



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 14, 2017 – 01:12 pm GMT

PDB ID : 1GYK
Title : SERUM AMYLOID P COMPONENT CO-CRYSTALLISED WITH MOBDG
AT NEUTRAL PH
Authors : Thompson, D.; Pepys, M.B.; Tickle, I.; Wood, S.P.
Deposited on : 2002-04-25
Resolution : 2.20 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 : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : 1.9-1692
EDS : trunk28620
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
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) : recalc28949

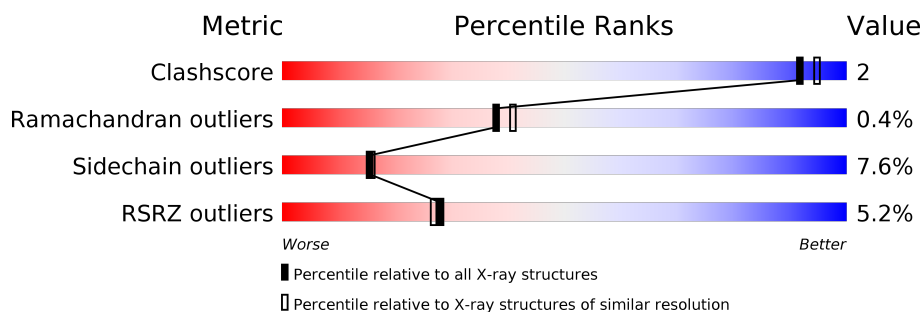
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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))
Clashscore	112137	4730 (2.20-2.20)
Ramachandran outliers	110173	4656 (2.20-2.20)
Sidechain outliers	110143	4657 (2.20-2.20)
RSRZ outliers	101464	4033 (2.20-2.20)

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	204	<div> <div>7%</div> <div>80%</div> <div>17%</div> <div>..</div> </div>
1	B	204	<div> <div>9%</div> <div>78%</div> <div>18%</div> <div>..</div> </div>
1	C	204	<div> <div>5%</div> <div>76%</div> <div>20%</div> <div>..</div> </div>
1	D	204	<div> <div>79%</div> <div>18%</div> <div>..</div> </div>
1	E	204	<div> <div>4%</div> <div>79%</div> <div>17%</div> <div>.</div> </div>

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	CDG	B	1207	-	-	-	X
3	CDG	D	1207	-	-	-	X

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 8326 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.

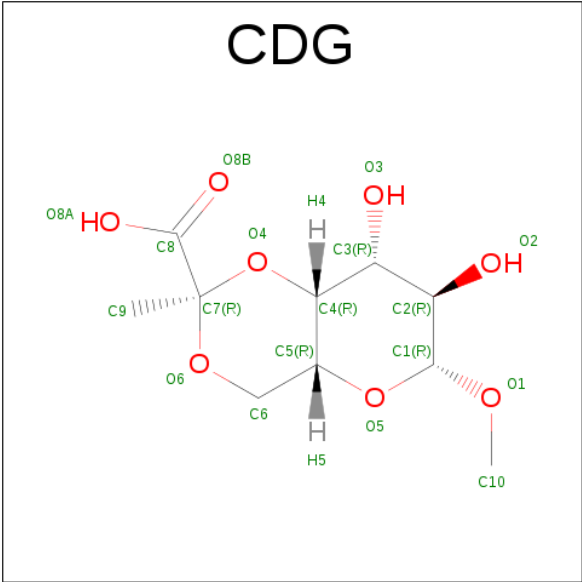
- Molecule 1 is a protein called SERUM AMYLOID P-COMPONENT.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	204	Total	C	N	O	S	0	0	0
			1649	1071	272	303	3			
1	B	204	Total	C	N	O	S	0	0	0
			1649	1071	272	303	3			
1	C	204	Total	C	N	O	S	0	0	0
			1649	1071	272	303	3			
1	D	204	Total	C	N	O	S	0	0	0
			1649	1071	272	303	3			
1	E	204	Total	C	N	O	S	0	0	0
			1649	1071	272	303	3			

- Molecule 2 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	2	Total	Ca	0	0
			2	2		
2	A	2	Total	Ca	0	0
			2	2		
2	D	2	Total	Ca	0	0
			2	2		
2	C	2	Total	Ca	0	0
			2	2		
2	E	1	Total	Ca	0	0
			1	1		

- Molecule 3 is METHYL 4,6-O-[(1R)-1-CARBOXYETHYLIDENE]-BETA-D-GALACTOPYRANOSIDE (three-letter code: CDG) (formula: C₁₀H₁₆O₈).

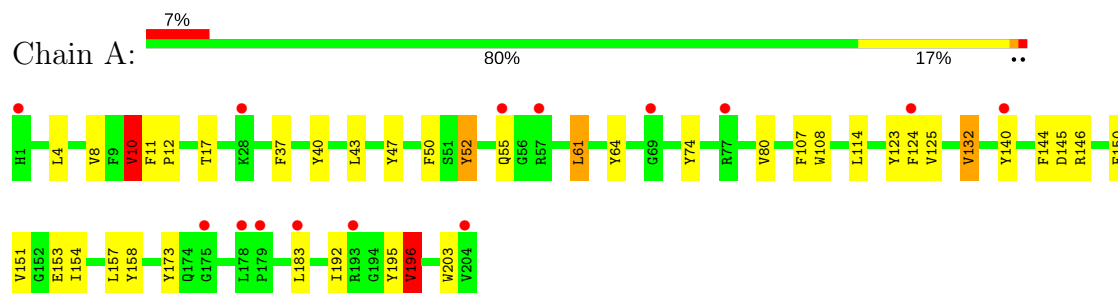


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	5	0
			18	10	8		
3	B	1	Total	C	O	5	0
			18	10	8		
3	C	1	Total	C	O	5	0
			18	10	8		
3	D	1	Total	C	O	5	0
			18	10	8		

