crystal structure of a chimeric DAH7PS
Authors : Cross, P.J.; Allison, T.M.; Dobson, R.C.J.; Jameson, G.B.; Parker, E.J.
Deposited on : 2012-08-26
Resolution : 3.00 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

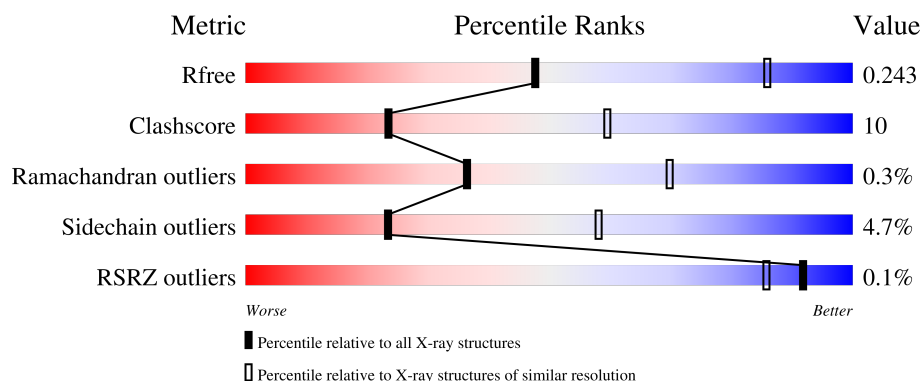
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 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	2672 (3.00-3.00)
Clashscore	190562	2977 (3.00-3.00)
Ramachandran outliers	187476	2877 (3.00-3.00)
Sidechain outliers	187428	2880 (3.00-3.00)
RSRZ outliers	180081	2671 (3.00-3.00)

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	333	78% 20% .
1	B	333	82% 17% .
1	C	333	79% 18% .
1	D	333	79% 19% ..

2 Entry composition [i](#)

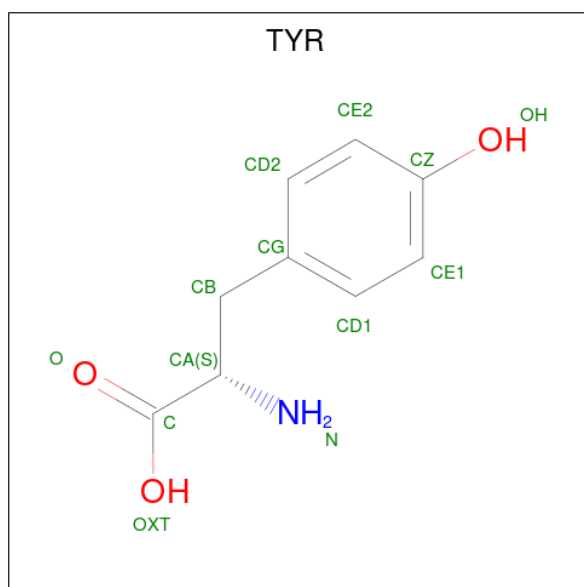
There are 3 unique types of molecules in this entry. The entry contains 10092 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Phospho-2-dehydro-3-deoxyheptonate aldolase, 2-dehydro-3-deoxyphosphoheptonate aldolase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	333	Total	C	N	O	S	0	0	0
			2533	1614	427	481	11			
1	B	333	Total	C	N	O	S	0	0	0
			2510	1600	422	477	11			
1	C	332	Total	C	N	O	S	0	0	0
			2474	1575	413	475	11			
1	D	331	Total	C	N	O	S	0	0	0
			2502	1595	419	477	11			

- Molecule 2 is TYROSINE (CCD ID: TYR) (formula: C₉H₁₁NO₃).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			13	9	1	3		
2	A	1	Total	C	N	O	0	0
			13	9	1	3		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	B	1	Total	C	N	O	0	0
			13	9	1	3		
2	D	1	Total	C	N	O	0	0
			13	9	1	3		

