



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 09:31 AM UTC

PDB ID : 8BSL / pdb_00008bsl
Title : Human GLS in complex with compound 12
Authors : Debreczeni, J.E.
Deposited on : 2022-11-25
Resolution : 2.38 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
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
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

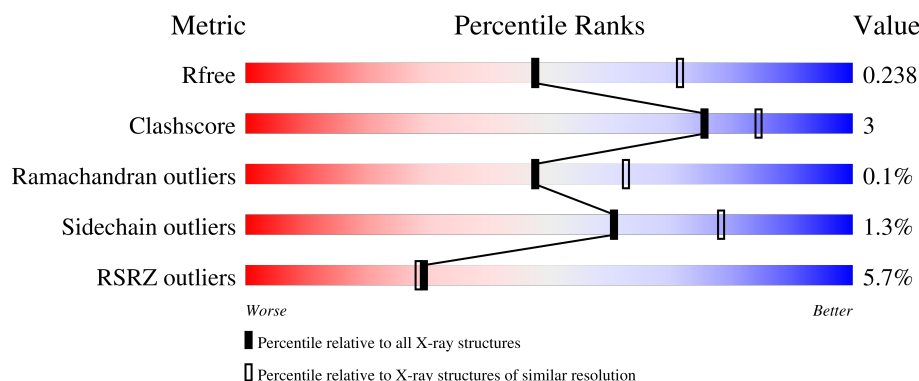
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.38 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	7164 (2.40-2.36)
Clashscore	190562	7722 (2.40-2.36)
Ramachandran outliers	187476	7626 (2.40-2.36)
Sidechain outliers	187428	7627 (2.40-2.36)
RSRZ outliers	180081	7170 (2.40-2.36)

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	478	5% 77% 8% 15%
1	B	478	4% 76% 8% 16%
1	C	478	5% 75% 9% 16%
1	D	478	4% 78% 6% 15%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 13408 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.

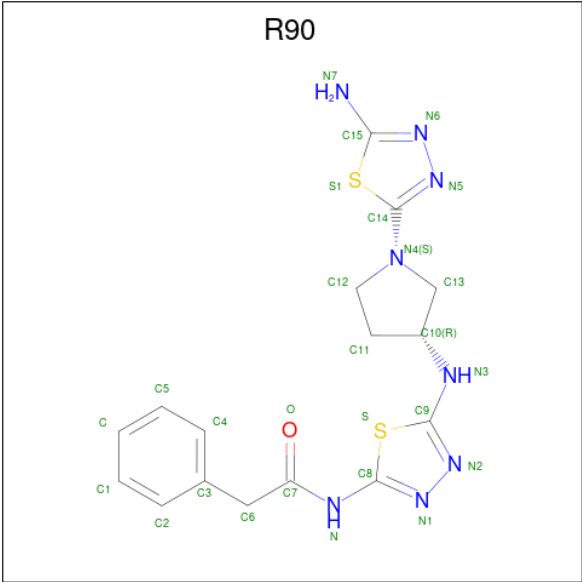
- Molecule 1 is a protein called Glutaminase kidney isoform, mitochondrial.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	408	Total	C	N	O	S	0	0	0
			3167	2017	534	588	28			
1	B	403	Total	C	N	O	S	0	0	0
			3139	2005	526	580	28			
1	C	403	Total	C	N	O	S	0	0	0
			3123	1995	523	577	28			
1	D	405	Total	C	N	O	S	0	0	0
			3154	2009	532	585	28			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	121	GLY	-	expression tag	UNP O94925
A	122	SER	-	expression tag	UNP O94925
B	121	GLY	-	expression tag	UNP O94925
B	122	SER	-	expression tag	UNP O94925
C	121	GLY	-	expression tag	UNP O94925
C	122	SER	-	expression tag	UNP O94925
D	121	GLY	-	expression tag	UNP O94925
D	122	SER	-	expression tag	UNP O94925

- Molecule 2 is {N}-[5-[(3 {R})-1-(5-azanyl-1,3,4-thiadiazol-2-yl)pyrrolidin-3-yl]amino]-1,3,4-thiadiazol-2-yl]-2-phenyl-ethanamide (CCD ID: R90) (formula: C₁₆H₁₈N₈OS₂) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	S	0	0
			27	16	8	1	2		
2	D	1	Total	C	N	O	S	0	0
			27	16	8	1	2		