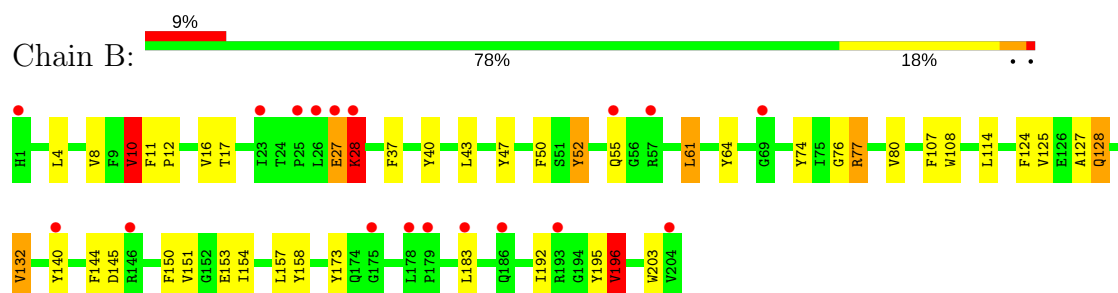
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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.

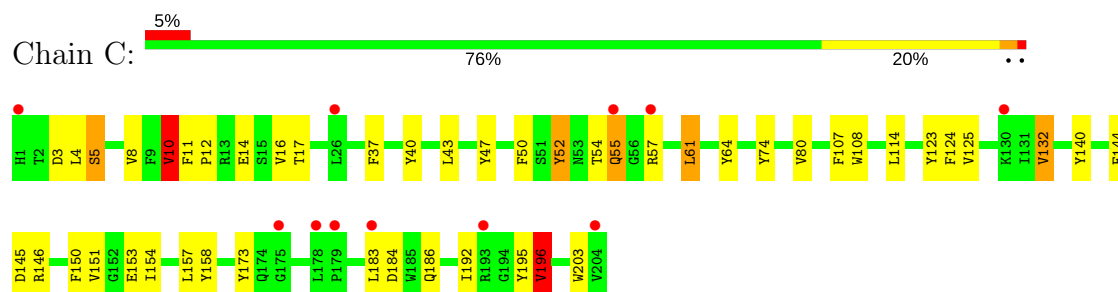
• Molecule 1: SERUM AMYLOID P-COMPONENT



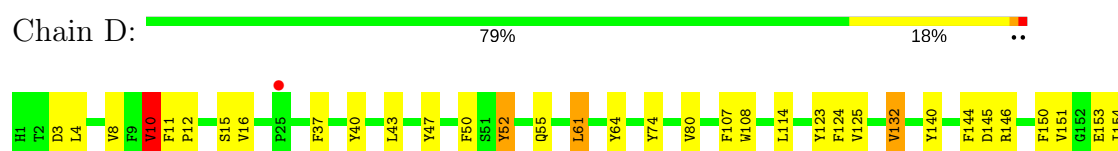
• Molecule 1: SERUM AMYLOID P-COMPONENT



• Molecule 1: SERUM AMYLOID P-COMPONENT

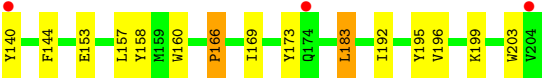
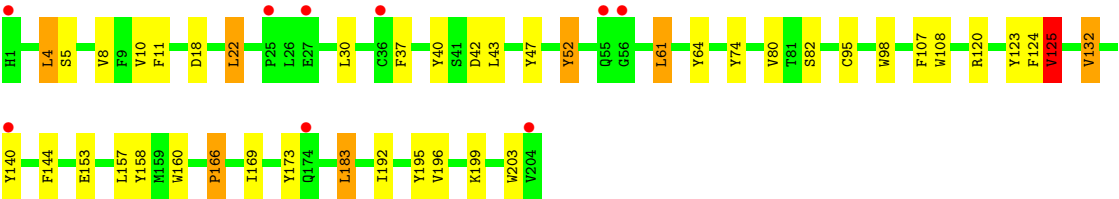
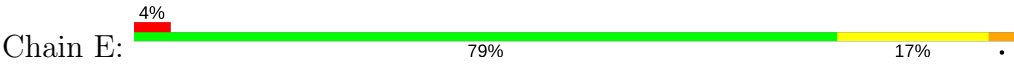


• Molecule 1: SERUM AMYLOID P-COMPONENT





● Molecule 1: SERUM AMYLOID P-COMPONENT



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	95.76Å 70.53Å 103.41Å 90.00° 96.80° 90.00°	Depositor
Resolution (Å)	20.00 – 2.20 21.21 – 2.20	Depositor EDS
% Data completeness (in resolution range)	95.2 (20.00-2.20) 95.4 (21.21-2.20)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	7.24 (at 2.19Å)	Xtriage
Refinement program	X-PLOR	Depositor
R, R_{free}	0.186 , 0.224 0.270 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	DCC
Wilson B-factor (Å ²)	20.3	Xtriage
Anisotropy	0.102	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 8.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.83	EDS
Total number of atoms	8326	wwPDB-VP
Average B, all atoms (Å ²)	16.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.96% 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: CA, CDG