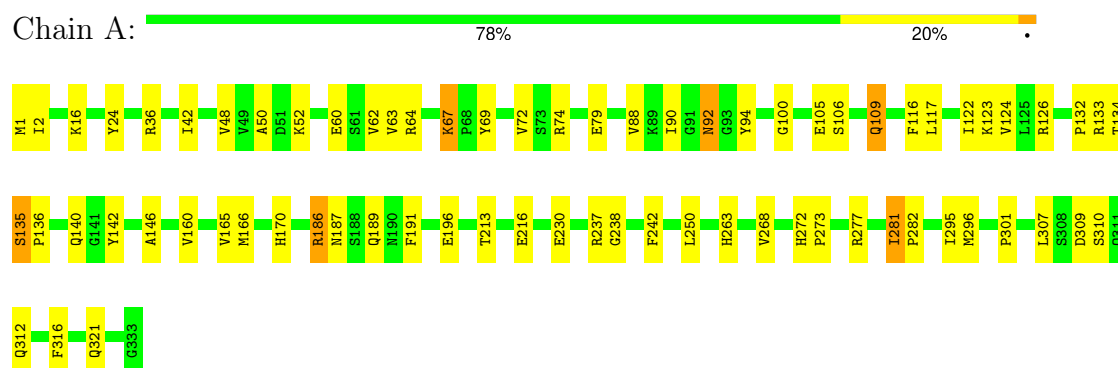
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	6	Total	O	0	0
			6	6		
3	B	7	Total	O	0	0
			7	7		
3	C	6	Total	O	0	0
			6	6		
3	D	2	Total	O	0	0
			2	2		

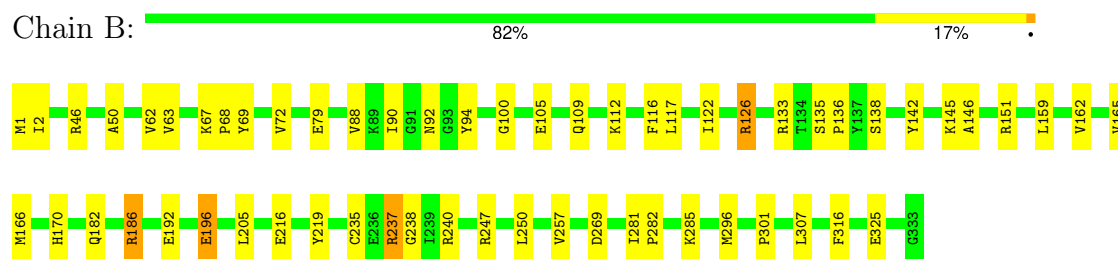
3 Residue-property plots

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.

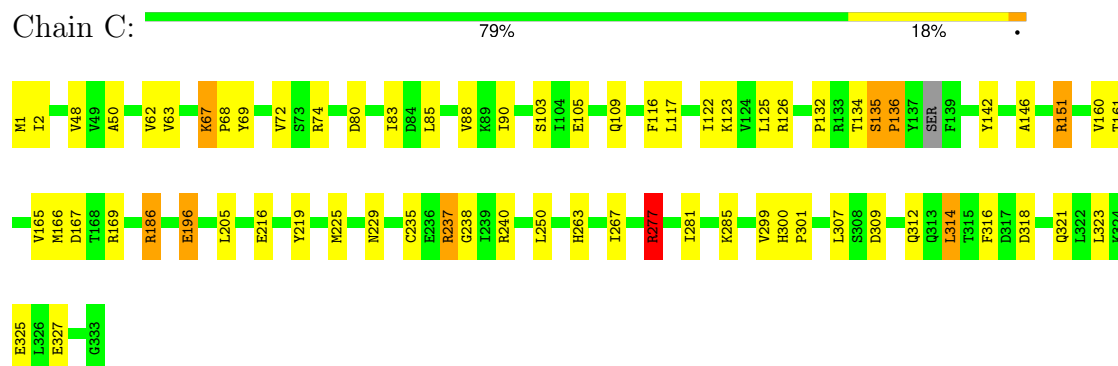
- Molecule 1: Phospho-2-dehydro-3-deoxyheptonate aldolase, 2-dehydro-3-deoxyphosphoheptona te aldolase