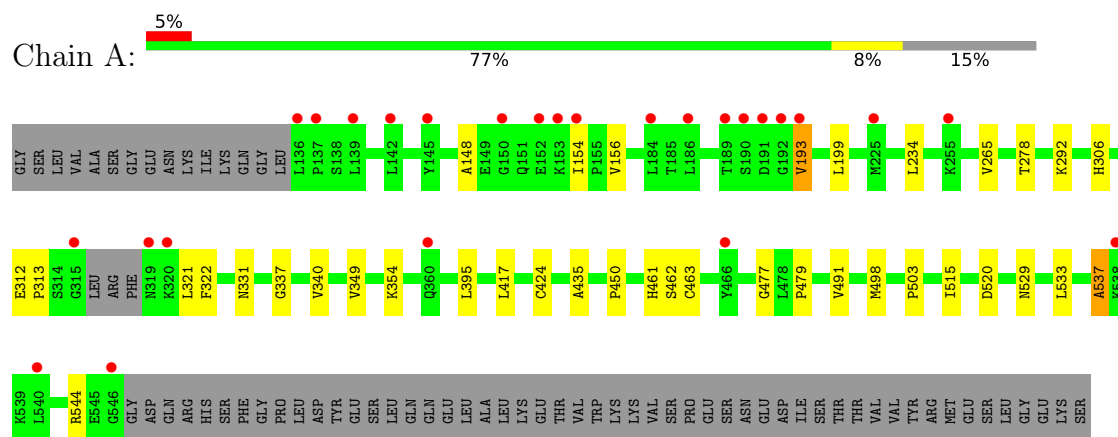
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	176	Total	O	0	0
			176	176		
3	B	216	Total	O	0	0
			216	216		
3	C	156	Total	O	0	0
			156	156		
3	D	223	Total	O	0	0
			223	223		

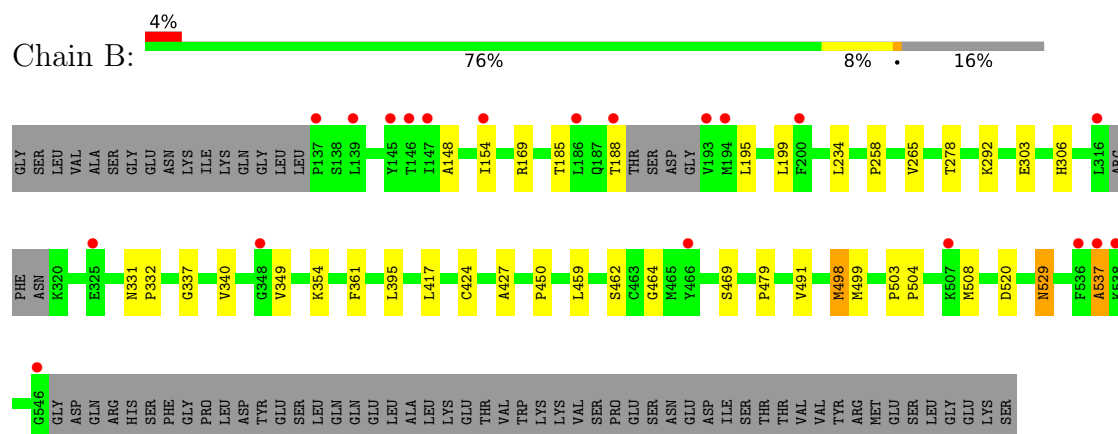
3 Residue-property plots [i](#)

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.

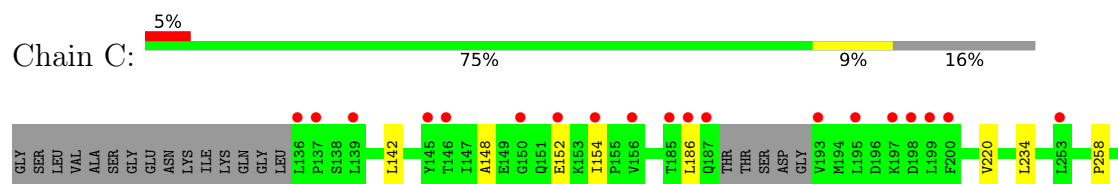
- Molecule 1: Glutaminase kidney isoform, mitochondrial