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	1.62	41/1696 (2.4%)	1.33	8/2306 (0.3%)
1	B	1.68	45/1696 (2.7%)	1.37	13/2306 (0.6%)
1	C	1.64	42/1696 (2.5%)	1.35	11/2306 (0.5%)
1	D	1.64	43/1696 (2.5%)	1.33	8/2306 (0.3%)
1	E	1.61	31/1696 (1.8%)	1.34	11/2306 (0.5%)
All	All	1.64	202/8480 (2.4%)	1.34	51/11530 (0.4%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	B	0	1

All (202) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	17	THR	CA-CB	-9.98	1.27	1.53
1	C	145	ASP	C-N	8.75	1.54	1.34
1	D	3	ASP	CA-CB	7.86	1.71	1.53
1	E	160	TRP	NE1-CE2	7.63	1.47	1.37
1	B	28	LYS	CA-C	-7.55	1.33	1.52
1	E	195	TYR	CD2-CE2	7.42	1.50	1.39
1	B	28	LYS	N-CA	7.27	1.60	1.46
1	E	52	TYR	CD1-CE1	7.14	1.50	1.39
1	A	40	TYR	CG-CD1	7.03	1.48	1.39
1	B	40	TYR	CG-CD1	7.01	1.48	1.39
1	C	40	TYR	CG-CD1	7.01	1.48	1.39
1	D	40	TYR	CG-CD1	7.01	1.48	1.39
1	E	74	TYR	CD2-CE2	6.99	1.49	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	158	TYR	CD1-CE1	6.81	1.49	1.39
1	B	158	TYR	CD1-CE1	6.79	1.49	1.39
1	D	158	TYR	CD1-CE1	6.76	1.49	1.39
1	C	158	TYR	CD1-CE1	6.71	1.49	1.39
1	E	140	TYR	CD1-CE1	6.67	1.49	1.39
1	E	173	TYR	CD2-CE2	6.62	1.49	1.39
1	A	140	TYR	CD2-CE2	6.61	1.49	1.39
1	B	140	TYR	CD2-CE2	6.60	1.49	1.39
1	D	140	TYR	CD2-CE2	6.59	1.49	1.39
1	C	140	TYR	CD2-CE2	6.55	1.49	1.39
1	A	40	TYR	CD2-CE2	6.49	1.49	1.39
1	D	40	TYR	CD2-CE2	6.48	1.49	1.39
1	A	173	TYR	CD2-CE2	6.47	1.49	1.39
1	C	40	TYR	CD2-CE2	6.45	1.49	1.39
1	B	195	TYR	CD2-CE2	6.44	1.49	1.39
1	B	40	TYR	CD2-CE2	6.44	1.49	1.39
1	B	108	TRP	CE3-CZ3	6.44	1.49	1.38
1	D	173	TYR	CD2-CE2	6.43	1.49	1.39
1	B	173	TYR	CD2-CE2	6.42	1.49	1.39
1	D	108	TRP	CE3-CZ3	6.42	1.49	1.38
1	A	108	TRP	CE3-CZ3	6.41	1.49	1.38
1	C	195	TYR	CD2-CE2	6.41	1.49	1.39
1	B	128	GLN	CA-CB	6.41	1.68	1.53
1	D	195	TYR	CD2-CE2	6.40	1.49	1.39
1	C	173	TYR	CD2-CE2	6.40	1.49	1.39
1	E	140	TYR	CD2-CE2	6.39	1.49	1.39
1	C	108	TRP	CE3-CZ3	6.39	1.49	1.38
1	A	195	TYR	CD2-CE2	6.38	1.49	1.39
1	A	140	TYR	CD1-CE1	6.29	1.48	1.39
1	D	140	TYR	CD1-CE1	6.26	1.48	1.39
1	C	140	TYR	CD1-CE1	6.23	1.48	1.39
1	B	128	GLN	CB-CG	6.22	1.69	1.52
1	B	140	TYR	CD1-CE1	6.20	1.48	1.39
1	E	40	TYR	CG-CD1	6.13	1.47	1.39
1	D	15	SER	C-N	-6.12	1.20	1.34
1	B	10	VAL	CA-CB	6.08	1.67	1.54
1	D	10	VAL	CA-CB	6.06	1.67	1.54
1	C	10	VAL	CA-CB	6.05	1.67	1.54
1	A	10	VAL	CA-CB	6.04	1.67	1.54
1	A	52	TYR	CD2-CE2	5.95	1.48	1.39
1	A	40	TYR	CE2-CZ	5.93	1.46	1.38
1	B	40	TYR	CE2-CZ	5.91	1.46	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	52	TYR	CD2-CE2	5.91	1.48	1.39
1	D	40	TYR	CE2-CZ	5.91	1.46	1.38
1	D	52	TYR	CD2-CE2	5.89	1.48	1.39
1	C	52	TYR	CD2-CE2	5.88	1.48	1.39
1	C	40	TYR	CE2-CZ	5.88	1.46	1.38
1	C	40	TYR	CD1-CE1	5.87	1.48	1.39
1	D	40	TYR	CD1-CE1	5.87	1.48	1.39
1	A	40	TYR	CD1-CE1	5.87	1.48	1.39
1	A	158	TYR	CD2-CE2	5.85	1.48	1.39
1	C	132	VAL	CA-CB	5.84	1.67	1.54
1	B	40	TYR	CD1-CE1	5.83	1.48	1.39
1	A	132	VAL	CA-CB	5.82	1.67	1.54
1	B	158	TYR	CD2-CE2	5.82	1.48	1.39
1	D	158	TYR	CD2-CE2	5.82	1.48	1.39
1	D	132	VAL	CA-CB	5.81	1.67	1.54
1	C	158	TYR	CD2-CE2	5.80	1.48	1.39
1	B	132	VAL	CA-CB	5.80	1.67	1.54
1	B	47	TYR	CD2-CE2	5.75	1.48	1.39
1	C	11	PHE	CE1-CZ	5.75	1.48	1.37
1	B	11	PHE	CE1-CZ	5.75	1.48	1.37
1	E	52	TYR	CD2-CE2	5.75	1.48	1.39
1	A	11	PHE	CE1-CZ	5.75	1.48	1.37
1	D	11	PHE	CE1-CZ	5.74	1.48	1.37
1	A	47	TYR	CD2-CE2	5.74	1.48	1.39
1	D	47	TYR	CD2-CE2	5.74	1.48	1.39
1	C	47	TYR	CD2-CE2	5.72	1.48	1.39
1	E	37	PHE	CE2-CZ	5.71	1.48	1.37
1	E	195	TYR	CE2-CZ	5.68	1.46	1.38
1	C	196	VAL	CA-CB	5.64	1.66	1.54
1	C	158	TYR	CE2-CZ	5.63	1.45	1.38
1	D	196	VAL	CA-CB	5.62	1.66	1.54
1	B	196	VAL	CA-CB	5.62	1.66	1.54
1	A	203	TRP	CE3-CZ3	5.62	1.48	1.38
1	B	203	TRP	CE3-CZ3	5.61	1.48	1.38
1	A	196	VAL	CA-CB	5.61	1.66	1.54
1	D	203	TRP	CE3-CZ3	5.61	1.48	1.38
1	C	203	TRP	CE3-CZ3	5.58	1.48	1.38
1	D	158	TYR	CE2-CZ	5.57	1.45	1.38
1	E	158	TYR	CD2-CE2	5.56	1.47	1.39
1	B	158	TYR	CE1-CZ	5.54	1.45	1.38