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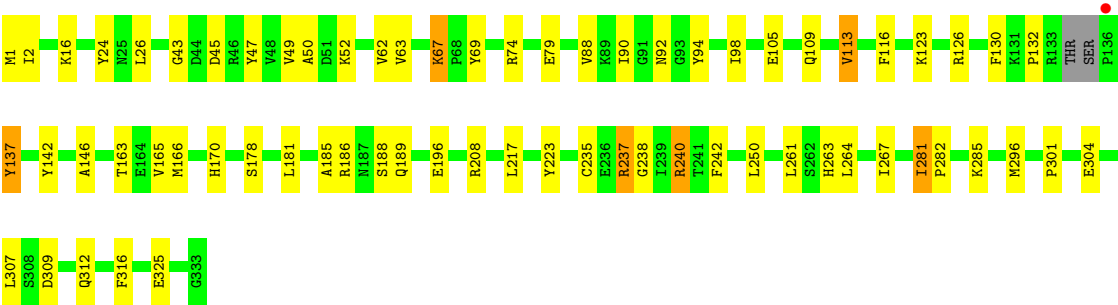
● Molecule 1: Phospho-2-dehydro-3-deoxyheptonate aldolase, 2-dehydro-3-deoxyphosphoheptona te aldolase

Chain D:

79%

19%

..



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	76.90Å 130.85Å 138.07Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	37.94 – 3.00 37.94 – 3.00	Depositor EDS
% Data completeness (in resolution range)	94.5 (37.94-3.00) 94.5 (37.94-3.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.10	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.81 (at 3.01Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.192 , 0.248 0.189 , 0.243	Depositor DCC
R_{free} test set	1431 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	67.5	Xtriage
Anisotropy	0.200	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 56.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	10092	wwPDB-VP
Average B, all atoms (Å ²)	81.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.18% 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 [i](#)

5.1 Standard geometry [i](#)

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.59	0/2576	0.90	3/3497 (0.1%)
1	B	0.58	0/2552	0.88	3/3467 (0.1%)
1	C	0.60	0/2514	0.93	7/3422 (0.2%)
1	D	0.60	0/2544	0.89	4/3455 (0.1%)
All	All	0.59	0/10186	0.90	17/13841 (0.1%)

There are no bond length outliers.

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	135	SER	CA-C-N	7.79	129.57	119.84
1	C	135	SER	C-N-CA	7.79	129.57	119.84
1	D	67	LYS	CA-C-N	7.62	127.66	119.28
1	D	67	LYS	C-N-CA	7.62	127.66	119.28
1	B	67	LYS	CA-C-N	7.25	127.59	119.32
1	B	67	LYS	C-N-CA	7.25	127.59	119.32
1	A	67	LYS	CA-C-N	6.49	126.42	119.28
1	A	67	LYS	C-N-CA	6.49	126.42	119.28
1	C	67	LYS	CA-C-N	6.18	126.08	119.28
1	C	67	LYS	C-N-CA	6.18	126.08	119.28
1	D	137	TYR	N-CA-C	-5.56	107.74	114.75
1	D	49	VAL	N-CA-C	5.46	117.18	108.89
1	C	277	ARG	NE-CZ-NH2	5.44	124.09	119.20
1	C	300	HIS	CA-C-N	5.19	124.37	118.97
1	C	300	HIS	C-N-CA	5.19	124.37	118.97
1	A	140	GLN	N-CA-C	5.11	118.77	112.54
1	B	257	VAL	CG1-CB-CG2	-5.04	99.72	110.80

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	2533	0	2519	65	0
1	B	2510	0	2484	45	0
1	C	2474	0	2402	53	0
1	D	2502	0	2462	61	0
2	A	26	0	16	1	0
2	B	13	0	8	0	0
2	D	13	0	8	0	0
3	A	6	0	0	2	0
3	B	7	0	0	0	0
3	C	6	0	0	0	0
3	D	2	0	0	0	0
All	All	10092	0	9899	203	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 10.

