



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 20, 2026 – 08:21 AM UTC

PDB ID : 5UYY / pdb_00005uyy
Title : Crystal structure of prephenate dehydrogenase tyrA from Bacillus anthracis in complex with L-tyrosine
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Deposited on : 2017-02-24
Resolution : 2.60 Å(reported)

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

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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

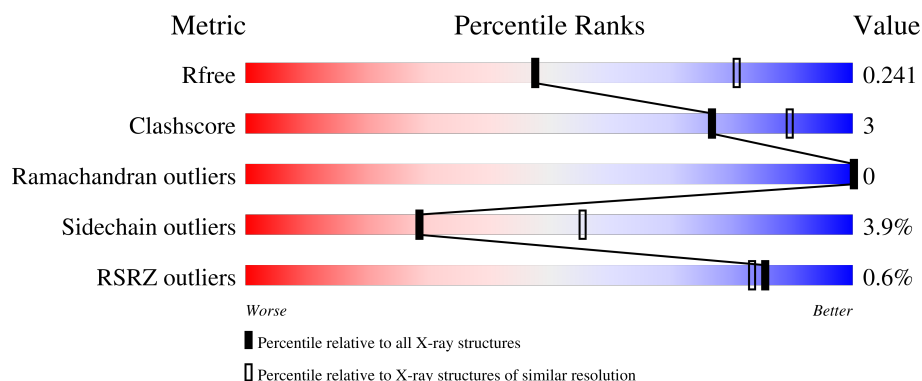
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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	4008 (2.60-2.60)
Clashscore	190562	4347 (2.60-2.60)
Ramachandran outliers	187476	4277 (2.60-2.60)
Sidechain outliers	187428	4277 (2.60-2.60)
RSRZ outliers	180081	4008 (2.60-2.60)

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	381	
1	B	381	
1	C	381	
1	D	381	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 11890 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.

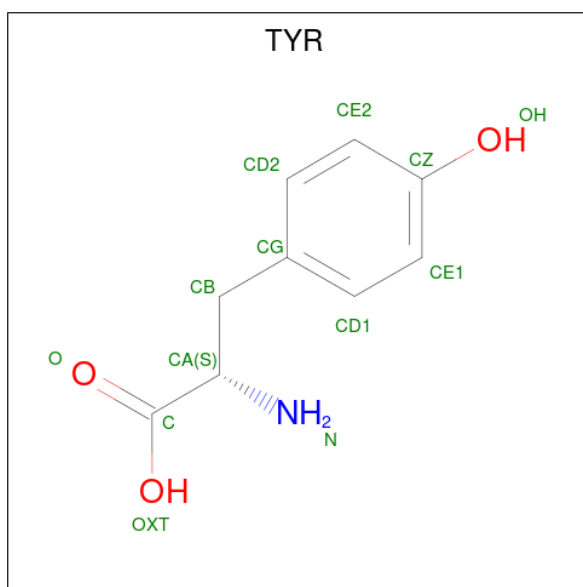
- Molecule 1 is a protein called Prephenate dehydrogenase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	373	Total	C	N	O	S	0	0	0
			2881	1831	490	550	10			
1	B	365	Total	C	N	O	S	0	0	0
			2792	1777	484	523	8			
1	C	373	Total	C	N	O	S	0	0	0
			2876	1829	493	544	10			
1	D	365	Total	C	N	O	S	0	0	0
			2783	1773	478	524	8			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	SER	-	expression tag	UNP Q81P63
A	-1	ASN	-	expression tag	UNP Q81P63
A	0	ALA	-	expression tag	UNP Q81P63
B	-2	SER	-	expression tag	UNP Q81P63
B	-1	ASN	-	expression tag	UNP Q81P63
B	0	ALA	-	expression tag	UNP Q81P63
C	-2	SER	-	expression tag	UNP Q81P63
C	-1	ASN	-	expression tag	UNP Q81P63
C	0	ALA	-	expression tag	UNP Q81P63
D	-2	SER	-	expression tag	UNP Q81P63
D	-1	ASN	-	expression tag	UNP Q81P63
D	0	ALA	-	expression tag	UNP Q81P63

- 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	B	1	Total	C	N	O	0	0
			13	9	1	3		
2	C	1	Total	C	N	O	0	0
			13	9	1	3		
2	D	1	Total	C	N	O	0	0
			13	9	1	3		