1	A	50	PHE	CE1-CZ	5.54	1.47	1.37
1	B	158	TYR	CE2-CZ	5.54	1.45	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	158	TYR	CE2-CZ	5.53	1.45	1.38
1	D	50	PHE	CE1-CZ	5.51	1.47	1.37
1	D	158	TYR	CE1-CZ	5.51	1.45	1.38
1	B	50	PHE	CE1-CZ	5.50	1.47	1.37
1	C	50	PHE	CE1-CZ	5.49	1.47	1.37
1	C	74	TYR	CE1-CZ	5.49	1.45	1.38
1	D	74	TYR	CE1-CZ	5.48	1.45	1.38
1	B	74	TYR	CE1-CZ	5.47	1.45	1.38
1	C	158	TYR	CE1-CZ	5.47	1.45	1.38
1	C	140	TYR	CE1-CZ	5.46	1.45	1.38
1	A	74	TYR	CE1-CZ	5.46	1.45	1.38
1	A	158	TYR	CE1-CZ	5.45	1.45	1.38
1	B	107	PHE	CE2-CZ	5.45	1.47	1.37
1	C	107	PHE	CE2-CZ	5.45	1.47	1.37
1	D	64	TYR	CD2-CE2	5.43	1.47	1.39
1	C	64	TYR	CD2-CE2	5.43	1.47	1.39
1	B	140	TYR	CE1-CZ	5.42	1.45	1.38
1	B	124	PHE	CE1-CZ	5.42	1.47	1.37
1	D	107	PHE	CE2-CZ	5.42	1.47	1.37
1	A	107	PHE	CE2-CZ	5.41	1.47	1.37
1	B	64	TYR	CD2-CE2	5.41	1.47	1.39
1	D	40	TYR	CE1-CZ	5.41	1.45	1.38
1	B	173	TYR	CE2-CZ	5.41	1.45	1.38
1	C	124	PHE	CE1-CZ	5.41	1.47	1.37
1	A	40	TYR	CE1-CZ	5.40	1.45	1.38
1	C	173	TYR	CE2-CZ	5.40	1.45	1.38
1	D	140	TYR	CE1-CZ	5.40	1.45	1.38
1	A	64	TYR	CD2-CE2	5.39	1.47	1.39
1	C	40	TYR	CE1-CZ	5.39	1.45	1.38
1	D	124	PHE	CE1-CZ	5.39	1.47	1.37
1	B	40	TYR	CE1-CZ	5.39	1.45	1.38
1	A	140	TYR	CE1-CZ	5.38	1.45	1.38
1	E	11	PHE	CE1-CZ	5.37	1.47	1.37
1	A	124	PHE	CE1-CZ	5.37	1.47	1.37
1	A	37	PHE	CE1-CZ	5.37	1.47	1.37
1	A	173	TYR	CE2-CZ	5.36	1.45	1.38
1	D	173	TYR	CE2-CZ	5.36	1.45	1.38
1	E	47	TYR	CD2-CE2	5.36	1.47	1.39
1	E	52	TYR	CG-CD1	5.35	1.46	1.39
1	E	98	TRP	CE3-CZ3	5.34	1.47	1.38
1	D	37	PHE	CE1-CZ	5.33	1.47	1.37
1	E	195	TYR	CG-CD1	5.33	1.46	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	37	PHE	CE1-CZ	5.32	1.47	1.37
1	B	37	PHE	CE1-CZ	5.31	1.47	1.37
1	E	158	TYR	CD1-CE1	5.30	1.47	1.39
1	E	124	PHE	CE2-CZ	5.30	1.47	1.37
1	D	64	TYR	CD1-CE1	5.30	1.47	1.39
1	B	64	TYR	CD1-CE1	5.29	1.47	1.39
1	B	150	PHE	CE2-CZ	5.28	1.47	1.37
1	E	74	TYR	CD1-CE1	5.28	1.47	1.39
1	B	52	TYR	CG-CD1	5.26	1.46	1.39
1	C	64	TYR	CD1-CE1	5.26	1.47	1.39
1	A	64	TYR	CD1-CE1	5.26	1.47	1.39
1	A	52	TYR	CG-CD1	5.25	1.46	1.39
1	C	144	PHE	CE2-CZ	5.24	1.47	1.37
1	B	144	PHE	CE2-CZ	5.24	1.47	1.37
1	C	150	PHE	CE2-CZ	5.24	1.47	1.37
1	D	150	PHE	CE2-CZ	5.24	1.47	1.37
1	E	37	PHE	CE1-CZ	5.24	1.47	1.37
1	D	52	TYR	CG-CD1	5.23	1.46	1.39
1	E	64	TYR	CD2-CE2	5.23	1.47	1.39
1	C	52	TYR	CG-CD1	5.22	1.46	1.39
1	D	144	PHE	CE2-CZ	5.22	1.47	1.37
1	A	144	PHE	CE2-CZ	5.22	1.47	1.37
1	C	37	PHE	CE2-CZ	5.22	1.47	1.37
1	E	144	PHE	CE2-CZ	5.22	1.47	1.37
1	B	37	PHE	CE2-CZ	5.20	1.47	1.37
1	D	37	PHE	CE2-CZ	5.20	1.47	1.37
1	A	150	PHE	CE2-CZ	5.20	1.47	1.37
1	A	37	PHE	CE2-CZ	5.18	1.47	1.37
1	B	74	TYR	CD2-CE2	5.18	1.47	1.39
1	E	160	TRP	CD2-CE3	-5.18	1.32	1.40
1	D	74	TYR	CD2-CE2	5.18	1.47	1.39
1	A	173	TYR	CD1-CE1	5.18	1.47	1.39
1	A	173	TYR	CG-CD1	5.17	1.45	1.39
1	B	107	PHE	CE1-CZ	5.17	1.47	1.37
1	A	107	PHE	CE1-CZ	5.17	1.47	1.37
1	A	74	TYR	CD2-CE2	5.16	1.47	1.39
1	C	107	PHE	CE1-CZ	5.16	1.47	1.37
1	D	107	PHE	CE1-CZ	5.16	1.47	1.37
1	C	74	TYR	CD2-CE2	5.16	1.47	1.39
1	C	173	TYR	CD1-CE1	5.16	1.47	1.39
1	C	173	TYR	CG-CD1	5.16	1.45	1.39
1	D	173	TYR	CD1-CE1	5.16	1.47	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	123	TYR	CD1-CE1	5.15	1.47	1.39
1	E	203	TRP	CE3-CZ3	5.14	1.47	1.38
1	B	173	TYR	CG-CD1	5.14	1.45	1.39
1	E	132	VAL	CA-CB	5.14	1.65	1.54
1	D	173	TYR	CG-CD1	5.14	1.45	1.39
1	A	50	PHE	CG-CD2	5.13	1.46	1.38
1	B	173	TYR	CD1-CE1	5.13	1.47	1.39
1	C	50	PHE	CG-CD2	5.13	1.46	1.38
1	B	50	PHE	CG-CD2	5.11	1.46	1.38
1	A	195	TYR	CE2-CZ	5.10	1.45	1.38
1	E	107	PHE	CE2-CZ	5.10	1.47	1.37
1	D	50	PHE	CG-CD2	5.09	1.46	1.38
1	E	124	PHE	CE1-CZ	5.07	1.47	1.37
1	C	123	TYR	CD2-CE2	5.03	1.46	1.39
1	E	125	VAL	CA-CB	5.02	1.65	1.54
1	E	64	TYR	CD1-CE1	5.02	1.46	1.39
1	B	195	TYR	CE2-CZ	5.02	1.45	1.38
1	D	123	TYR	CD2-CE2	5.02	1.46	1.39
1	D	195	TYR	CE2-CZ	5.02	1.45	1.38
1	A	123	TYR	CD2-CE2	5.01	1.46	1.39
1	C	195	TYR	CE2-CZ	5.00	1.45	1.38