All (203) 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:166:MET:HE2	1:D:186:ARG:HH21	1.26	1.01
1:D:166:MET:CE	1:D:186:ARG:HH21	1.76	0.97
1:C:196:GLU:HA	1:C:196:GLU:OE1	1.69	0.93
1:A:186:ARG:NH2	1:D:189:GLN:O	2.02	0.93
1:A:134:THR:O	1:D:223:TYR:CD1	2.22	0.92
1:B:105:GLU:H	1:B:109:GLN:HE21	1.19	0.91
1:A:135:SER:H	1:A:136:PRO:CD	1.84	0.90
1:C:277:ARG:HB2	1:C:277:ARG:HH21	1.39	0.88
1:D:1:MET:HE2	1:D:62:VAL:HG11	1.56	0.84
1:A:1:MET:HE2	1:A:62:VAL:HG11	1.64	0.80
1:A:135:SER:H	1:A:136:PRO:HD3	1.45	0.80
1:D:105:GLU:H	1:D:109:GLN:HE21	1.30	0.79
1:B:301:PRO:HA	1:B:316:PHE:CE1	2.18	0.78
1:A:105:GLU:H	1:A:109:GLN:HE21	1.29	0.77
1:D:166:MET:HE2	1:D:186:ARG:NH2	2.00	0.76
1:D:24:TYR:OH	1:D:52:LYS:HG3	1.86	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:133:ARG:CB	1:B:138:SER:HB2	2.17	0.74
1:A:135:SER:N	1:A:136:PRO:CD	2.49	0.73
1:A:301:PRO:HA	1:A:316:PHE:CE1	2.23	0.72
1:C:105:GLU:H	1:C:109:GLN:HE21	1.39	0.70
1:B:301:PRO:CA	1:B:316:PHE:HE1	2.05	0.70
1:D:301:PRO:HA	1:D:316:PHE:CE1	2.27	0.69
1:A:189:GLN:O	1:D:186:ARG:NH1	2.26	0.69
1:B:196:GLU:HA	1:B:196:GLU:OE1	1.92	0.68
1:B:196:GLU:CD	1:C:169:ARG:HH22	2.03	0.67
1:B:196:GLU:OE2	1:C:169:ARG:NH2	2.28	0.67
1:B:105:GLU:N	1:B:109:GLN:HE21	1.91	0.66
1:B:1:MET:HE2	1:B:62:VAL:HG11	1.79	0.65
1:D:1:MET:HE1	1:D:50:ALA:HA	1.76	0.64
1:C:74:ARG:NH2	1:C:263:HIS:HA	2.14	0.63
1:A:191:PHE:H	1:D:186:ARG:HH12	1.47	0.62
1:A:281:ILE:HD12	1:A:281:ILE:H	1.65	0.60
1:B:69:TYR:HB2	1:B:72:VAL:HG22	1.83	0.60
1:D:281:ILE:HB	1:D:282:PRO:HD3	1.82	0.59
1:A:136:PRO:HB3	1:D:47:TYR:CD1	2.37	0.59
1:C:301:PRO:HA	1:C:316:PHE:CE1	2.37	0.59
1:C:88:VAL:CG2	1:C:123:LYS:CB	2.81	0.59
1:D:109:GLN:O	1:D:113:VAL:HG23	2.03	0.58
1:A:2:ILE:HD13	1:C:2:ILE:HD13	1.84	0.58
1:A:105:GLU:HB2	1:A:109:GLN:HG3	1.85	0.58
1:A:48:VAL:O	1:A:64:ARG:NH2	2.36	0.57
1:C:88:VAL:CG2	1:C:123:LYS:HB3	2.35	0.57
1:D:88:VAL:CG2	1:D:123:LYS:HB2	2.34	0.57
1:A:24:TYR:OH	1:A:52:LYS:HG3	2.05	0.56
1:A:301:PRO:CA	1:A:316:PHE:HE1	2.19	0.56
1:B:301:PRO:HA	1:B:316:PHE:CD1	2.40	0.56
1:A:1:MET:HE1	1:A:50:ALA:HA	1.86	0.56
1:D:105:GLU:N	1:D:109:GLN:HE21	2.03	0.55
1:C:85:LEU:HD23	1:C:160:VAL:HG21	1.88	0.55
1:D:88:VAL:CG2	1:D:123:LYS:CB	2.84	0.55
1:A:88:VAL:CG2	1:A:123:LYS:CB	2.85	0.55
1:C:323:LEU:O	1:C:327:GLU:HG2	2.07	0.54