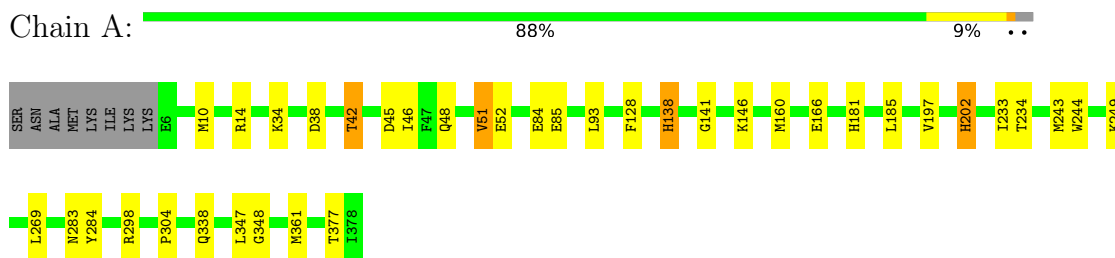
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	117	Total	O	0	0
			117	117		
3	B	113	Total	O	0	0
			113	113		
3	C	178	Total	O	0	0
			178	178		
3	D	98	Total	O	0	0
			98	98		

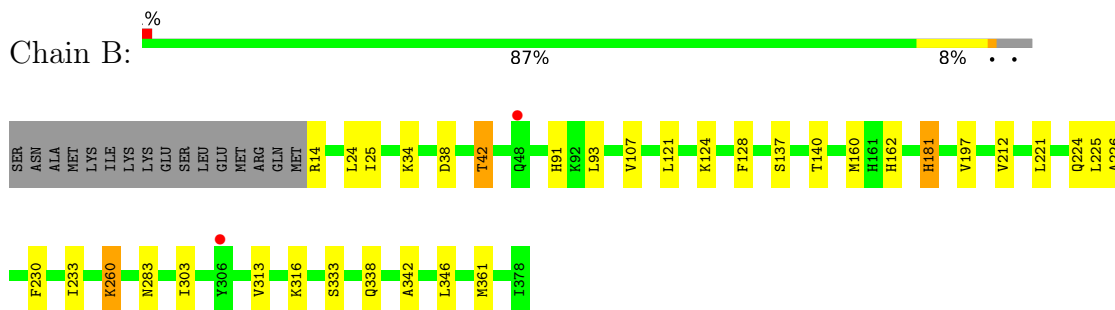
3 Residue-property plots [i](#)

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.