All (51) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	28	LYS	O-C-N	-9.73	102.62	121.10
1	E	157	LEU	CA-CB-CG	9.00	136.01	115.30
1	C	16	VAL	C-N-CA	7.57	140.63	121.70
1	B	43	LEU	CA-CB-CG	7.11	131.66	115.30
1	C	43	LEU	CA-CB-CG	7.11	131.66	115.30
1	D	43	LEU	CA-CB-CG	7.11	131.64	115.30
1	A	43	LEU	CA-CB-CG	7.08	131.59	115.30
1	C	61	LEU	CA-CB-CG	7.03	131.46	115.30
1	D	61	LEU	CA-CB-CG	7.02	131.44	115.30
1	A	61	LEU	CA-CB-CG	7.00	131.40	115.30
1	B	61	LEU	CA-CB-CG	6.99	131.38	115.30
1	C	16	VAL	O-C-N	-6.86	111.73	122.70
1	E	43	LEU	CA-CB-CG	6.84	131.03	115.30
1	E	61	LEU	CA-CB-CG	6.65	130.60	115.30
1	B	52	TYR	CA-CB-CG	6.23	125.23	113.40
1	C	52	TYR	CA-CB-CG	6.21	125.20	113.40
1	D	52	TYR	CA-CB-CG	6.21	125.20	113.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	52	TYR	CA-CB-CG	6.19	125.17	113.40
1	B	17	THR	O-C-N	-6.11	112.92	122.70
1	B	28	LYS	CA-C-N	5.92	133.67	117.10
1	C	17	THR	O-C-N	-5.86	113.33	122.70
1	B	16	VAL	C-N-CA	5.85	136.33	121.70
1	E	52	TYR	CA-CB-CG	5.84	124.49	113.40
1	B	27	GLU	C-N-CA	-5.83	107.13	121.70
1	E	4	LEU	CA-CB-CG	5.68	128.37	115.30
1	E	120	ARG	NE-CZ-NH1	5.64	123.12	120.30
1	D	3	ASP	O-C-N	5.51	131.51	122.70
1	E	183	LEU	CA-CB-CG	5.50	127.96	115.30
1	A	145	ASP	CB-CG-OD1	5.50	123.25	118.30
1	D	145	ASP	CB-CG-OD1	5.48	123.23	118.30
1	B	145	ASP	CB-CG-OD1	5.47	123.22	118.30
1	A	17	THR	O-C-N	-5.43	114.01	122.70
1	E	22	LEU	CA-CB-CG	5.29	127.46	115.30
1	C	145	ASP	C-N-CA	5.27	134.87	121.70
1	E	42	ASP	CB-CG-OD1	5.22	123.00	118.30
1	E	22	LEU	CB-CG-CD2	-5.21	102.14	111.00
1	C	114	LEU	CB-CG-CD2	5.13	119.72	111.00
1	E	120	ARG	NE-CZ-NH2	-5.13	117.73	120.30
1	A	114	LEU	CB-CG-CD2	5.12	119.70	111.00
1	D	114	LEU	CB-CG-CD2	5.11	119.69	111.00
1	B	114	LEU	CB-CG-CD2	5.10	119.67	111.00
1	C	196	VAL	CB-CA-C	5.07	121.03	111.40
1	B	196	VAL	CB-CA-C	5.06	121.02	111.40
1	B	17	THR	CB-CA-C	-5.05	97.98	111.60
1	D	196	VAL	CB-CA-C	5.05	120.99	111.40
1	A	196	VAL	CB-CA-C	5.03	120.96	111.40
1	A	12	PRO	N-CA-C	5.03	125.18	112.10
1	C	12	PRO	N-CA-C	5.03	125.18	112.10
1	D	12	PRO	N-CA-C	5.02	125.16	112.10
1	B	12	PRO	N-CA-C	5.02	125.16	112.10
1	C	16	VAL	CA-C-N	5.00	128.21	117.20