1:D:301:PRO:CA	1:D:316:PHE:HE1	2.19	0.54
1:A:105:GLU:N	1:A:109:GLN:HE21	2.03	0.54
1:A:186:ARG:NH2	1:A:186:ARG:HG3	2.23	0.54
1:A:166:MET:HE2	1:A:186:ARG:HH11	1.73	0.54
1:A:135:SER:H	1:A:136:PRO:HD2	1.71	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:301:PRO:CA	1:B:316:PHE:CE1	2.84	0.53
1:A:135:SER:N	1:A:136:PRO:HD2	2.22	0.53
1:D:301:PRO:CA	1:D:316:PHE:CE1	2.92	0.53
1:B:238:GLY:HA2	1:B:250:LEU:HA	1.91	0.53
1:C:69:TYR:HB2	1:C:72:VAL:HG22	1.91	0.52
1:D:301:PRO:HA	1:D:316:PHE:CD1	2.44	0.52
1:C:238:GLY:HA2	1:C:250:LEU:HA	1.91	0.52
1:A:106:SER:OG	1:A:109:GLN:HB2	2.09	0.52
1:A:134:THR:O	1:D:223:TYR:CE1	2.61	0.52
1:B:281:ILE:H	1:B:281:ILE:HD12	1.74	0.52
1:D:166:MET:CE	1:D:186:ARG:NH2	2.59	0.52
1:D:116:PHE:HB2	1:D:316:PHE:HE2	1.76	0.51
1:A:166:MET:H	1:A:170:HIS:HE1	1.57	0.51
1:A:105:GLU:H	1:A:109:GLN:NE2	2.04	0.51
1:A:186:ARG:HG3	1:A:186:ARG:HH21	1.76	0.51
1:A:88:VAL:CG2	1:A:123:LYS:HB3	2.42	0.50
1:A:67:LYS:HD3	1:A:69:TYR:OH	2.12	0.50
1:A:126:ARG:NH2	3:A:501:HOH:O	2.45	0.50
1:C:281:ILE:H	1:C:281:ILE:HD12	1.77	0.50
1:B:63:VAL:HG21	1:D:63:VAL:HG11	1.92	0.50
1:C:88:VAL:CG2	1:C:123:LYS:HB2	2.42	0.50
1:D:196:GLU:HA	1:D:196:GLU:OE1	2.10	0.50
1:B:281:ILE:HB	1:B:282:PRO:HD3	1.94	0.50
1:B:135:SER:HB2	1:B:136:PRO:HD2	1.93	0.49
1:A:133:ARG:CB	1:A:136:PRO:HG2	2.43	0.49
1:D:1:MET:HE2	1:D:62:VAL:CG1	2.35	0.49
1:A:88:VAL:CG2	1:A:123:LYS:HB2	2.43	0.49
1:B:1:MET:HE1	1:B:50:ALA:HA	1.94	0.49
1:D:69:TYR:OH	1:D:261:LEU:HD12	2.12	0.49
1:B:2:ILE:HD13	1:D:2:ILE:HD13	1.94	0.49
1:C:1:MET:HE2	1:C:62:VAL:HG11	1.95	0.49
1:C:105:GLU:N	1:C:109:GLN:HE21	2.06	0.49
1:A:63:VAL:HG11	1:C:63:VAL:HG21	1.95	0.49
1:C:74:ARG:NH1	1:C:80:ASP:OD1	2.42	0.49
1:D:142:TYR:HB2	1:D:146:ALA:HB2	1.93	0.49
1:A:242:PHE:CG	1:C:240:ARG:HG2	2.48	0.48
1:A:301:PRO:HA	1:A:316:PHE:CD1	2.48	0.48
1:B:117:LEU:HB3	1:B:122:ILE:HB	1.95	0.48
1:D:238:GLY:HA2	1:D:250:LEU:HA	1.95	0.48
1:C:277:ARG:HH21	1:C:277:ARG:CB	2.19	0.47
1:A:117:LEU:HB3	1:A:122:ILE:HB	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:166:MET:CE	1:A:186:ARG:HH11	2.27	0.47
1:B:182:GLN:OE1	1:B:296:MET:HE1	2.15	0.47
1:D:237:ARG:C	1:D:237:ARG:HD3	2.39	0.47
1:A:196:GLU:OE1	1:A:196:GLU:HA	2.14	0.47
1:A:277:ARG:NH2	1:A:310:SER:O	2.48	0.47
1:B:240:ARG:HG2	1:D:242:PHE:CB	2.45	0.47