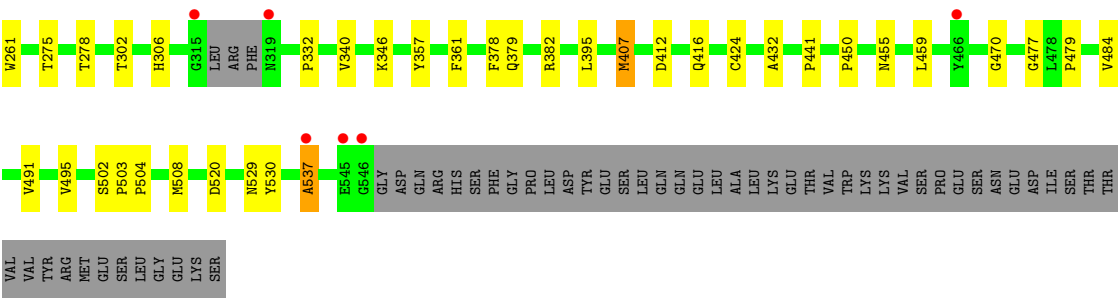


- Molecule 1: Glutaminase kidney isoform, mitochondrial

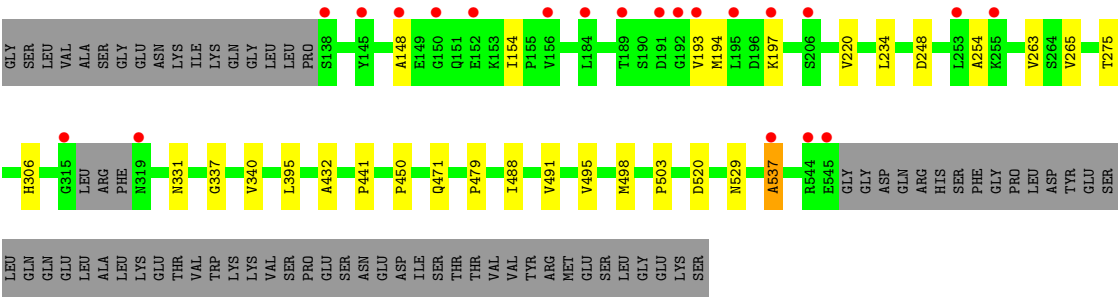
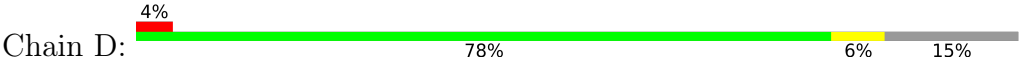


- Molecule 1: Glutaminase kidney isoform, mitochondrial





● Molecule 1: Glutaminase kidney isoform, mitochondrial



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	50.99Å 139.03Å 177.72Å 90.00° 96.01° 90.00°	Depositor
Resolution (Å)	47.64 – 2.38 47.64 – 2.38	Depositor EDS
% Data completeness (in resolution range)	95.5 (47.64-2.38) 95.5 (47.64-2.38)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.63 (at 2.37Å)	Xtriage
Refinement program	BUSTER 2.11.8	Depositor
R, R_{free}	0.209 , 0.246 0.202 , 0.238	Depositor DCC
R_{free} test set	4678 reflections (4.74%)	wwPDB-VP
Wilson B-factor (Å ²)	39.5	Xtriage
Anisotropy	0.476	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 55.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.028 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	13408	wwPDB-VP
Average B, all atoms (Å ²)	46.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.82% 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](#)

Bond lengths and bond angles in the following residue types are not validated in this section: R90

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	0.69	1/3237 (0.0%)	1.09	2/4371 (0.0%)
1	B	0.75	2/3208 (0.1%)	1.09	3/4328 (0.1%)
1	C	0.71	2/3192 (0.1%)	1.09	2/4309 (0.0%)
1	D	0.72	1/3223 (0.0%)	1.10	3/4350 (0.1%)
All	All	0.72	6/12860 (0.0%)	1.09	10/17358 (0.1%)

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	537	ALA	CA-C	9.79	1.61	1.53
1	D	537	ALA	CA-C	8.48	1.61	1.53
1	C	537	ALA	CA-C	6.72	1.61	1.52
1	C	407	MET	SD-CE	6.01	1.94	1.79
1	A	537	ALA	CA-C	5.91	1.60	1.53
1	B	498	MET	SD-CE	-5.50	1.65	1.79

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	464	GLY	N-CA-C	7.38	122.79	114.67
1	A	503	PRO	N-CA-C	6.65	118.81	110.70
1	D	488	ILE	N-CA-CB	5.84	120.86	111.23
1	B	306	HIS	CA-CB-CG	-5.79	108.02	113.80
1	B	503	PRO	N-CA-C	5.71	117.67	110.70
1	C	503	PRO	N-CA-C	5.68	117.63	110.70
1	D	503	PRO	N-CA-C	5.64	117.58	110.70
1	A	306	HIS	CA-CB-CG	-5.53	108.27	113.80
1	D	306	HIS	CA-CB-CG	-5.05	108.75	113.80
1	C	306	HIS	CA-CB-CG	-5.04	108.75	113.80