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	28	LYS	Mainchain

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	1649	0	1626	2	0
1	B	1649	0	1626	8	0
1	C	1649	0	1626	8	0
1	D	1649	0	1626	3	0
1	E	1649	0	1626	6	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
2	E	1	0	0	0	0
3	A	18	0	15	0	0
3	B	18	0	15	0	0
3	C	18	0	15	0	0
3	D	18	0	15	0	0
All	All	8326	0	8190	27	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 2.

All (27) 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:B:27:GLU:HA	1:B:127:ALA:HB1	1.56	0.85
1:E:95:CYS:HB2	1:E:108:TRP:HB2	1.59	0.83
1:C:14:GLU:HB3	1:C:146:ARG:HH12	1.60	0.65
1:C:184:ASP:OD1	1:C:186:GLN:HB2	1.99	0.62
1:C:3:ASP:OD1	1:C:5:SER:HB2	2.02	0.59
1:A:192:ILE:HG23	1:A:196:VAL:HG13	1.85	0.59
1:B:192:ILE:HG23	1:B:196:VAL:HG13	1.85	0.59
1:C:192:ILE:HG23	1:C:196:VAL:HG13	1.85	0.58
1:D:192:ILE:HG23	1:D:196:VAL:HG13	1.85	0.57
1:E:30:LEU:HB2	1:E:125:VAL:HG22	1.86	0.57
1:B:27:GLU:HG2	1:B:128:GLN:HG3	1.89	0.55
1:D:16:VAL:O	1:D:16:VAL:HG22	2.12	0.49
1:E:52:TYR:HB3	1:E:61:LEU:HB3	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:192:ILE:HG23	1:E:196:VAL:HG13	1.98	0.46
1:B:27:GLU:CG	1:B:128:GLN:HG3	2.47	0.45
1:B:76:GLY:O	1:B:77:ARG:HB2	2.17	0.45
1:B:77:ARG:HH11	1:B:77:ARG:HD3	1.64	0.44
1:C:14:GLU:HB3	1:C:146:ARG:NH1	2.31	0.44
1:C:54:THR:OG1	1:C:57:ARG:HD3	2.18	0.44
1:C:55:GLN:O	1:C:57:ARG:HG3	2.18	0.43
1:B:27:GLU:CA	1:B:127:ALA:HB1	2.38	0.42
1:E:166:PRO:O	1:E:169:ILE:HB	2.18	0.42
1:C:10:VAL:HB	1:C:153:GLU:HG2	2.02	0.42
1:E:10:VAL:HG22	1:E:153:GLU:HG2	2.02	0.42
1:A:10:VAL:HB	1:A:153:GLU:HG2	2.02	0.41
1:B:10:VAL:HB	1:B:153:GLU:HG2	2.02	0.41
1:D:10:VAL:HB	1:D:153:GLU:HG2	2.02	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	202/204 (99%)	199 (98%)	2 (1%)	1 (0%)	32	34
1	B	202/204 (99%)	199 (98%)	2 (1%)	1 (0%)	32	34
1	C	202/204 (99%)	198 (98%)	3 (2%)	1 (0%)	32	34
1	D	202/204 (99%)	199 (98%)	2 (1%)	1 (0%)	32	34
1	E	202/204 (99%)	194 (96%)	8 (4%)	0	100	100
All	All	1010/1020 (99%)	989 (98%)	17 (2%)	4 (0%)	38	41