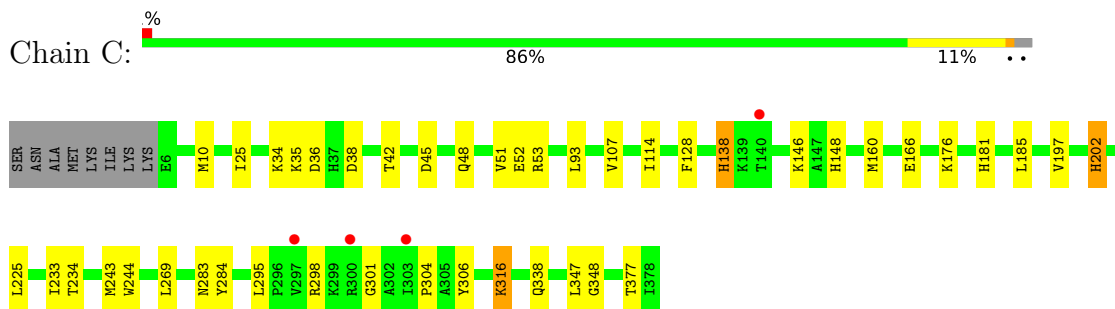
- Molecule 1: Prephenate dehydrogenase



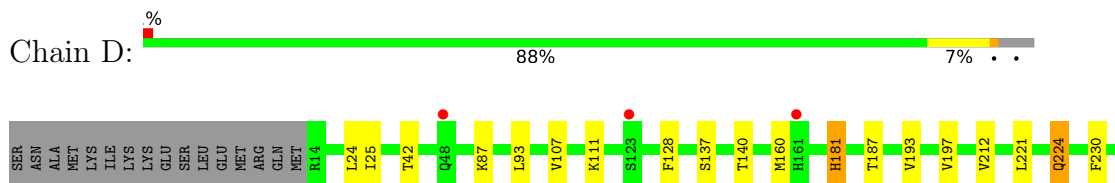
- Molecule 1: Prephenate dehydrogenase



- Molecule 1: Prephenate dehydrogenase



- Molecule 1: Prephenate dehydrogenase





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	84.68Å 105.59Å 179.62Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.60 50.00 – 2.60	Depositor EDS
% Data completeness (in resolution range)	99.9 (50.00-2.60) 99.9 (50.00-2.60)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	0.07	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.90 (at 2.58Å)	Xtriage
Refinement program	REFMAC 5.8.0107	Depositor
R, R_{free}	0.189 , 0.246 0.189 , 0.241	Depositor DCC
R_{free} test set	2490 reflections (4.87%)	wwPDB-VP
Wilson B-factor (Å ²)	61.9	Xtriage
Anisotropy	0.368	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 54.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	11890	wwPDB-VP
Average B, all atoms (Å ²)	76.0	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 35.78 % 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 5.5304e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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	1.06	0/2937	1.13	10/3976 (0.3%)
1	B	1.07	2/2848 (0.1%)	1.08	4/3860 (0.1%)
1	C	1.15	1/2933 (0.0%)	1.13	5/3970 (0.1%)
1	D	1.07	2/2839 (0.1%)	1.12	6/3848 (0.2%)
All	All	1.09	5/11557 (0.0%)	1.12	25/15654 (0.2%)

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	295	LEU	CA-C	8.41	1.62	1.52
1	D	346	LEU	CA-C	-7.84	1.43	1.53
1	D	224	GLN	N-CA	-6.24	1.39	1.46
1	B	346	LEU	CA-C	-5.32	1.46	1.53
1	B	342	ALA	N-CA	5.11	1.53	1.46

All (25) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	303	ILE	CA-C-N	-6.99	112.56	119.76
1	D	303	ILE	C-N-CA	-6.99	112.56	119.76
1	A	377	THR	N-CA-C	6.87	120.71	109.85
1	C	377	THR	N-CA-C	6.78	120.56	109.85
1	D	87	LYS	CB-CA-C	-6.55	100.50	110.92
1	C	347	LEU	CA-C-N	6.52	127.19	121.58
1	C	347	LEU	C-N-CA	6.52	127.19	121.58
1	B	181	HIS	N-CA-CB	6.38	120.36	110.21
1	B	303	ILE	CA-C-N	-6.35	113.22	119.76
1	B	303	ILE	C-N-CA	-6.35	113.22	119.76
1	A	141	GLY	N-CA-C	6.09	121.83	112.51
1	A	347	LEU	CA-C-N	6.04	126.78	121.58
1	A	347	LEU	C-N-CA	6.04	126.78	121.58
1	D	181	HIS	N-CA-CB	6.04	119.82	110.21
1	A	51	VAL	N-CA-CB	5.95	119.50	110.58

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	84	GLU	N-CA-CB	5.59	118.08	109.91
1	D	224	GLN	N-CA-CB	-5.58	101.89	109.98
1	D	25	ILE	CB-CA-C	-5.55	104.86	111.97
1	C	10	MET	CB-CG-SD	-5.45	96.35	112.70
1	C	348	GLY	N-CA-C	-5.43	102.81	111.18
1	B	42	THR	CB-CA-C	5.38	118.63	109.75
1	A	51	VAL	CB-CA-C	-5.38	104.80	112.22
1	A	10	MET	CB-CG-SD	-5.27	96.90	112.70
1	A	42	THR	CB-CA-C	5.21	118.34	109.75
1	A	348	GLY	N-CA-C	-5.13	103.28	111.18