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	3167	0	3130	23	0
1	B	3139	0	3118	21	0
1	C	3123	0	3088	24	0
1	D	3154	0	3127	16	0
2	A	27	0	0	2	0
2	D	27	0	0	0	0
3	A	176	0	0	0	0
3	B	216	0	0	0	0
3	C	156	0	0	0	0
3	D	223	0	0	0	0
All	All	13408	0	12463	76	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 (76) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:533:LEU:O	1:A:544:ARG:NH2	1.98	0.97
1:B:234:LEU:HD22	1:B:520:ASP:HB3	1.59	0.84
1:B:265:VAL:HG22	1:B:498:MET:HE3	1.61	0.82
1:A:234:LEU:HD22	1:A:520:ASP:HB3	1.63	0.80
1:D:234:LEU:HD22	1:D:520:ASP:HB3	1.71	0.72
1:A:537:ALA:HB2	1:C:450:PRO:HG2	1.72	0.71
1:B:537:ALA:HB2	1:D:450:PRO:HG2	1.71	0.71
1:B:450:PRO:HG2	1:D:537:ALA:HB2	1.73	0.71
1:C:234:LEU:HD22	1:C:520:ASP:HB3	1.75	0.69
1:A:278:THR:HA	1:A:424:CYS:HB2	1.80	0.62
1:A:450:PRO:HG2	1:C:537:ALA:HB2	1.81	0.62
1:B:340:VAL:HG23	1:B:395:LEU:HD13	1.83	0.60
1:A:193:VAL:HG12	1:A:193:VAL:O	2.02	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:302:THR:OG1	1:C:455:ASN:ND2	2.32	0.58
1:A:156:VAL:HG12	1:A:193:VAL:HG13	1.86	0.57
1:A:477:GLY:O	1:A:529:ASN:HB2	2.05	0.57
1:A:340:VAL:HG23	1:A:395:LEU:HD13	1.87	0.56
1:B:479:PRO:HD2	1:B:491:VAL:O	2.08	0.54
1:A:322:PHE:N	2:A:601:R90:N5	2.54	0.53
1:C:379:GLN:HA	1:C:382:ARG:HD3	1.89	0.53
1:D:432:ALA:HB1	1:D:441:PRO:HG2	1.90	0.53
1:B:427:ALA:HB3	1:B:499:MET:HG2	1.91	0.53
1:C:378:PHE:CZ	1:C:382:ARG:HD2	2.45	0.51
1:D:265:VAL:HG22	1:D:498:MET:HE3	1.91	0.51
1:B:349:VAL:O	1:B:354:LYS:HE3	2.11	0.51
1:A:312:GLU:HG2	1:C:470:GLY:HA3	1.94	0.50
1:C:432:ALA:HB1	1:C:441:PRO:HG3	1.94	0.50
1:A:148:ALA:HA	1:A:154:ILE:HG12	1.95	0.48
1:B:148:ALA:HA	1:B:154:ILE:HG12	1.95	0.47
1:B:278:THR:HA	1:B:424:CYS:HB2	1.96	0.47
1:B:265:VAL:CG2	1:B:498:MET:HE3	2.40	0.47
1:C:261:TRP:CE3	1:C:502:SER:HB2	2.49	0.47
1:D:340:VAL:HG23	1:D:395:LEU:HD13	1.96	0.47
1:C:340:VAL:HG23	1:C:395:LEU:HD13	1.97	0.47
1:C:382:ARG:NH2	1:C:412:ASP:OD1	2.48	0.47
1:A:321:LEU:HB3	2:A:601:R90:N6	2.31	0.46
1:A:292:LYS:HD3	1:A:417:LEU:HD13	1.98	0.46
1:B:292:LYS:HD3	1:B:417:LEU:HD13	1.98	0.46
1:C:479:PRO:HD2	1:C:491:VAL:O	2.16	0.45
1:B:529:ASN:ND2	1:D:529:ASN:HD21	2.14	0.45
1:D:479:PRO:HD2	1:D:491:VAL:O	2.16	0.45
1:B:332:PRO:CD	1:B:459:LEU:HD13	2.46	0.45
1:D:148:ALA:HA	1:D:154:ILE:HG12	1.99	0.45
1:C:220:VAL:HG21	1:C:495:VAL:HA	1.97	0.45
1:A:313:PRO:HG3	1:A:462:SER:HB2	1.97	0.45
1:D:193:VAL:HG23	1:D:194:MET:HE2	1.97	0.45
1:D:432:ALA:CB	1:D:441:PRO:HG2	2.47	0.44
1:B:258:PRO:HB3	1:B:504:PRO:HG3	1.99	0.44
1:B:185:THR:O	1:B:188:THR:OG1	2.36	0.44
1:A:349:VAL:O	1:A:354:LYS:HE3	2.17	0.44
1:C:407:MET:HE3	1:C:407:MET:HB3	1.78	0.43
1:C:477:GLY:O	1:C:529:ASN:HB2	2.19	0.43
1:D:248:ASP:HA	1:D:254:ALA:HB2	2.00	0.43
1:A:435:ALA:HB2	1:A:491:VAL:HG13	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:148:ALA:HA	1:C:154:ILE:HG12	2.00	0.43
1:B:462:SER:O	1:B:469:SER:HB3	2.19	0.43
1:C:378:PHE:CE1	1:C:416:GLN:HG3	2.54	0.43
1:A:479:PRO:HG3	1:C:530:TYR:CE1	2.54	0.43
1:D:220:VAL:HG21	1:D:495:VAL:HA	2.01	0.43
1:B:265:VAL:HG22	1:B:498:MET:CE	2.43	0.42
1:C:278:THR:HA	1:C:424:CYS:HB2	2.02	0.42
1:A:265:VAL:HG22	1:A:498:MET:HE3	2.01	0.42
1:C:332:PRO:HD2	1:C:459:LEU:HD13	2.01	0.42
1:D:265:VAL:CG2	1:D:498:MET:HE3	2.49	0.42
1:A:461:HIS:CE1	1:A:529:ASN:HD22	2.37	0.42
1:C:258:PRO:HB3	1:C:504:PRO:HG3	2.00	0.42
1:C:432:ALA:CB	1:C:441:PRO:HG3	2.50	0.42
1:A:331:ASN:O	1:A:337:GLY:HA3	2.20	0.41
1:B:195:LEU:HD23	1:B:199:LEU:HD23	2.01	0.41
1:D:331:ASN:O	1:D:337:GLY:HA3	2.20	0.41
1:A:515:ILE:HD13	1:A:515:ILE:HA	1.97	0.41
1:B:331:ASN:O	1:B:337:GLY:HA3	2.21	0.41
1:C:332:PRO:CD	1:C:459:LEU:HD13	2.51	0.41
1:A:479:PRO:HD2	1:A:491:VAL:O	2.21	0.41
1:B:529:ASN:HD21	1:D:529:ASN:HD21	1.69	0.40
1:C:346:LYS:HG3	1:C:357:TYR:CD2	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	404/478 (84%)	393 (97%)	10 (2%)	1 (0%)	43	56
1	B	397/478 (83%)	391 (98%)	6 (2%)	0	100	100
1	C	397/478 (83%)	388 (98%)	9 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	D	401/478 (84%)	391 (98%)	10 (2%)	0	100	100
All	All	1599/1912 (84%)	1563 (98%)	35 (2%)	1 (0%)	48	62