1:C:116:PHE:CG	1:C:316:PHE:CD2	3.02	0.47
1:C:132:PRO:HA	1:C:166:MET:HE1	1.95	0.47
1:D:26:LEU:HD22	1:D:43:GLY:HA3	1.96	0.47
1:A:301:PRO:CA	1:A:316:PHE:CE1	2.92	0.46
1:C:105:GLU:HB2	1:C:109:GLN:HG2	1.97	0.46
1:C:117:LEU:HB3	1:C:122:ILE:HB	1.96	0.46
1:D:1:MET:HB2	1:D:45:ASP:OD2	2.15	0.46
1:A:74:ARG:NH2	1:A:263:HIS:HA	2.31	0.46
1:C:196:GLU:OE1	1:C:196:GLU:CA	2.53	0.46
1:A:142:TYR:HB2	1:A:146:ALA:HB2	1.98	0.46
1:C:235:CYS:HA	1:C:267:ILE:O	2.15	0.46
1:A:69:TYR:HB2	1:A:72:VAL:HG22	1.97	0.46
1:B:205:LEU:HD11	1:B:235:CYS:HB2	1.96	0.46
1:A:216:GLU:OE1	1:D:240:ARG:NH1	2.49	0.46
1:C:314:LEU:HG	1:C:318:ASP:HB3	1.97	0.46
1:B:79:GLU:H	1:B:79:GLU:CD	2.24	0.46
1:D:67:LYS:HD3	1:D:69:TYR:OH	2.15	0.46
1:A:242:PHE:CB	1:C:240:ARG:HG2	2.45	0.45
1:B:240:ARG:HH12	1:C:216:GLU:CD	2.25	0.45
1:B:92:ASN:C	1:B:94:TYR:H	2.23	0.45
1:A:124:VAL:HG13	1:A:160:VAL:HG23	1.98	0.45
1:B:240:ARG:HG2	1:D:242:PHE:CG	2.51	0.45
1:B:116:PHE:CG	1:B:316:PHE:CD2	3.04	0.45
1:C:88:VAL:HG22	1:C:123:LYS:CB	2.46	0.45
1:C:186:ARG:H	1:C:186:ARG:HG2	1.57	0.45
1:D:88:VAL:HG22	1:D:123:LYS:HB2	1.98	0.45
1:B:237:ARG:HD3	1:B:237:ARG:C	2.41	0.45
1:A:100:GLY:HA3	1:A:126:ARG:HG3	1.98	0.44
1:A:238:GLY:HA2	1:A:250:LEU:HA	1.99	0.44
1:C:301:PRO:CA	1:C:316:PHE:CE1	3.00	0.44
1:C:125:LEU:O	1:C:161:THR:HA	2.17	0.44
1:D:309:ASP:HB3	1:D:312:GLN:HG2	1.99	0.44
1:B:166:MET:H	1:B:170:HIS:HE1	1.64	0.44
1:C:285:LYS:HD3	1:C:325:GLU:HB3	1.99	0.44
1:A:42:ILE:HA	2:A:401:TYR:O	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:92:ASN:O	1:D:92:ASN:CG	2.61	0.44
1:A:36:ARG:HH12	1:A:60:GLU:CD	2.26	0.44
1:A:166:MET:H	1:A:170:HIS:CE1	2.35	0.44
1:B:151:ARG:HE	1:B:151:ARG:HA	1.83	0.44
1:C:1:MET:HE1	1:C:50:ALA:HA	2.00	0.44
1:D:16:LYS:HA	1:D:16:LYS:HD2	1.89	0.44
1:D:166:MET:H	1:D:170:HIS:HE1	1.66	0.44
1:B:68:PRO:CB	1:B:219:TYR:OH	2.66	0.43
1:D:88:VAL:HG21	1:D:123:LYS:HB2	1.99	0.43
1:B:142:TYR:HB2	1:B:146:ALA:HB2	2.00	0.43
1:C:116:PHE:HB2	1:C:316:PHE:HE2	1.83	0.43
1:C:309:ASP:HB3	1:C:312:GLN:HG2	1.99	0.43
1:B:285:LYS:HD3	1:B:325:GLU:HB3	2.01	0.43
1:C:68:PRO:HB2	1:C:219:TYR:CE1	2.54	0.43
1:B:116:PHE:HB2	1:B:316:PHE:HE2	1.83	0.43
1:D:185:ALA:O	1:D:188:SER:HB2	2.19	0.43
1:D:304:GLU:H	1:D:304:GLU:CD	2.26	0.43
1:C:142:TYR:HB2	1:C:146:ALA:HB2	2.01	0.43
1:D:116:PHE:CG	1:D:316:PHE:CD2	3.05	0.43