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	55	GLN
1	B	55	GLN
1	C	55	GLN
1	D	55	GLN

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	181/181 (100%)	167 (92%)	14 (8%)	15	15
1	B	181/181 (100%)	166 (92%)	15 (8%)	13	13
1	C	181/181 (100%)	167 (92%)	14 (8%)	15	15
1	D	181/181 (100%)	167 (92%)	14 (8%)	15	15
1	E	181/181 (100%)	169 (93%)	12 (7%)	19	21
All	All	905/905 (100%)	836 (92%)	69 (8%)	15	16

All (69) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	4	LEU
1	A	8	VAL
1	A	10	VAL
1	A	52	TYR
1	A	61	LEU
1	A	80	VAL
1	A	125	VAL
1	A	132	VAL
1	A	146	ARG
1	A	151	VAL
1	A	154	ILE
1	A	157	LEU
1	A	183	LEU
1	A	196	VAL
1	B	4	LEU
1	B	8	VAL

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Mol	Chain	Res	Type
1	B	10	VAL
1	B	28	LYS
1	B	52	TYR
1	B	61	LEU
1	B	77	ARG
1	B	80	VAL
1	B	125	VAL
1	B	132	VAL
1	B	151	VAL
1	B	154	ILE
1	B	157	LEU
1	B	183	LEU
1	B	196	VAL
1	C	4	LEU
1	C	5	SER
1	C	8	VAL
1	C	10	VAL
1	C	52	TYR
1	C	61	LEU
1	C	80	VAL
1	C	125	VAL
1	C	132	VAL
1	C	151	VAL
1	C	154	ILE
1	C	157	LEU
1	C	183	LEU
1	C	196	VAL
1	D	4	LEU
1	D	8	VAL
1	D	10	VAL
1	D	52	TYR
1	D	61	LEU
1	D	80	VAL
1	D	125	VAL
1	D	132	VAL
1	D	146	ARG
1	D	151	VAL
1	D	154	ILE
1	D	157	LEU
1	D	183	LEU
1	D	196	VAL
1	E	4	LEU

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Mol	Chain	Res	Type
1	E	5	SER
1	E	8	VAL
1	E	18	ASP
1	E	22	LEU
1	E	80	VAL
1	E	82	SER
1	E	125	VAL
1	E	132	VAL
1	E	166	PRO
1	E	183	LEU
1	E	199	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	1	HIS
1	B	1	HIS
1	C	1	HIS
1	D	1	HIS
1	E	32	ASN
1	E	148	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 13 ligands modelled in this entry, 9 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	CDG	A	1207	2	15,19,19	2.50	6 (40%)	23,29,29	2.65	7 (30%)
3	CDG	B	1207	2	15,19,19	2.50	6 (40%)	23,29,29	2.64	7 (30%)
3	CDG	C	1207	2	15,19,19	2.50	6 (40%)	23,29,29	2.64	7 (30%)
3	CDG	D	1207	2	15,19,19	2.49	6 (40%)	23,29,29	2.64	7 (30%)

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	CDG	A	1207	2	-	0/2/39/39	0/2/2/2
3	CDG	B	1207	2	-	0/2/39/39	0/2/2/2
3	CDG	C	1207	2	-	0/2/39/39	0/2/2/2
3	CDG	D	1207	2	-	0/2/39/39	0/2/2/2

All (24) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	1207	CDG	O6-C6	2.03	1.46	1.43
3	A	1207	CDG	O6-C6	2.04	1.46	1.43
3	B	1207	CDG	O6-C6	2.06	1.46	1.43
3	C	1207	CDG	O6-C6	2.08	1.46	1.43
3	B	1207	CDG	C6-C5	2.34	1.55	1.51
3	D	1207	CDG	C6-C5	2.35	1.55	1.51
3	A	1207	CDG	C6-C5	2.36	1.55	1.51
3	C	1207	CDG	C6-C5	2.36	1.55	1.51
3	C	1207	CDG	O5-C1	2.44	1.47	1.41
3	D	1207	CDG	O5-C1	2.45	1.47	1.41
3	B	1207	CDG	O5-C1	2.47	1.48	1.41
3	A	1207	CDG	O5-C1	2.48	1.48	1.41
3	B	1207	CDG	O4-C4	2.61	1.48	1.44
3	A	1207	CDG	O4-C4	2.63	1.48	1.44
3	C	1207	CDG	O4-C4	2.65	1.48	1.44

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	1207	CDG	O4-C4	2.65	1.48	1.44
3	D	1207	CDG	O1-C1	3.64	1.46	1.40
3	B	1207	CDG	O1-C1	3.64	1.46	1.40
3	C	1207	CDG	O1-C1	3.64	1.46	1.40
3	A	1207	CDG	O1-C1	3.66	1.46	1.40
3	D	1207	CDG	O6-C7	6.77	1.49	1.42
3	C	1207	CDG	O6-C7	6.78	1.49	1.42
3	A	1207	CDG	O6-C7	6.78	1.49	1.42
3	B	1207	CDG	O6-C7	6.79	1.49	1.42