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	193	VAL

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	350/415 (84%)	348 (99%)	2 (1%)	78	88
1	B	348/415 (84%)	343 (99%)	5 (1%)	59	77
1	C	345/415 (83%)	338 (98%)	7 (2%)	48	68
1	D	350/415 (84%)	346 (99%)	4 (1%)	65	81
All	All	1393/1660 (84%)	1375 (99%)	18 (1%)	61	78

All (18) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	199	LEU
1	A	463	CYS
1	B	169	ARG
1	B	303	GLU
1	B	361	PHE
1	B	508	MET
1	B	529	ASN
1	C	142	LEU
1	C	152	GLU
1	C	186	LEU
1	C	275	THR
1	C	361	PHE
1	C	484	VAL

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Mol	Chain	Res	Type
1	C	508	MET
1	D	197	LYS
1	D	263	VAL
1	D	275	THR
1	D	471	GLN

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	416	GLN
1	A	461	HIS
1	A	516	HIS
1	B	516	HIS
1	B	535	HIS
1	C	157	HIS
1	C	271	GLN
1	C	330	HIS
1	C	335	ASN
1	D	330	HIS
1	D	335	ASN
1	D	388	ASN
1	D	416	GLN
1	D	529	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 oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

2 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	R90	D	601	-	30,30,30	0.61	1 (3%)	36,41,41	0.93	2 (5%)
2	R90	A	601	-	30,30,30	0.59	0	36,41,41	0.98	2 (5%)

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	R90	D	601	-	-	0/16/25/25	0/4/4/4
2	R90	A	601	-	-	0/16/25/25	0/4/4/4

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	601	R90	C13-C10	2.51	1.57	1.53

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	601	R90	N4-C14-N5	3.12	122.94	116.91
2	A	601	R90	N4-C14-N5	3.09	122.88	116.91
2	A	601	R90	C12-N4-C13	-2.35	109.63	112.38
2	D	601	R90	C12-N4-C13	-2.33	109.66	112.38

There are no chirality outliers.