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	2881	0	2808	17	0
1	B	2792	0	2726	19	0
1	C	2876	0	2808	25	0
1	D	2783	0	2692	16	0
2	A	13	0	8	1	0
2	B	13	0	8	0	0
2	C	13	0	8	1	0
2	D	13	0	8	0	0
3	A	117	0	0	0	0
3	B	113	0	0	0	0
3	C	178	0	0	4	0
3	D	98	0	0	2	0
All	All	11890	0	11066	65	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 (65) 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:185:LEU:HD21	1:D:221:LEU:HD11	1.66	0.77
1:A:185:LEU:HD21	1:B:221:LEU:HD11	1.70	0.73
1:C:128:PHE:HB3	1:C:160:MET:HE2	1.71	0.72
1:B:128:PHE:HB3	1:B:160:MET:HE2	1.74	0.70
1:D:128:PHE:HB3	1:D:160:MET:HE2	1.74	0.69
1:A:128:PHE:HB3	1:A:160:MET:HE2	1.76	0.65
1:B:361:MET:HE2	1:C:301:GLY:HA3	1.81	0.63
1:D:24:LEU:HD21	1:D:137:SER:HB3	1.81	0.61
1:B:25:ILE:HG21	1:B:107:VAL:HG11	1.83	0.60
1:B:24:LEU:HD21	1:B:137:SER:HB3	1.83	0.60
1:C:38:ASP:OD2	3:C:501:HOH:O	2.17	0.59
1:A:45:ASP:HB2	1:A:51:VAL:HG13	1.84	0.59
3:C:602:HOH:O	1:D:260:LYS:HE2	2.02	0.58
1:C:45:ASP:HB2	1:C:51:VAL:HG13	1.87	0.56
1:C:128:PHE:CB	1:C:160:MET:HE2	2.36	0.56
1:C:138:HIS:HB2	1:C:243:MET:HE2	1.87	0.56
1:D:128:PHE:CB	1:D:160:MET:HE2	2.37	0.54
1:B:128:PHE:CB	1:B:160:MET:HE2	2.37	0.54
1:A:185:LEU:CD2	1:B:221:LEU:HD11	2.40	0.52
1:A:298:ARG:HH12	1:B:224:GLN:HA	1.75	0.52
1:A:128:PHE:CB	1:A:160:MET:HE2	2.40	0.51
1:C:185:LEU:HD21	1:D:221:LEU:CD1	2.39	0.50
2:A:401:TYR:N	1:B:333:SER:HG	2.10	0.50
1:A:138:HIS:HB2	1:A:243:MET:HE2	1.93	0.49
1:A:202:HIS:CE1	1:A:244:TRP:CE2	3.01	0.48
1:D:361:MET:HA	1:D:361:MET:HE2	1.95	0.47
1:C:202:HIS:CE1	1:C:244:TRP:CE2	3.03	0.47
1:C:35:LYS:HG2	1:C:36:ASP:OD1	2.16	0.46
1:C:316:LYS:HE3	3:C:659:HOH:O	2.14	0.46
1:C:225:LEU:HD12	1:D:193:VAL:HG11	1.98	0.45
1:D:260:LYS:HD2	1:D:260:LYS:HA	1.80	0.45
1:C:48:GLN:O	1:C:52:GLU:HG3	2.17	0.45
1:C:225:LEU:HD12	1:D:193:VAL:CG1	2.47	0.45
2:C:401:TYR:N	1:D:333:SER:HG	2.15	0.45
1:B:260:LYS:HA	1:B:260:LYS:HD2	1.82	0.44
1:C:25:ILE:HG21	1:C:107:VAL:HG11	1.98	0.44
1:B:361:MET:HE2	1:C:301:GLY:CA	2.45	0.44
1:B:212:VAL:HG21	1:B:230:PHE:CE1	2.53	0.44
1:A:48:GLN:O	1:A:52:GLU:HG3	2.18	0.43
1:C:233:ILE:HG22	1:C:234:THR:HG23	2.00	0.43
1:B:124:LYS:HA	1:B:162:HIS:CD2	2.54	0.43
1:D:187:THR:HG22	3:D:589:HOH:O	2.17	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:298:ARG:HG3	1:C:306:TYR:CE2	2.54	0.43
1:D:235:ARG:HG2	1:D:306:TYR:CZ	2.53	0.43
1:D:212:VAL:HG21	1:D:230:PHE:CE1	2.54	0.43
1:A:181:HIS:ND1	1:A:304:PRO:HG3	2.34	0.43
1:A:14:ARG:NH1	1:A:38:ASP:OD1	2.48	0.42
1:A:298:ARG:NH1	1:B:224:GLN:HA	2.34	0.42
1:A:46:ILE:HG23	1:A:85:GLU:OE2	2.20	0.42
1:A:233:ILE:HG23	1:B:233:ILE:HG13	2.01	0.42
1:B:91:HIS:CE1	1:B:121:LEU:HD21	2.55	0.42
1:C:176:LYS:NZ	3:C:507:HOH:O	2.53	0.42
1:A:181:HIS:CG	1:A:304:PRO:HG3	2.55	0.41
1:C:114:ILE:HD12	1:C:114:ILE:HA	1.89	0.41
1:B:361:MET:CE	1:C:301:GLY:HA3	2.50	0.41
1:A:269:LEU:HD13	1:A:284:TYR:CZ	2.56	0.41
1:C:181:HIS:ND1	1:C:304:PRO:HG3	2.35	0.41
1:D:338:GLN:HG2	3:D:534:HOH:O	2.21	0.41
1:C:181:HIS:CG	1:C:304:PRO:HG3	2.56	0.41
1:B:225:LEU:O	1:B:226:ALA:C	2.62	0.40
1:B:14:ARG:HD3	1:B:38:ASP:OD1	2.21	0.40
1:A:233:ILE:HG22	1:A:234:THR:HG23	2.03	0.40
1:C:269:LEU:HD13	1:C:284:TYR:CZ	2.57	0.40
1:C:146:LYS:HD2	1:C:148:HIS:CE1	2.56	0.40
1:D:111:LYS:HA	1:D:111:LYS:HE2	2.04	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	371/381 (97%)	367 (99%)	4 (1%)	0	100	100
1	B	363/381 (95%)	357 (98%)	6 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	371/381 (97%)	366 (99%)	5 (1%)	0	100	100
1	D	363/381 (95%)	358 (99%)	5 (1%)	0	100	100
All	All	1468/1524 (96%)	1448 (99%)	20 (1%)	0	100	100