1:D:163:THR:HG22	1:D:178:SER:CB	2.48	0.43
1:C:205:LEU:HD11	1:C:235:CYS:HB2	1.99	0.43
1:A:281:ILE:HD12	1:A:281:ILE:N	2.32	0.43
1:A:116:PHE:HB2	1:A:316:PHE:HE2	1.83	0.42
1:A:268:VAL:O	1:A:295:ILE:HA	2.18	0.42
1:C:237:ARG:C	1:C:237:ARG:HD3	2.44	0.42
1:C:67:LYS:HD3	1:C:69:TYR:OH	2.19	0.42
1:C:83:ILE:HG22	1:C:85:LEU:CD1	2.49	0.42
1:D:285:LYS:HD3	1:D:325:GLU:HB3	1.99	0.42
1:A:79:GLU:H	1:A:79:GLU:CD	2.27	0.42
1:B:105:GLU:HB2	1:B:109:GLN:HG2	2.00	0.42
1:C:225:MET:HA	1:C:229:ASN:O	2.19	0.42
1:D:92:ASN:C	1:D:94:TYR:H	2.27	0.42
1:B:63:VAL:HG11	1:D:63:VAL:HG21	2.00	0.42
1:B:112:LYS:HB2	1:B:112:LYS:HE3	1.92	0.42
1:A:116:PHE:CG	1:A:316:PHE:CD2	3.08	0.42
1:B:216:GLU:CD	1:C:240:ARG:HH12	2.27	0.42
1:C:167:ASP:OD1	1:C:169:ARG:HD2	2.19	0.42
1:C:151:ARG:HA	1:C:151:ARG:HD3	1.43	0.42
1:D:79:GLU:H	1:D:79:GLU:CD	2.28	0.42
1:A:281:ILE:HB	1:A:282:PRO:HD3	2.01	0.42
1:D:88:VAL:CG2	1:D:123:LYS:HB3	2.50	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:116:PHE:CB	1:B:316:PHE:HE2	2.33	0.42
1:B:186:ARG:H	1:B:186:ARG:HG2	1.56	0.41
1:D:98:ILE:O	1:D:296:MET:HA	2.19	0.41
1:B:192:GLU:HG2	1:C:167:ASP:HB2	2.02	0.41
1:A:309:ASP:HB3	1:A:312:GLN:HG2	2.03	0.41
1:D:208:ARG:HB2	1:D:217:LEU:HD13	2.01	0.41
1:C:88:VAL:HG22	1:C:123:LYS:HB2	2.02	0.41
1:D:105:GLU:HB2	1:D:109:GLN:HG2	2.03	0.41
1:A:126:ARG:HD2	1:A:296:MET:HE2	2.03	0.41
1:C:116:PHE:CB	1:C:316:PHE:CE2	3.04	0.41
1:D:116:PHE:CB	1:D:316:PHE:CE2	3.04	0.41
1:A:213:THR:HB	3:A:504:HOH:O	2.20	0.41
1:D:130:PHE:CD1	1:D:130:PHE:N	2.88	0.41
1:D:264:LEU:HD23	1:D:264:LEU:HA	1.94	0.41
1:B:1:MET:CE	1:B:50:ALA:HA	2.50	0.41
1:D:74:ARG:NH2	1:D:263:HIS:HA	2.35	0.40
1:D:235:CYS:HA	1:D:267:ILE:O	2.21	0.40
1:A:186:ARG:HG2	1:A:187:ASN:N	2.36	0.40
1:C:135:SER:HA	1:C:136:PRO:HD2	1.77	0.40
1:A:272:HIS:N	1:A:273:PRO:HD2	2.36	0.40
1:B:100:GLY:HA3	1:B:126:ARG:O	2.22	0.40
1:B:269:ASP:OD1	1:B:269:ASP:C	2.64	0.40
1:A:92:ASN:C	1:A:94:TYR:H	2.30	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	331/333 (99%)	316 (96%)	13 (4%)	2 (1%)	21 56
1	B	331/333 (99%)	317 (96%)	14 (4%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	328/333 (98%)	313 (95%)	14 (4%)	1 (0%)	36	70
1	D	327/333 (98%)	311 (95%)	15 (5%)	1 (0%)	36	70
All	All	1317/1332 (99%)	1257 (95%)	56 (4%)	4 (0%)	36	70