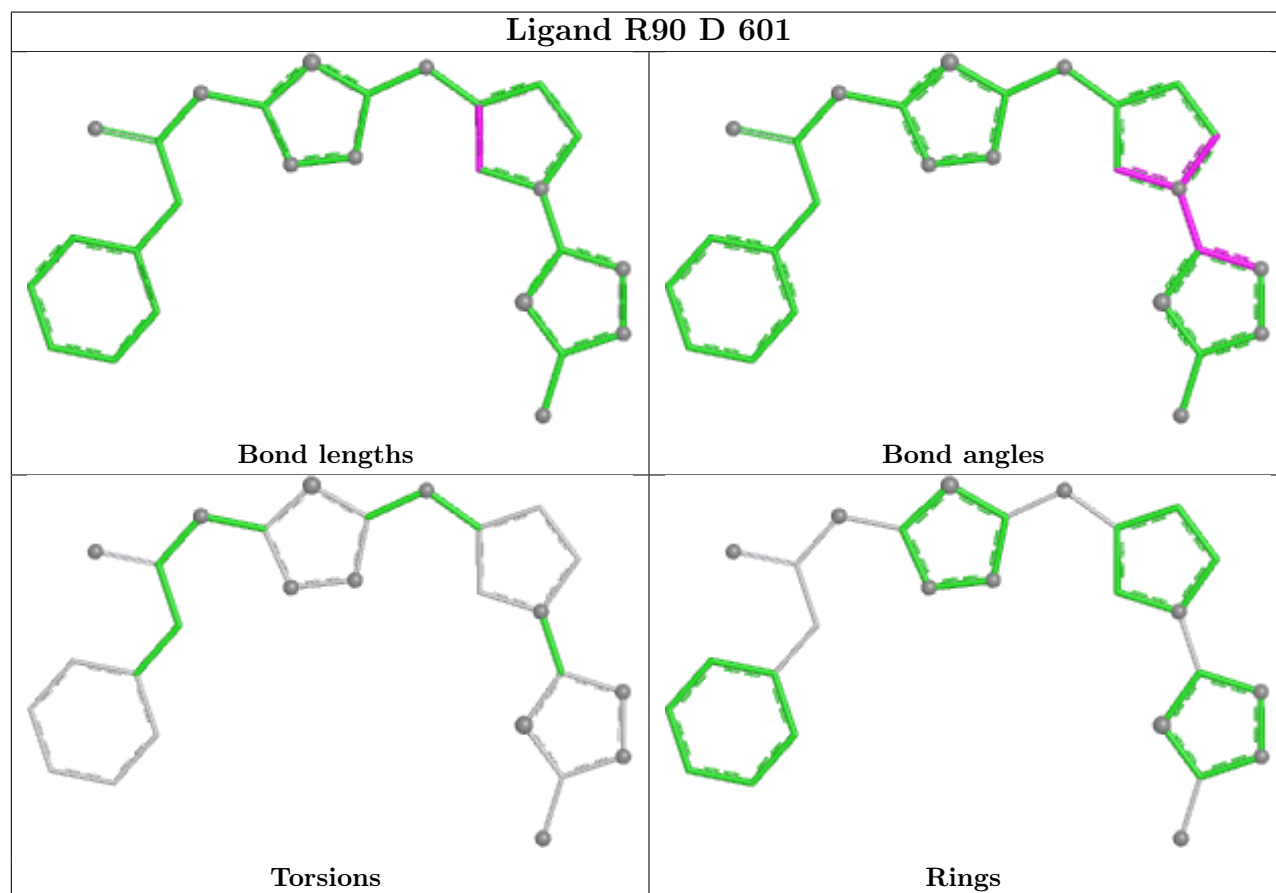
There are no torsion outliers.