All (28) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	1207	CDG	C9-C7-C8	-6.22	100.84	111.11
3	A	1207	CDG	C9-C7-C8	-6.21	100.85	111.11
3	D	1207	CDG	C9-C7-C8	-6.21	100.85	111.11
3	C	1207	CDG	C9-C7-C8	-6.21	100.86	111.11
3	A	1207	CDG	C7-O4-C4	2.18	118.75	114.01
3	D	1207	CDG	C7-O4-C4	2.18	118.77	114.01
3	C	1207	CDG	C7-O4-C4	2.18	118.77	114.01
3	B	1207	CDG	C7-O4-C4	2.18	118.77	114.01
3	C	1207	CDG	C10-O1-C1	2.44	117.10	113.29
3	A	1207	CDG	O1-C1-C2	2.46	111.06	108.14
3	D	1207	CDG	O1-C1-C2	2.47	111.07	108.14
3	B	1207	CDG	O1-C1-C2	2.47	111.08	108.14
3	B	1207	CDG	C10-O1-C1	2.48	117.15	113.29
3	D	1207	CDG	C10-O1-C1	2.48	117.16	113.29
3	A	1207	CDG	C10-O1-C1	2.50	117.19	113.29
3	C	1207	CDG	O1-C1-C2	2.52	111.14	108.14
3	C	1207	CDG	O4-C7-C9	4.31	117.15	107.62
3	D	1207	CDG	O4-C7-C9	4.31	117.15	107.62
3	B	1207	CDG	O4-C7-C9	4.32	117.17	107.62
3	A	1207	CDG	O4-C7-C9	4.34	117.20	107.62
3	B	1207	CDG	C6-O6-C7	6.10	119.27	113.94
3	C	1207	CDG	C6-O6-C7	6.11	119.28	113.94
3	D	1207	CDG	C6-O6-C7	6.12	119.28	113.94
3	A	1207	CDG	C6-O6-C7	6.13	119.29	113.94
3	B	1207	CDG	O6-C7-C9	6.61	114.68	106.25
3	C	1207	CDG	O6-C7-C9	6.62	114.69	106.25
3	A	1207	CDG	O6-C7-C9	6.65	114.72	106.25
3	D	1207	CDG	O6-C7-C9	6.65	114.72	106.25

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

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	204/204 (100%)	0.59	14 (6%) 18 16	5, 14, 30, 53	0
1	B	204/204 (100%)	0.69	18 (8%) 11 9	5, 14, 30, 53	0
1	C	204/204 (100%)	0.64	11 (5%) 26 26	5, 14, 30, 53	0
1	D	204/204 (100%)	0.16	1 (0%) 90 90	5, 14, 30, 53	0
1	E	204/204 (100%)	0.33	9 (4%) 35 33	6, 15, 41, 53	0
All	All	1020/1020 (100%)	0.48	53 (5%) 28 27	5, 15, 33, 53	0

All (53) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	179	PRO	7.6
1	B	175	GLY	5.6
1	C	55	GLN	4.9
1	B	28	LYS	4.8
1	E	204	VAL	4.5
1	B	27	GLU	4.4
1	E	56	GLY	4.1
1	C	57	ARG	4.0
1	C	1	HIS	4.0
1	B	178	LEU	3.9
1	E	140	TYR	3.8
1	B	193	ARG	3.8
1	B	25	PRO	3.7
1	B	26	LEU	3.5
1	B	146	ARG	3.4
1	A	55	GLN	3.2
1	E	27	GLU	3.2
1	C	26	LEU	3.2
1	B	204	VAL	3.2
1	E	55	GLN	2.9

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Mol	Chain	Res	Type	RSRZ
1	C	175	GLY	2.8
1	C	178	LEU	2.8
1	B	1	HIS	2.7
1	E	1	HIS	2.7
1	B	183	LEU	2.7
1	B	179	PRO	2.6
1	A	77	ARG	2.6
1	A	193	ARG	2.6
1	A	28	LYS	2.6
1	B	55	GLN	2.5
1	A	69	GLY	2.5
1	A	204	VAL	2.4
1	B	57	ARG	2.4
1	A	1	HIS	2.4
1	C	183	LEU	2.4
1	C	193	ARG	2.4
1	D	25	PRO	2.4
1	C	130	LYS	2.4
1	B	69	GLY	2.3
1	A	57	ARG	2.3
1	A	179	PRO	2.3
1	B	23	ILE	2.3
1	A	183	LEU	2.2
1	A	124	PHE	2.2
1	E	174	GLN	2.2
1	E	25	PRO	2.2
1	A	175	GLY	2.2
1	A	140	TYR	2.1
1	A	178	LEU	2.1
1	B	140	TYR	2.1
1	E	36	CYS	2.1
1	C	204	VAL	2.0
1	B	186	GLN	2.0

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

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

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 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(Å ²)	Q<0.9
3	CDG	B	1207	18/18	0.86	0.24	3.28	14,37,43,45	5
3	CDG	D	1207	18/18	0.90	0.23	2.92	14,37,43,45	5
3	CDG	A	1207	18/18	0.84	0.22	1.86	14,37,43,45	5
3	CDG	C	1207	18/18	0.88	0.22	1.54	14,37,43,45	5
2	CA	A	1205	1/1	0.96	0.14	-1.17	14,14,14,14	0
2	CA	E	1205	1/1	0.91	0.10	-1.83	33,33,33,33	0
2	CA	D	1206	1/1	0.96	0.05	-2.42	14,14,14,14	0
2	CA	A	1206	1/1	0.97	0.08	-2.50	14,14,14,14	0
2	CA	B	1206	1/1	0.98	0.07	-2.59	14,14,14,14	0
2	CA	B	1205	1/1	0.95	0.09	-3.06	14,14,14,14	0
2	CA	C	1206	1/1	0.97	0.08	-3.51	14,14,14,14	0
2	CA	C	1205	1/1	0.98	0.06	-4.11	14,14,14,14	0
2	CA	D	1205	1/1	0.98	0.06	-5.46	14,14,14,14	0

6.5 Other polymers [i](#)

There are no such residues in this entry.