There are no Ramachandran outliers to report.

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	299/324 (92%)	287 (96%)	12 (4%)	28	55
1	B	286/324 (88%)	275 (96%)	11 (4%)	29	56
1	C	298/324 (92%)	287 (96%)	11 (4%)	30	57
1	D	281/324 (87%)	269 (96%)	12 (4%)	26	51
All	All	1164/1296 (90%)	1118 (96%)	46 (4%)	28	55

All (46) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	34	LYS
1	A	42	THR
1	A	93	LEU
1	A	138	HIS
1	A	146	LYS
1	A	166	GLU
1	A	197	VAL
1	A	202	HIS
1	A	249	LYS
1	A	283	ASN
1	A	338	GLN
1	A	361	MET
1	B	34	LYS
1	B	42	THR

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Mol	Chain	Res	Type
1	B	93	LEU
1	B	140	THR
1	B	181	HIS
1	B	197	VAL
1	B	260	LYS
1	B	283	ASN
1	B	313	VAL
1	B	316	LYS
1	B	338	GLN
1	C	34	LYS
1	C	42	THR
1	C	53	ARG
1	C	93	LEU
1	C	138	HIS
1	C	166	GLU
1	C	197	VAL
1	C	202	HIS
1	C	283	ASN
1	C	316	LYS
1	C	338	GLN
1	D	42	THR
1	D	93	LEU
1	D	107	VAL
1	D	140	THR
1	D	181	HIS
1	D	197	VAL
1	D	224	GLN
1	D	250	GLN
1	D	283	ASN
1	D	313	VAL
1	D	338	GLN
1	D	361	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	186	ASN
1	A	202	HIS
1	A	283	ASN
1	B	69	HIS
1	B	165	ASN
1	B	181	HIS

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Mol	Chain	Res	Type
1	B	202	HIS
1	B	283	ASN
1	C	165	ASN
1	C	202	HIS
1	C	283	ASN
1	D	181	HIS
1	D	186	ASN
1	D	283	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	B	401	-	12,13,13	0.88	1 (8%)	13,17,17	0.63	0
2	TYR	D	401	-	12,13,13	0.75	0	13,17,17	0.98	1 (7%)
2	TYR	C	401	-	12,13,13	0.66	0	13,17,17	0.35	0
2	TYR	A	401	-	12,13,13	0.66	0	13,17,17	0.54	0

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

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	401	TYR	OXT-C	-2.08	1.24	1.30

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	401	TYR	OXT-C-O	-3.08	117.09	124.08

There are no chirality outliers.

All (1) torsion outliers are listed below:

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

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	401	TYR	1	0
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	373/381 (97%)	-0.27	0 100 100	48, 76, 111, 131	0
1	B	365/381 (95%)	-0.20	2 (0%) 87 85	42, 76, 126, 150	0
1	C	373/381 (97%)	-0.35	4 (1%) 78 74	41, 63, 112, 149	0
1	D	365/381 (95%)	-0.16	3 (0%) 82 80	41, 78, 128, 168	0
All	All	1476/1524 (96%)	-0.24	9 (0%) 85 83	41, 72, 123, 168	0

All (9) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	300	ARG	3.3
1	D	123	SER	3.0
1	C	303	ILE	2.5
1	C	297	VAL	2.4
1	C	140	THR	2.4
1	D	48	GLN	2.3
1	B	306	TYR	2.2
1	B	48	GLN	2.2
1	D	161	HIS	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 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($\text{\AA}^2$)	Q<0.9
2	TYR	B	401	13/13	0.93	0.07	36,39,45,46	0
2	TYR	D	401	13/13	0.95	0.06	34,36,43,44	0
2	TYR	C	401	13/13	0.97	0.05	44,54,62,62	0
2	TYR	A	401	13/13	0.97	0.05	45,57,65,65	0

6.5 Other polymers [i](#)

There are no such residues in this entry.