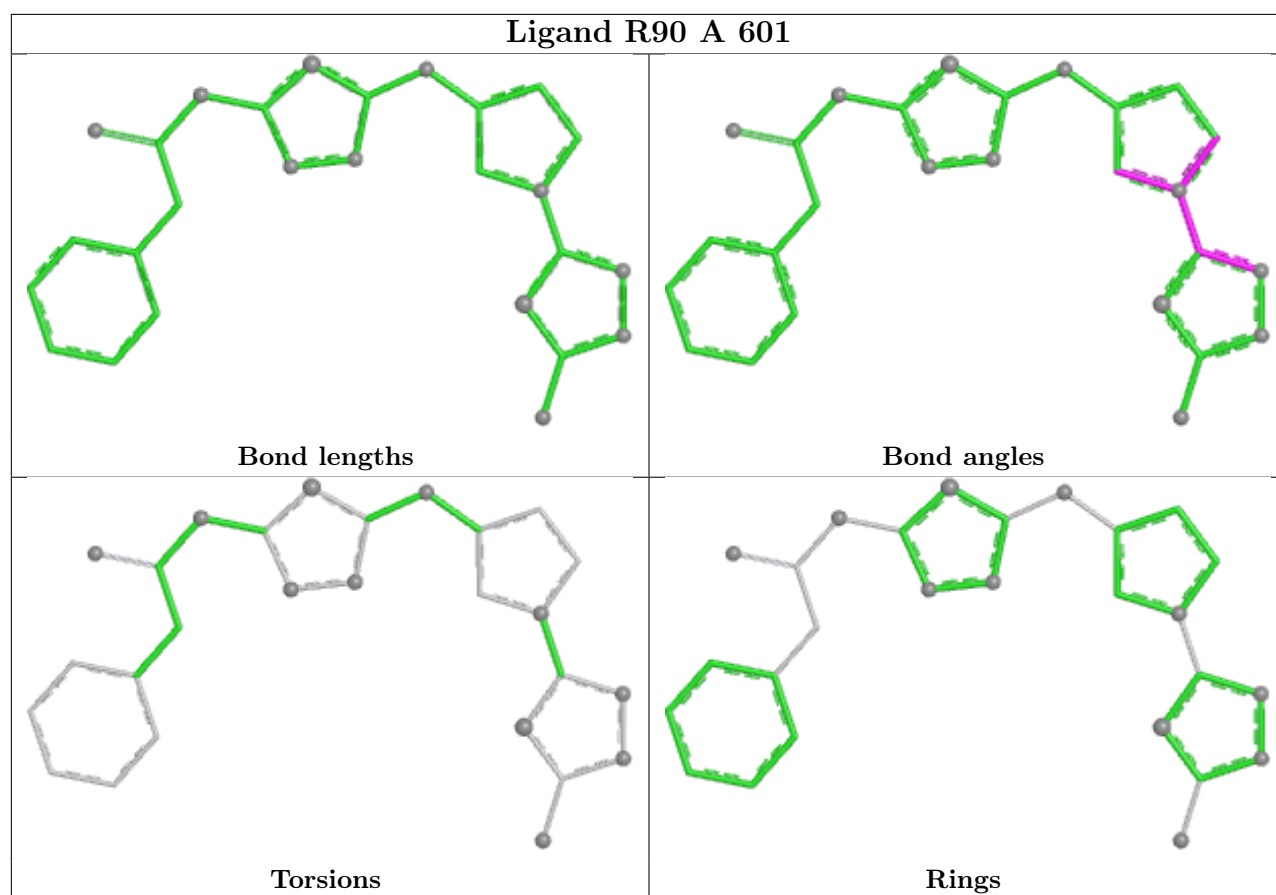
There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	601	R90	2	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





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	408/478 (85%)	0.45	26 (6%) 25 24	31, 45, 81, 98	0
1	B	403/478 (84%)	0.26	20 (4%) 34 34	26, 37, 72, 88	0
1	C	403/478 (84%)	0.48	25 (6%) 26 25	31, 44, 85, 103	0
1	D	405/478 (84%)	0.33	21 (5%) 33 32	27, 40, 76, 95	0
All	All	1619/1912 (84%)	0.38	92 (5%) 29 28	26, 42, 79, 103	0

All (92) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	193	VAL	5.4
1	C	136	LEU	5.4
1	C	187	GLN	5.3
1	A	191	ASP	4.5
1	B	137	PRO	4.5
1	C	193	VAL	4.4
1	A	546	GLY	4.2
1	C	319	ASN	4.2
1	B	188	THR	4.0
1	A	192	GLY	3.9
1	A	136	LEU	3.8
1	A	139	LEU	3.7
1	A	137	PRO	3.6
1	C	546	GLY	3.5
1	C	137	PRO	3.5
1	B	536	PHE	3.4
1	C	186	LEU	3.3
1	C	152	GLU	3.3
1	D	192	GLY	3.3
1	A	193	VAL	3.2
1	D	193	VAL	3.2

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Mol	Chain	Res	Type	RSRZ
1	B	186	LEU	3.2
1	C	139	LEU	3.2
1	C	195	LEU	3.2
1	D	319	ASN	3.1
1	C	466	TYR	3.1
1	A	145	TYR	3.0
1	A	190	SER	3.0
1	A	189	THR	3.0
1	D	191	ASP	3.0
1	A	255	LYS	2.9
1	B	546	GLY	2.9
1	A	540	LEU	2.9
1	D	148	ALA	2.8
1	A	154	ILE	2.7
1	A	319	ASN	2.7
1	D	195	LEU	2.7
1	B	154	ILE	2.7
1	A	538	LYS	2.7
1	C	145	TYR	2.6
1	D	145	TYR	2.6
1	D	255	LYS	2.6
1	C	154	ILE	2.6
1	C	545	GLU	2.6
1	D	152	GLU	2.6
1	D	189	THR	2.5
1	A	320	LYS	2.5
1	B	139	LEU	2.5
1	D	206	SER	2.4
1	C	199	LEU	2.4
1	D	150	GLY	2.4
1	B	194	MET	2.4
1	D	253	LEU	2.4
1	D	545	GLU	2.4
1	B	537	ALA	2.4
1	D	315	GLY	2.4
1	A	153	LYS	2.4
1	B	200	PHE	2.4
1	C	200	PHE	2.4
1	B	316	LEU	2.4
1	A	315	GLY	2.4
1	D	156	VAL	2.4
1	D	544	ARG	2.4