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	132	PRO
1	A	132	PRO
1	A	135	SER
1	C	136	PRO

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	267/285 (94%)	256 (96%)	11 (4%)	27	61
1	B	262/285 (92%)	249 (95%)	13 (5%)	22	56
1	C	253/285 (89%)	238 (94%)	15 (6%)	18	50
1	D	261/285 (92%)	251 (96%)	10 (4%)	29	63
All	All	1043/1140 (92%)	994 (95%)	49 (5%)	23	58

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

Mol	Chain	Res	Type
1	A	16	LYS
1	A	90	ILE
1	A	92	ASN
1	A	109	GLN
1	A	165	VAL
1	A	186	ARG
1	A	230	GLU
1	A	237	ARG

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Mol	Chain	Res	Type
1	A	281	ILE
1	A	307	LEU
1	A	321	GLN
1	B	46	ARG
1	B	88	VAL
1	B	90	ILE
1	B	126	ARG
1	B	145	LYS
1	B	159	LEU
1	B	162	VAL
1	B	165	VAL
1	B	186	ARG
1	B	196	GLU
1	B	237	ARG
1	B	247	ARG
1	B	307	LEU
1	C	48	VAL
1	C	90	ILE
1	C	103	SER
1	C	126	ARG
1	C	134	THR
1	C	151	ARG
1	C	165	VAL
1	C	186	ARG
1	C	196	GLU
1	C	237	ARG
1	C	277	ARG
1	C	299	VAL
1	C	307	LEU
1	C	314	LEU
1	C	321	GLN
1	D	90	ILE
1	D	113	VAL
1	D	126	ARG
1	D	137	TYR
1	D	165	VAL
1	D	181	LEU
1	D	237	ARG
1	D	240	ARG
1	D	281	ILE
1	D	307	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18)

such sidechains are listed below:

Mol	Chain	Res	Type
1	A	92	ASN
1	A	109	GLN
1	A	170	HIS
1	A	212	ASN
1	A	231	ASN
1	B	109	GLN
1	B	212	ASN
1	B	231	ASN
1	B	312	GLN
1	C	109	GLN
1	C	189	GLN
1	C	212	ASN
1	C	231	ASN
1	C	312	GLN
1	C	321	GLN
1	D	109	GLN
1	D	170	HIS
1	D	212	ASN

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 oligosaccharides 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	TYR	A	401	-	12,13,13	0.77	1 (8%)	13,17,17	0.81	1 (7%)
2	TYR	B	401	-	12,13,13	0.68	0	13,17,17	0.77	1 (7%)
2	TYR	D	401	-	12,13,13	0.78	1 (8%)	13,17,17	0.73	1 (7%)
2	TYR	A	402	-	12,13,13	0.72	1 (8%)	13,17,17	0.83	1 (7%)

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	TYR	A	401	-	-	2/8/8/8	0/1/1/1
2	TYR	B	401	-	-	0/8/8/8	0/1/1/1
2	TYR	D	401	-	-	1/8/8/8	0/1/1/1
2	TYR	A	402	-	-	1/8/8/8	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	401	TYR	OXT-C	-2.20	1.23	1.30
2	A	402	TYR	OXT-C	-2.15	1.23	1.30
2	A	401	TYR	OXT-C	-2.00	1.24	1.30

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	402	TYR	OXT-C-O	-2.86	117.58	124.08
2	A	401	TYR	OXT-C-O	-2.77	117.80	124.08
2	B	401	TYR	OXT-C-O	-2.54	118.31	124.08
2	D	401	TYR	OXT-C-O	-2.54	118.31	124.08

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	401	TYR	OXT-C-CA-N
2	A	402	TYR	OXT-C-CA-N

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Mol	Chain	Res	Type	Atoms
2	A	401	TYR	O-C-CA-N
2	D	401	TYR	O-C-CA-N

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	401	TYR	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	333/333 (100%)	-0.63	0	100	100	37, 75, 126, 167	0
1	B	333/333 (100%)	-0.52	0	100	100	39, 80, 127, 165	0
1	C	332/333 (99%)	-0.44	0	100	100	35, 79, 173, 221	0
1	D	331/333 (99%)	-0.61	1 (0%)	90	79	33, 76, 115, 166	0
All	All	1329/1332 (99%)	-0.55	1 (0%)	92	86	33, 77, 139, 221	0

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	136	PRO	2.6

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 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
2	TYR	A	402	13/13	0.91	0.08	68,70,86,89	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	TYR	A	401	13/13	0.94	0.06	57,66,74,76	0
2	TYR	B	401	13/13	0.94	0.06	52,59,69,69	0
2	TYR	D	401	13/13	0.95	0.06	45,61,70,73	0

6.5 Other polymers [i](#)

There are no such residues in this entry.