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Mol	Chain	Res	Type	RSRZ
1	B	145	TYR	2.3
1	C	185	THR	2.3
1	A	142	LEU	2.3
1	B	466	TYR	2.3
1	D	197	LYS	2.3
1	B	348	GLY	2.3
1	B	538	LYS	2.3
1	C	198	ASP	2.2
1	A	150	GLY	2.2
1	A	466	TYR	2.2
1	D	537	ALA	2.2
1	C	315	GLY	2.2
1	A	186	LEU	2.2
1	B	325	GLU	2.2
1	A	225	MET	2.2
1	A	184	LEU	2.1
1	C	253	LEU	2.1
1	C	156	VAL	2.1
1	C	150	GLY	2.1
1	C	537	ALA	2.1
1	B	147	ILE	2.1
1	C	146	THR	2.1
1	D	138	SER	2.1
1	A	152	GLU	2.1
1	C	197	LYS	2.0
1	B	507	LYS	2.0
1	B	146	THR	2.0
1	A	360	GLN	2.0
1	D	184	LEU	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 ⓘ

There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

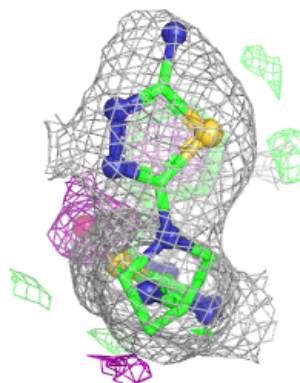
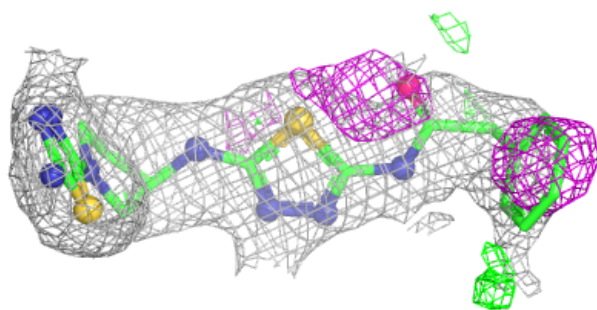
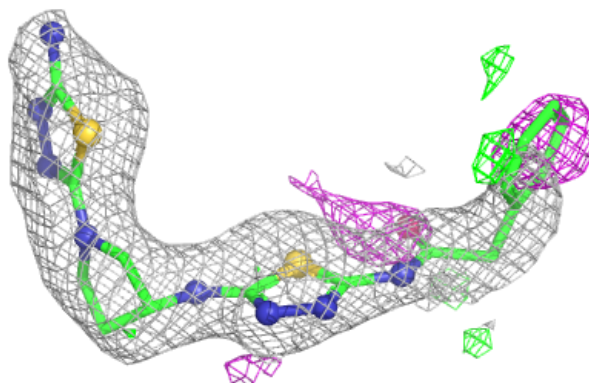
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q<0.9' lists 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	R90	A	601	27/27	0.89	0.15	58,59,67,67	0
2	R90	D	601	27/27	0.91	0.13	53,58,67,67	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

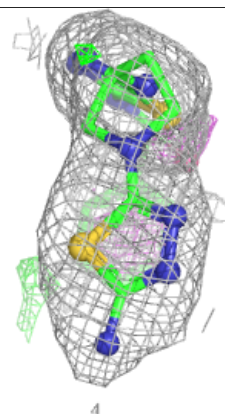
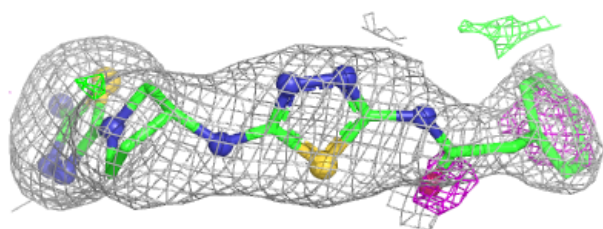
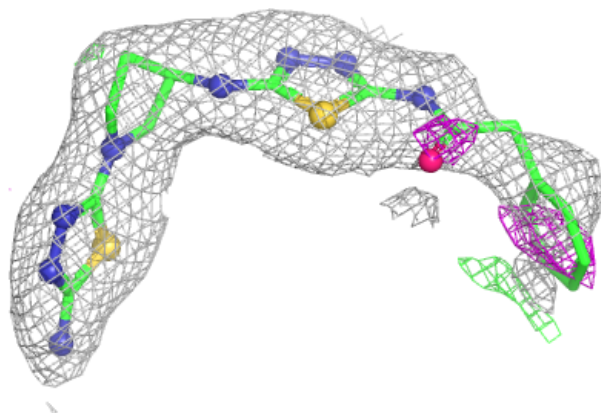
Electron density around R90 A 601:

2mF_o-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around R90 D 601:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers ⓘ

There are no such residues in this entry.